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Seq. ID zvd700460606.h1

Seq. No. 385029
Seq. ID zvd700460616.h1

Seq. No. 385030
Seq. ID zvd700460650.h1

Seq. No. 385031
Seq. ID zvd700460655.h1

Seq. No. 385032
Seq. ID zvd700460656.h1

Seq. No. 385033
Seq. ID zvd700460664.h1

Seq. No. 385034
Seq. ID zvd700460674.h1

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Seq. No. 385035
Contig ID 0_1.R1084
5'-most EST uC-osflcyp024a06b1
Method BLASTX
NCBI GI g1345809
BLAST score 1954
E value 0.0e+00
Match length 376
% identity 100
NCBI Description CHALCONE SYNTHASE (NAREGENIN-CHALCONE SYNTHASE) >gi_2117713_pir__S58190 naringenin-chalcone synthase (EC 2.3.1.74) - rice >gi_927491_emb_CAA61955_ (X89859) naringenin-chalcone synthase [Oryza sativa]

Seq. No. 385036
Contig ID 0_2.R1084
5'-most EST g571870
Method BLASTX
NCBI GI g1816444
BLAST score 1953

E value	0.0e+00
Match length	376
% identity	100
NCBI Description	(AB000801) chalcone synthase [Oryza sativa]

Seq. No.	385037
Contig ID	1_1.R1084
5'-most EST	g2427201
Method	BLASTX
NCBI GI	g3618308
BLAST score	1626
E value	0.0e+00
Match length	403
% identity	78
NCBI Description	(AB001882) zinc finger protein [Oryza sati

Seq. No.	385038
Contig ID	2_1.R1084
5'-most EST	LIB3431-016-P1-K1-D7
Method	BLASTX
NCBI GI	g3618310
BLAST score	999
E value	1.0e-108
Match length	257
% identity	76
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	385039
Contig ID	2_2.R1084
5'-most EST	g3618313
Method	BLASTX
NCBI GI	g3618314
BLAST score	1089
E value	1.0e-119
Match length	240
% identity	86
NCBI Description	(AB001885) zinc finger protein [Oryza sativa]

Seq. No.	385040
Contig ID	2_3.R1084
5'-most EST	LIB3432-060-P1-K1-D5
Method	BLASTX
NCBI GI	g3618310
BLAST score	599
E value	7.0e-62
Match length	188
% identity	64
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	385041
Contig ID	2_4.R1084
5'-most EST	LIB3432-022-P1-K1-F8
Method	BLASTX
NCBI GI	g3618310
BLAST score	337
E value	2.0e-31
Match length	114

% identity	61
NCBI Description	(AB001883) zinc finger protein [Oryza sativa]

Seq. No.	385042
Contig ID	3_1.R1084
5'-most EST	uC-osroM202014c04b1
Method	BLASTX
NCBI GI	g3618312
BLAST score	1062
E value	1.0e-116
Match length	308
% identity	66
NCBI Description	(AB001884) zinc finger protein [Oryza sativa]

Seq. No.	385043
Contig ID	5_1.R1084
5'-most EST	g3618315
Method	BLASTX
NCBI GI	g3618316
BLAST score	1732
E value	0.0e+00
Match length	360
% identity	91
NCBI Description	(AB001886) zinc finger protein [Oryza sativa]

Seq. No.	385044
Contig ID	6_1.R1084
5'-most EST	g3618317
Method	BLASTX
NCBI GI	g3618318
BLAST score	1298
E value	1.0e-143
Match length	335
% identity	77
NCBI Description	(AB001887) zinc finger protein [Oryza sativa]

Seq. No.	385045
Contig ID	7_1.R1084
5'-most EST	g572029
Method	BLASTX
NCBI GI	g3618320
BLAST score	1856
E value	0.0e+00
Match length	407
% identity	86
NCBI Description	(AB001888) zinc finger protein [Oryza sativa]

Seq. No.	385046
Contig ID	9_1.R1084
5'-most EST	LIB3431-012-P1-K1-C7
Method	BLASTN
NCBI GI	g1944204
BLAST score	494
E value	0.0e+00
Match length	498
% identity	100
NCBI Description	Oryza sativa mRNA for RicMT, complete cds

Seq. No.	385047
Contig ID	10_1.R1084
5'-most EST	g1631507
Method	BLASTX
NCBI GI	g2055262
BLAST score	1248
E value	1.0e-138
Match length	229
% identity	100
NCBI Description	(AB003194) chitinase IIb [Oryza sativa]

Seq. No.	385048
Contig ID	11_1.R1084
5'-most EST	g572424
Method	BLASTX
NCBI GI	g2696227
BLAST score	1419
E value	1.0e-158
Match length	305
% identity	88
NCBI Description	(D55711) chitinase [Oryza sativa]

Seq. No.	385049
Contig ID	12_1.R1084
5'-most EST	g5295977
Method	BLASTX
NCBI GI	g5295978
BLAST score	962
E value	1.0e-104
Match length	211
% identity	92
NCBI Description	(AB003322) MADS box-like protein [Oryza sativa]

Seq. No.	385050
Contig ID	13_1.R1084
5'-most EST	LIB3479-010-Q6-K1-G2
Method	BLASTX
NCBI GI	g4406132
BLAST score	1063
E value	1.0e-116
Match length	223
% identity	92
NCBI Description	(AF077760) MADS box protein [Oryza sativa]

Seq. No.	385051
Contig ID	14_1.R1084
5'-most EST	g5295983
Method	BLASTX
NCBI GI	g5295984
BLAST score	975
E value	1.0e-105
Match length	263
% identity	75
NCBI Description	(AB003325) MADS box-like protein [Oryza sativa]

Seq. No.	385052

Contig ID	15_1.R1084
5'-most EST	g5295985
Method	BLASTX
NCBI GI	g5295986
BLAST score	1126
E value	1.0e-123
Match length	222
% identity	100
NCBI Description	(AB003326) MADS box-like protein [Oryza sativa]

Seq. No.	385053
Contig ID	16_1.R1084
5'-most EST	g3061187
Method	BLASTX
NCBI GI	g5295988
BLAST score	708
E value	2.0e-74
Match length	158
% identity	91
NCBI Description	(AB003327) MADS box-like protein [Oryza sativa]

Seq. No.	385054
Contig ID	17_1.R1084
5'-most EST	g5295989
Method	BLASTX
NCBI GI	g5295990
BLAST score	1153
E value	1.0e-126
Match length	230
% identity	100
NCBI Description	(AB003328) MADS box-like protein [Oryza sativa]

Seq. No.	385055
Contig ID	19_1.R1084
5'-most EST	g1743364
Method	BLASTX
NCBI GI	g4062936
BLAST score	1809
E value	0.0e+00
Match length	372
% identity	94
NCBI Description	(AB003495) dihydroflavonol 4-reductase [Oryza sativa] >gi_4062938_dbj_BAA36183_ (AB003496) dihydroflavonol 4-reductase [Oryza sativa]

Seq. No.	385056
Contig ID	21_1.R1084
5'-most EST	g5002877
Method	BLASTX
NCBI GI	g3273243
BLAST score	2430
E value	0.0e+00
Match length	509
% identity	94
NCBI Description	(AB004660) NLS receptor [Oryza sativa] >gi_3273245_dbj_BAA31166_ (AB004814) NLS receptor [Oryza sativa]

Seq. No.	385057
Contig ID	22_1.R1084
5'-most EST	g2208904
Method	BLASTX
NCBI GI	g2208905
BLAST score	1924
E value	0.0e+00
Match length	376
% identity	95
NCBI Description	(AB004799) ascorbate ox[illegible] [Oryza sativa]

Seq. No.	385058
Contig ID	23_1.R1084
5'-most EST	g5607356
Method	BLASTX
NCBI GI	g3218544
BLAST score	1493
E value	1.0e-166
Match length	332
% identity	85
NCBI Description	(AB004813) alternative oxidase [Oryza sativa] >gi_3218546_dbj_BAA28773_ (AB004864) alternative oxidase [Oryza sativa]

Seq. No.	385059
Contig ID	23_2.R1084
5'-most EST	LIB3475-003-P1-K2-E4
Method	BLASTX
NCBI GI	g3218543
BLAST score	1666
E value	0.0e+00
Match length	335
% identity	95
NCBI Description	(AB004813) alternative oxidase [Oryza sativa] >gi_3218548_dbj_BAA28774_ (AB004865) alternative oxidase [Oryza sativa]

Seq. No.	385060
Contig ID	23_4.R1084
5'-most EST	g2311951
Method	BLASTN
NCBI GI	g3218545
BLAST score	137
E value	6.0e-71
Match length	328
% identity	95
NCBI Description	Oryza sativa AOX1a mRNA for alternative oxidase, complete cds

Seq. No.	385061
Contig ID	25_1.R1084
5'-most EST	g2780745
Method	BLASTX
NCBI GI	g2780746
BLAST score	2147
E value	0.0e+00

Match length	519
% identity	84
NCBI Description	(AB005290) plastid RNA polymerase sigma factor [Oryza sativa]

Seq. No.	385062
Contig ID	27_1.R1084
5'-most EST	g4826581
Method	BLASTX
NCBI GI	g2696231
BLAST score	1425
E value	1.0e-158
Match length	301
% identity	90
NCBI Description	(D55713) chitinase [Oryza sativa] >gi_4826582_dbj_BAA21743.2_ (AB006188) acidic class III chitinase OsChib3a [Oryza sativa] >gi_4827249_dbj_BAA77605.1_ (AB026998) acidic class III chitinase OsChib3a [Oryza sativa]

Seq. No.	385063
Contig ID	28_1.R1084
5'-most EST	uC-osflm202110c01b1
Method	BLASTX
NCBI GI	g3913808
BLAST score	2421
E value	0.0e+00
Match length	494
% identity	95
NCBI Description	FERROCHELATASE PRECURSOR (PROTOHEME FERRO-LYASE) (HEME SYNTHETASE) >gi_2429618_dbj_BAA22284_ (AB007120) ferrochelatase [Oryza sativa]

Seq. No.	385064
Contig ID	29_1.R1084
5'-most EST	LIB3479-004-Q6-K1-H8
Method	BLASTX
NCBI GI	g3913640
BLAST score	1758
E value	0.0e+00
Match length	339
% identity	100
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041775_dbj_BAA25422_ (AB007193) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	385065
Contig ID	29_2.R1084
5'-most EST	LIB3432-053-P1-K1-H10
Method	BLASTX
NCBI GI	g3913640
BLAST score	292
E value	2.0e-35
Match length	82
% identity	92
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CYTOSOLIC

(D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)
>gi_3041775_dbj_BAA25422_ (AB007193)
fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	385066
Contig ID	30_1.R1084
5'-most EST	LIB3432-059-P1-K1-E3
Method	BLASTX
NCBI GI	g3913641
BLAST score	1869
E value	0.0e+00
Match length	382
% identity	95
NCBI Description	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) >gi_3041777_dbj_BAA25423_ (AB007194) fructose-1,6-bisphosphatase [Oryza sativa]

Seq. No.	385067
Contig ID	31_1.R1084
5'-most EST	g2428328
Method	BLASTX
NCBI GI	g4730884
BLAST score	2300
E value	0.0e+00
Match length	475
% identity	94
NCBI Description	(AB007404) alanine aminotransferase [Oryza sativa] >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine aminotransferase [Oryza sativa]

Seq. No.	385068
Contig ID	31_2.R1084
5'-most EST	g2800423
Method	BLASTX
NCBI GI	g4730884
BLAST score	364
E value	2.0e-34
Match length	127
% identity	70
NCBI Description	(AB007404) alanine aminotransferase [Oryza sativa] >gi_4730886_dbj_BAA77261.1_ (AB007405) alanine aminotransferase [Oryza sativa]

Seq. No.	385069
Contig ID	33_1.R1084
5'-most EST	g2463564
Method	BLASTX
NCBI GI	g2463565
BLAST score	1999
E value	0.0e+00
Match length	383
% identity	100
NCBI Description	(AB007501) squalene synthase [Oryza sativa]

Seq. No.	385070
Contig ID	34_1.R1084

5'-most EST	g4887607
Method	BLASTX
NCBI GI	g3327240
BLAST score	1187
E value	1.0e-130
Match length	374
% identity	68
NCBI Description	(AB016071) homeobox gene [Oryza sativa]

Seq. No.	385071
Contig ID	34_2.R1084
5'-most EST	g2935572
Method	BLASTX
NCBI GI	g2935573
BLAST score	1161
E value	1.0e-127
Match length	311
% identity	73
NCBI Description	(AF050180) KNOX class homeodomain protein [Oryza sativa] >gi_4887610_dbj_BAA77818.1_ (AB007624) homeobox gene [Oryza sativa] >gi_5103729_dbj_BAA79226.1_ (AB028885) knotted1-type homeobox protein OSH71 [Oryza sativa]

Seq. No.	385072
Contig ID	34_3.R1084
5'-most EST	g5103724
Method	BLASTX
NCBI GI	g5103725
BLAST score	1217
E value	1.0e-134
Match length	301
% identity	79
NCBI Description	(AB028883) knotted1-type homeobox protein OSH6 [Oryza sativa]

Seq. No.	385073
Contig ID	36_1.R1084
5'-most EST	g5103722
Method	BLASTX
NCBI GI	g5103723
BLAST score	1079
E value	1.0e-118
Match length	344
% identity	63
NCBI Description	(AB028882) knotted1-type homeobox protein OSH3 [Oryza sativa]

Seq. No.	385074
Contig ID	38_1.R1084
5'-most EST	g2312070
Method	BLASTX
NCBI GI	g4887618
BLAST score	946
E value	1.0e-102
Match length	192
% identity	93
NCBI Description	(AB007628) homeobox gene [Oryza sativa]

Seq. No.	385075
Contig ID	39_1.R1084
5'-most EST	g4887617
Method	BLASTX
NCBI GI	g4887618
BLAST score	1012
E value	1.0e-110
Match length	205
% identity	94
NCBI Description	(AB007628) eobox gene [Oryza sativa]

Seq. No.	38
Contig ID	084
5'-most EST	3432-053-P1-K. H12
Method	BLASTX
NCBI GI	g4887618
BLAST score	688
E value	2.0e-72
Match length	128
% identity	
NCBI Descrip	

Seq.	385077
Con	39_3.R1084
5'-mo.	LIB3432-036-P2-K1-C2
Method	BLA
NCBI GI	
BLAST score	
E valu	
Match	
% id	98
NCBI Descr ption	Oryza sativa HOS59 mRNA, partial cds

Seq. No.	385078
Contig ID	40_1.R1084
5'-most EST	g4887619
Method	BLASTX
NCBI GI	g4887620
BLAST score	960
E value	1.0e-104
Match length	196
% identity	93
NCBI Description	(AB007629) homeobox gene [Oryza sativa]

Seq. No.	385079
Contig ID	41_1.R1084
5'-most EST	g3641660
Method	BLASTX
NCBI GI	g3641661
BLAST score	2594
E value	0.0e+00
Match length	533
% identity	94
NCBI Description	(AB008519) high affinity nitrate transporter [Oryza sativa]

Seq. No.	385080

Contig ID	42_1.R1084
5'-most EST	g2428095
Method	BLASTX
NCBI GI	g4008156
BLAST score	10387
E value	0.0e+00
Match length	2158
% identity	93
NCBI Description	(AB008845) NADH dependent Glutamate Synthase [Oryza sativa]

Seq. No.	385081
Contig ID	43_1.R1084
5'-most EST	uC-osflcyp022b06b1
Method	BLASTX
NCBI GI	g2894534
BLAST score	1438
E value	1.0e-160
Match length	286
% identity	97
NCBI Description	(AJ224327) aquaporin [Oryza sativa]

Seq. No.	385082
Contig ID	43_2.R1084
5'-most EST	g2798686
Method	BLASTX
NCBI GI	g1632822
BLAST score	1545
E value	1.0e-172
Match length	291
% identity	99
NCBI Description	(Y08962) transmembrane protein [Oryza sativa] >gi_1667594 (U77297) transmembrane protein [Oryza sativa]

Seq. No.	385083
Contig ID	43_3.R1084
5'-most EST	LIB3475-007-P1-K1-F5
Method	BLASTX
NCBI GI	g4768911
BLAST score	860
E value	2.0e-92
Match length	174
% identity	94
NCBI Description	(AF131201) plasma membrane MIP protein [Zea mays]

Seq. No.	385084
Contig ID	44_1.R1084
5'-most EST	uC-osflcyp176a12b1
Method	BLASTX
NCBI GI	g3550985
BLAST score	1277
E value	1.0e-141
Match length	385
% identity	69
NCBI Description	(AB010740) OsS5a [Oryza sativa]

Seq. No.	385085
Contig ID	44_2.R1084

5'-most EST	LIB3477-001-P1-K1-F2
Method	BLASTX
NCBI GI	g3337091
BLAST score	644
E value	7.0e-67
Match length	300
% identity	46
NCBI Description	(AB016204) polygalacturonase inhibitor (PGIP) [Citrus unshiu]

Seq. No.	385086
Contig ID	44_3.R1084
5'-most EST	g2799226
Method	BLASTN
NCBI GI	g3550984
BLAST score	187
E value	1.0e-100
Match length	194
% identity	99
NCBI Description	Oryza sativa mRNA for OsS5a, complete cds

Seq. No.	385087
Contig ID	45_1.R1084
5'-most EST	g2655292
Method	BLASTX
NCBI GI	g2655293
BLAST score	919
E value	3.0e-99
Match length	201
% identity	91
NCBI Description	(AF032975) germin-like protein 5 [Oryza sativa]

Seq. No.	385088
Contig ID	46_1.R1084
5'-most EST	LIB3475-010-P1-K1-B2
Method	BLASTX
NCBI GI	g5360221
BLAST score	626
E value	4.0e-65
Match length	117
% identity	100
NCBI Description	(AB011262) nuclear transport factor 2 (NTF2) [Oryza sativa]

Seq. No.	385089
Contig ID	47_1.R1084
5'-most EST	g3983662
Method	BLASTX
NCBI GI	g3983663
BLAST score	4280
E value	0.0e+00
Match length	868
% identity	98
NCBI Description	(AB011270) importin-beta1 [Oryza sativa]

Seq. No.	385090
Contig ID	48_1.R1084
5'-most EST	g3983664

Method	BLASTX
NCBI GI	g3983665
BLAST score	4233
E value	0.0e+00
Match length	872
% identity	96
NCBI Description	(AB011271) importin-beta2 [Oryza sativa]

Seq. No.	385091
Contig ID	49_1.R1084
5'-most EST	g4716578
Method	BLASTX
NCBI GI	g2913891
BLAST score	517
E value	3.0e-52
Match length	128
% identity	79
NCBI Description	(AB011367) LIP9 [Oryza sativa]

Seq. No.	385092
Contig ID	49_2.R1084
5'-most EST	g2442778
Method	BLASTX
NCBI GI	g1657843
BLAST score	188
E value	6.0e-14
Match length	52
% identity	75
NCBI Description	(U73210) cold acclimation protein WCOR410b [Triticum aestivum]

Seq. No.	385093
Contig ID	50_1.R1084
5'-most EST	g3760863
Method	BLASTN
NCBI GI	g2913892
BLAST score	287
E value	1.0e-160
Match length	537
% identity	98
NCBI Description	Oryza sativa mRNA for LIP5, complete cds

Seq. No.	385094
Contig ID	51_1.R1084
5'-most EST	uC-osrocyp005d08b1
Method	BLASTX
NCBI GI	g3913811
BLAST score	2122
E value	0.0e+00
Match length	489
% identity	88
NCBI Description	GLUTAMYL-TRNA REDUCTASE PRECURSOR (GLUTR) >gi_2920320_dbj_BAA25003_ (AB011416) glutamyl-tRNA reductase [Oryza sativa]

Seq. No.	385095
Contig ID	52_1.R1084

5'-most EST	g3077789
Method	BLASTX
NCBI GI	g3062907
BLAST score	2627
E value	0.0e+00
Match length	510
% identity	100
NCBI Description	(AB012107) myo-inositol phosphate synthase [Oryza sativa]

Seq. No.	385096
Contig ID	53_1.R1084
5'-most EST	LIB3433-031-P1-K1-E2
Method	BLASTX
NCBI GI	g2992160
BLAST score	1064
E value	1.0e-116
Match length	239
% identity	85
NCBI Description	(AB012392) MuDR-like element [Oryza sativa]

Seq. No.	385097
Contig ID	54_1.R1084
5'-most EST	g3061268
Method	BLASTX
NCBI GI	g3721942
BLAST score	1422
E value	1.0e-158
Match length	341
% identity	79
NCBI Description	(AB018248) chitinase [Oryza sativa]

Seq. No.	385098
Contig ID	56_1.R1084
5'-most EST	g4164148
Method	BLASTX
NCBI GI	g4164149
BLAST score	1220
E value	1.0e-134
Match length	255
% identity	91
NCBI Description	(AB014056) iron-superoxide dismutase [Oryza sativa]

Seq. No.	385099
Contig ID	57_1.R1084
5'-most EST	g3138798
Method	BLASTX
NCBI GI	g3138799
BLAST score	1131
E value	1.0e-124
Match length	217
% identity	100
NCBI Description	(AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]

Seq. No.	385100
Contig ID	58_1.R1084
5'-most EST	g3767896
Method	BLASTX

NCBI GI	g5360230
BLAST score	1053
E value	1.0e-115
Match length	193
% identity	100
NCBI Description	(AB015287) Ran [Oryza sativa]

Seq. No.	385101
Contig ID	59_1.R1084
5'-most EST	g2310184
Method	BLASTX
NCBI GI	g3288883
BLAST score	2384
E value	0.0e+00
Match length	476
% identity	100
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]

Seq. No.	385102
Contig ID	59_2.R1084
5'-most EST	g2442903

Seq. No.	385103
Contig ID	59_4.R1084
5'-most EST	g4878682
Method	BLASTN
NCBI GI	g3288882
BLAST score	113
E value	8.0e-57
Match length	156
% identity	97
NCBI Description	Oryza sativa mRNA for SAR DNA binding protein, partial cds

Seq. No.	385104
Contig ID	60_1.R1084
5'-most EST	g3252793
Method	BLASTX
NCBI GI	g3252794
BLAST score	3975
E value	0.0e+00
Match length	733
% identity	98
NCBI Description	(AB015615) isoamylase [Oryza sativa]

Seq. No.	385105
Contig ID	61_1.R1084
5'-most EST	g3318614
Method	BLASTX
NCBI GI	g3318615
BLAST score	1658
E value	0.0e+00
Match length	360
% identity	91
NCBI Description	(AB016065) mitochondrial phosphate transporter [Oryza sativa]

Seq. No.	385106

Contig ID	61_2.R1084
5'-most EST	uC-osflcyp153g01b1
Method	BLASTX
NCBI GI	g3318615
BLAST score	385
E value	1.0e-47
Match length	180
% identity	65
NCBI Description	(AB016065) mitochondrial phosphate transporter [Oryza sativa]

Seq. No.	385107
Contig ID	[illegible]
5'-mo[illegible]	[illegible]
Metho[illegible]	BLASTX
NCBI G	g3370780
BLAST score	1263
E value	1.0e-139
Match length	261
% identity	90
NCBI Description	(AB016497) chitinase [Oryza sativ[illegible]

Seq. No.	385108
Contig ID	6[illegible]
5'-most EST	g
Method	[illegible]
NCBI GI	g[illegible]3455
BLAST score	1251
E value	1.0e-138
Mat[illegible]	258
% ide[illegible]	90
NCBI Description	(AF001500) chitinase [Oryza sativa]

Seq. No.	385109
Contig ID	64_1.R1084
5'-most EST	LIB3434-030-P1-K1-D1
Method	BLASTX
NCBI GI	g4126687
BLAST score	2488
E value	0.0e+00
Match length	510
% identity	95
NCBI Description	(AB016501) glutelin [Oryza sativa]

Seq. No.	385110
Contig ID	64_2.R1084
5'-most EST	g2798805
Method	BLASTX
NCBI GI	g4126687
BLAST score	560
E value	2.0e-57
Match length	112
% identity	97
NCBI Description	(AB016501) glutelin [Oryza sativa]

Seq. No.	385111
Contig ID	65_1.R1084

5'-most EST	LIB3479-009-Q6-K1-E2
Method	BLASTX
NCBI GI	g4126691
BLAST score	372
E value	2.0e-35
Match length	150
% identity	54
NCBI Description	(AB016503) prolamin [Oryza sativa]

Seq. No.	385112
Contig ID	65_2.R1084
5'-most EST	g2798847
Method	BLASTX
NCBI GI	g296129
BLAST score	428
E value	1.0e-41
Match length	253
% identity	59
NCBI Description	(X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_ (D63901) 13kDa prolamin [Oryza sativa]

Seq. No.	385113
Contig ID	65_9.R1084
5'-most EST	LIB3479-008-Q6-K1-F8
Method	BLASTX
NCBI GI	g283007
BLAST score	310
E value	4.0e-28
Match length	124
% identity	53
NCBI Description	14K prolamin precursor - rice >gi_20306_emb_CAA43295_ (X60979) prolamin [Oryza sativa]

Seq. No.	385114
Contig ID	65_12.R1084
5'-most EST	g2798845
Method	BLASTX
NCBI GI	g296129
BLAST score	215
E value	6.0e-17
Match length	167
% identity	28
NCBI Description	(X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_ (D63901) 13kDa prolamin [Oryza sativa]

Seq. No.	385115
Contig ID	65_13.R1084
5'-most EST	g2798436
Method	BLASTN
NCBI GI	g20305
BLAST score	235
E value	1.0e-129
Match length	372
% identity	94
NCBI Description	O.sativa mRNA for prolamin storage protein

Seq. No. 385116

Contig ID	65_15.R1084
5'-most EST	g2799638
Method	BLASTX
NCBI GI	g296129
BLAST score	149
E value	5.0e-12
Match length	82
% identity	66
NCBI Description	(X65064) prolamin [Oryza sativa] >gi_971122_dbj_BAA09940_ (D63901) 13kDa prolamin [Oryza sativa]

Seq. No.	385117
Contig ID	65_17.R1084
5'-most EST	g2796717
Method	BLASTN
NCBI GI	g971121
BLAST score	152
E value	4.0e-80
Match length	228
% identity	95
NCBI Description	Rice DNA for 13kDa prolamin, complete cds

Seq. No.	385118
Contig ID	66_1.R1084
5'-most EST	g20297
Method	BLASTX
NCBI GI	g4126693
BLAST score	352
E value	7.0e-33
Match length	124
% identity	60
NCBI Description	(AB016504) prolamin [Oryza sativa]

Seq. No.	385119
Contig ID	66_2.R1084
5'-most EST	g2799051
Method	BLASTX
NCBI GI	g4126693
BLAST score	194
E value	1.0e-24
Match length	101
% identity	58
NCBI Description	(AB016504) prolamin [Oryza sativa]

Seq. No.	385120
Contig ID	66_8.R1084
5'-most EST	g1632585
Method	BLASTX
NCBI GI	g82501
BLAST score	361
E value	1.0e-41
Match length	95
% identity	97
NCBI Description	prolamin precursor (clone pS23) - rice >gi_20302_emb_CAA37849_ (X53856) prolamin [Oryza sativa]

Seq. No.	385121

Contig ID	66_14.R1084
5'-most EST	LIB3599-001-P1-N6-B6
Method	BLASTX
NCBI GI	g130956
BLAST score	208
E value	1.0e-16
Match length	60
% identity	67
NCBI Description	PROLAMIN PPROL 4A PRECURSOR >gi_82505_pir__JA0168 prolamin 4a precursor - rice >gi_557588 (M23746) prolamine [Oryza sativa]

Seq. No.	385122
Contig ID	67_1.R1084
5'-most EST	g2797310
Method	BLASTX
NCBI GI	g4126695
BLAST score	245
E value	1.0e-39
Match length	138
% identity	67
NCBI Description	(AB016505) prolamin [Oryza sativa]

Seq. No.	385123
Contig ID	67_2.R1084
5'-most EST	g2799076
Method	BLASTX
NCBI GI	g4126695
BLAST score	329
E value	3.0e-30
Match length	117
% identity	58
NCBI Description	(AB016505) prolamin [Oryza sativa]

Seq. No.	385124
Contig ID	67_6.R1084
5'-most EST	g2799639
Method	BLASTN
NCBI GI	g4126694
BLAST score	190
E value	1.0e-102
Match length	326
% identity	92
NCBI Description	Oryza sativa mRNA for prolamin, complete cds, clone:lambda RM9

Seq. No.	385125
Contig ID	68_1.R1084
5'-most EST	uC-osf1M202062g09b1
Method	BLASTX
NCBI GI	g1524383
BLAST score	1959
E value	0.0e+00
Match length	443
% identity	87
NCBI Description	(X63374) 3-phosphoshikimate 1-carboxyvinyltransferase [Zea mays]

Seq. No.	385126
Contig ID	69_1.R1084
5'-most EST	LIB3432-031-P1-K1-H10
Method	BLASTX
NCBI GI	g4126809
BLAST score	1533
E value	1.0e-171
Match length	291
% identity	100
NCBI Description	(AB017042) glyoxalase I [Oryza sativa]

Seq. No.	385127
Contig ID	70_1.R1084
5'-most EST	LIB3477-011-P1-K1-B10
Method	BLASTX
NCBI GI	g5688945
BLAST score	1560
E value	1.0e-174
Match length	306
% identity	94
NCBI Description	(AB017427) mitochondrial ribosomal protein S14 [Oryza sativa] >gi_5688950_dbj_BAA82751.1_ (AB017429) mitochondrial ribosomal portein S14 [Oryza sativa]

Seq. No.	385128
Contig ID	70_2.R1084
5'-most EST	g5688946
Method	BLASTX
NCBI GI	g5688947
BLAST score	1249
E value	1.0e-138
Match length	237
% identity	95
NCBI Description	(AB017428) succinate dehydrogenase iron-protein subunit (SDHB) [Oryza sativa] >gi_5688949_dbj_BAA82750.1_ (AB017429) succinate dehydrogenase iron-protein subunit (SDHB) [Oryza sativa]

Seq. No.	385129
Contig ID	74_1.R1084
5'-most EST	uC-osf1cyp153e08b1
Method	BLASTX
NCBI GI	g5803256
BLAST score	466
E value	2.0e-46
Match length	115
% identity	79
NCBI Description	(AP000399) ESTs C98280(C1391),D15843(C1391) correspond to a region of the predicted gene; similar to OsENOD93a gene for early nodulin (AB018375) [Oryza sativa]

Seq. No.	385130
Contig ID	74_2.R1084
5'-most EST	LIB3475-001-P1-K2-B9
Method	BLASTX
NCBI GI	g5803258

BLAST score	495
E value	8.0e-50
Match length	115
% identity	84
NCBI Description	(AP000399) EST AU077972(C53511) corresponds to a region of the predicted gene; similar to OsENOD93a gene for early nodulin (AB018375) [Oryza sativa]

Seq. No.	385131
Contig ID	74_3.R1084
5'-most EST	g2311688
Method	BLASTX
NCBI GI	g3763845
BLAST score	496
E value	9.0e-50
Match length	115
% identity	84
NCBI Description	(AB018375) early nodulin [Oryza sativa] >gi_3763847_dbj_BAA33814_ (AB018376) early nodulin [Oryza sativa] >gi_5803255_dbj_BAA83565.1_ (AP000399) ESTs C98096(C0688),C98097(C0688) correspond to a region of the predicted gene; similar to OsENOD93a gene for early nodulin (AB018375) [Oryza sativa]

Seq. No.	385132
Contig ID	74_4.R1084
5'-most EST	g4809190
Method	BLASTX
NCBI GI	g4809191
BLAST score	583
E value	3.0e-60
Match length	135
% identity	86
NCBI Description	(AF140229) early nodulin [Oryza sativa]

Seq. No.	385133
Contig ID	74_6.R1084
5'-most EST	g286791
Method	BLASTX
NCBI GI	g5803250
BLAST score	216
E value	2.0e-17
Match length	68
% identity	65
NCBI Description	(AP000399) EST AU077941(C12908) corresponds to a region of the predicted gene; similar to OsENOD93a gene for early nodulin (AB018375) [Oryza sativa]

Seq. No.	385134
Contig ID	75_1.R1084
5'-most EST	LIB3434-016-P1-K1-D2
Method	BLASTX
NCBI GI	g3763849
BLAST score	456
E value	3.0e-45
Match length	92
% identity	100

NCBI Description	(AB018377) early nodulin [Oryza sativa]

Seq. No.	385135
Contig ID	77_1.R1084
5'-most EST	g6006309
Method	BLASTX
NCBI GI	g6006310
BLAST score	4324
E value	0.0e+00
Match length	900
% identity	93
NCBI Description	(AB018443) nonphototrophic hypocotyl 1b [Oryza sativa]

Seq. No.	385136
Contig ID	78_1.R1084
5'-most EST	g6006311
Method	BLASTX
NCBI GI	g6006312
BLAST score	4603
E value	0.0e+00
Match length	921
% identity	96
NCBI Description	(AB018444) nonphototrophic hypocotyl 1a [Oryza sativa]

Seq. No.	385137
Contig ID	78_2.R1084
5'-most EST	g568957
Method	BLASTN
NCBI GI	g6006311
BLAST score	377
E value	0.0e+00
Match length	463
% identity	99
NCBI Description	Oryza sativa mRNA for nonphototrophic hypocotyl 1a, complete cds

Seq. No.	385138
Contig ID	79_1.R1084
5'-most EST	g4519935
Method	BLASTX
NCBI GI	g4519938
BLAST score	4355
E value	0.0e+00
Match length	901
% identity	95
NCBI Description	(AB019240) RPR1h [Oryza sativa]

Seq. No.	385139
Contig ID	81_1.R1084
5'-most EST	g4760552
Method	BLASTX
NCBI GI	g4760553
BLAST score	1835
E value	0.0e+00
Match length	376
% identity	93
NCBI Description	(AB019533) Nad-dependent formate dehydrogenase [Oryza

sativa]

Seq. No.	385140
Contig ID	82_1.R1084
5'-most EST	LIB3474-010-P1-K1-A10
Method	BLASTX
NCBI GI	g2130069
BLAST score	2553
E value	0.0e+00
Match length	492
% identity	96
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	385141
Contig ID	82_2.R1084
5'-most EST	LIB3432-059-P1-K1-F5
Method	BLASTX
NCBI GI	g3868756
BLAST score	2684
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	(D86611) catalase [Oryza sativa]

Seq. No.	385142
Contig ID	82_3.R1084
5'-most EST	g569169
Method	BLASTX
NCBI GI	g2244749
BLAST score	593
E value	5.0e-61
Match length	236
% identity	74
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	385143
Contig ID	82_7.R1084
5'-most EST	LIB3431-027-P1-K1-B12

Seq. No.	385144
Contig ID	82_11.R1084
5'-most EST	uC-osf1cyp051c08b1
Method	BLASTX
NCBI GI	g2130069
BLAST score	365
E value	5.0e-72
Match length	195
% identity	80
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	385145
Contig ID	82_12.R1084
5'-most EST	g3768438

Seq. No.	385146

Contig ID	82_13.R1084
5'-most EST	LIB3431-018-P1-K1-D6
Method	BLASTX
NCBI GI	g2130069
BLAST score	1031
E value	1.0e-112
Match length	199
% identity	96
NCBI Description	catalase (EC 1.11.1.6) catA - rice >gi_1261858_dbj_BAA06232_ (D29966) catalase [Oryza sativa]

Seq. No.	385147
Contig ID	82_17.R1084
5'-most EST	uC-osflcyp154d06b1
Method	BLASTX
NCBI GI	g66298
BLAST score	860
E value	2.0e-92
Match length	240
% identity	71
NCBI Description	catalase (EC 1.11.1.6) - rice >gi_20192_emb_CAA43814_ (X61626) catalase [Oryza sativa]

Seq. No.	385148
Contig ID	83_1.R1084
5'-most EST	g2311935

Seq. No.	385149
Contig ID	84_1.R1084
5'-most EST	g3090547
Method	BLASTX
NCBI GI	g4996284
BLAST score	991
E value	1.0e-107
Match length	227
% identity	88
NCBI Description	(AB020973) heat shock protein 26 [Oryza sativa]

Seq. No.	385150
Contig ID	85_1.R1084
5'-most EST	g702417
Method	BLASTX
NCBI GI	g5853117
BLAST score	1746
E value	0.0e+00
Match length	536
% identity	71
NCBI Description	(AF177200) chlorophyll a oxygenase [Arabidopsis thaliana]

Seq. No.	385151
Contig ID	86_1.R1084
5'-most EST	g428388
Method	BLASTX
NCBI GI	g4586378
BLAST score	1571
E value	1.0e-175
Match length	332

% identity	93
NCBI Description	(AB021746) nicotianamine synthase 1 [Oryza sativa]

Seq. No.	385152
Contig ID	86_2.R1084
5'-most EST	g5038779
Method	BLASTX
NCBI GI	g4586378
BLAST score	648
E value	6.0e-68
Match length	131
% identity	96
NCBI Description	(AB021746) nicotianamine synthase 1 [Oryza sativa]

Seq. No.	385153
Contig ID	86_3.R1084
5'-most EST	LIB3475-010-P1-K1-C4
Method	BLASTX
NCBI GI	g4586378
BLAST score	424
E value	4.0e-49
Match length	107
% identity	98
NCBI Description	(AB021746) nicotianamine synthase 1 [Oryza sativa]

Seq. No.	385154
Contig ID	87_1.R1084
5'-most EST	g5731736
Method	BLASTX
NCBI GI	g5731737
BLAST score	2356
E value	0.0e+00
Match length	532
% identity	88
NCBI Description	(AB021878) similar to yeast sodium/proton exchanger [Oryza sativa]

Seq. No.	385155
Contig ID	88_1.R1084
5'-most EST	g4115415
Method	BLASTX
NCBI GI	g4680193
BLAST score	965
E value	1.0e-105
Match length	186
% identity	100
NCBI Description	(AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica]

Seq. No.	385156
Contig ID	90_1.R1084
5'-most EST	g5360658
Method	BLASTX
NCBI GI	g5360659
BLAST score	2658
E value	0.0e+00
Match length	606

% identity	86
NCBI Description	(AB022603) anthranilate synthase alpha 2 subunit [Oryza sativa]

Seq. No.	385157
Contig ID	91_1.R1084
5'-most EST	g5456937
Method	BLASTX
NCBI GI	g5456938
BLAST score	799
E value	3.0e-85
Match length	223
% identity	74
NCBI Description	(AB022675) ribosomal protein S9 [Oryza sativa]

Seq. No.	385158
Contig ID	92_1.R1084
5'-most EST	g5821254
Method	BLASTX
NCBI GI	g5821255
BLAST score	1268
E value	1.0e-140
Match length	318
% identity	79
NCBI Description	(AB023288) TRAB1 [Oryza sativa]

Seq. No.	385159
Contig ID	95_1.R1084
5'-most EST	g436051
Method	BLASTX
NCBI GI	g477282
BLAST score	4197
E value	0.0e+00
Match length	811
% identity	96
NCBI Description	starch branching enzyme isoform RBE3 - rice >gi_436052_dbj_BAA03738_ (D16201) branching enzyme-3 precursor [Oryza sativa]

Seq. No.	385160
Contig ID	95_2.R1084
5'-most EST	g5689137
Method	BLASTX
NCBI GI	g5689138
BLAST score	4363
E value	0.0e+00
Match length	808
% identity	99
NCBI Description	(AB023498) starch branching enzyme rbe4 [Oryza sativa]

Seq. No.	385161
Contig ID	96_1.R1084
5'-most EST	g5689254
Method	BLASTX
NCBI GI	g5689255
BLAST score	2578
E value	0.0e+00

Match length	560
% identity	88
NCBI Description	(AB024337) blue-light photoreceptor [Oryza sativa]

Seq. No.	385162
Contig ID	97_1.R1084
5'-most EST	g6331694
Method	BLASTX
NCBI GI	g1399510
BLAST score	1684
E value	0.0e+00
Match length	437
% identity	76
NCBI Description	(U50064) type A-like cyclin [Zea mays]

Seq. No.	385163
Contig ID	98_1.R1084
5'-most EST	g6331703
Method	BLASTX
NCBI GI	g1076742
BLAST score	1238
E value	1.0e-136
Match length	242
% identity	100
NCBI Description	cyclin - rice >gi_558621_emb_CAA57555_ (X82035) cyclin [Oryza sativa]

Seq. No.	385164
Contig ID	99_1.R1084
5'-most EST	g4586675
Method	BLASTX
NCBI GI	g4586676
BLAST score	2176
E value	0.0e+00
Match length	427
% identity	98
NCBI Description	(AB025047) sterol 14-demethylase [Oryza sativa]

Seq. No.	385165
Contig ID	100_1.R1084
5'-most EST	g4586448
Method	BLASTX
NCBI GI	g4586449
BLAST score	682
E value	2.0e-71
Match length	156
% identity	83
NCBI Description	(AB025187) cytochrome c oxidase subunit 6b-1 [Oryza sativa]

Seq. No.	385166
Contig ID	101_1.R1084
5'-most EST	uC-osroM202004e11b1
Method	BLASTX
NCBI GI	g5926740
BLAST score	2432
E value	0.0e+00
Match length	469

% identity	97
NCBI Description	(AB025310) asparaginyl endopeptidase [Oryza sativa]
Seq. No.	385167
Contig ID	101_2.R1084
5'-most EST	LIB3432-045-P1-K1-F10
Method	BLASTX
NCBI GI	g4206195
BLAST score	265
E value	9.0e-23
Match length	113
% identity	75
NCBI Description	(AF071527) hypothetical protein [Arabidopsis thaliana] >gi_4262169_gb_AAD14469_ (AC005275) hypothetical protein [Arabidopsis thaliana]
Seq. No.	385168
Contig ID	102_1.R1084
5'-most EST	uC-osf1M202095g01b1
Method	BLASTX
NCBI GI	g1346104
BLAST score	1959
E value	0.0e+00
Match length	380
% identity	100
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN ALPHA-1 SUBUNIT (GP-ALPHA-1) >gi_540533_dbj_BAA07405_ (D38232) G protein alpha subunit [Oryza sativa]
Seq. No.	385169
Contig ID	102_2.R1084
5'-most EST	LIB3475-012-P1-K1-H1
Seq. No.	385170
Contig ID	102_3.R1084
5'-most EST	uC-osf1cyp174g03b1
Method	BLASTN
NCBI GI	g5852170
BLAST score	86
E value	2.0e-40
Match length	200
% identity	64
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804
Seq. No.	385171
Contig ID	102_5.R1084
5'-most EST	uC-osf1cyp092h10b1
Method	BLASTN
NCBI GI	g5852170
BLAST score	210
E value	1.0e-114
Match length	564
% identity	94
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	385172
Contig ID	102_6.R1084
5'-most EST	LIB3433-035-P1-K1-B10
Method	BLASTX
NCBI GI	g2911068
BLAST score	743
E value	1.0e-78
Match length	145
% identity	87
NCBI Description	(AL021960) G10-like protein [Arabidopsis thaliana]

Seq. No.	385173
Contig ID	102_11.R1084
5'-most EST	LIB3432-048-P2-K1-C7
Method	BLASTN
NCBI GI	g5852170
BLAST score	229
E value	1.0e-125
Match length	488
% identity	81
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	385174
Contig ID	102_14.R1084
5'-most EST	uC-osflm202110d12b1
Method	BLASTN
NCBI GI	g5822826
BLAST score	188
E value	1.0e-101
Match length	273
% identity	93
NCBI Description	Oryza sativa D1 gene for alpha-subunit of GTP-binding protein, wild type, partial sequence

Seq. No.	385175
Contig ID	107_1.R1084
5'-most EST	g568524
Method	BLASTX
NCBI GI	g4760483
BLAST score	2054
E value	0.0e+00
Match length	398
% identity	100
NCBI Description	(AB026731) monodehydroascorbate reductase [Oryza sativa]

Seq. No.	385176
Contig ID	109_1.R1084
5'-most EST	g286492
Method	BLASTX
NCBI GI	g4835588
BLAST score	1743
E value	0.0e+00
Match length	362
% identity	92
NCBI Description	(AB027054) nitrilase-like protein [Oryza sativa]

Seq. No.	385177
Contig ID	109_2.R1084
5'-most EST	g2800552
Method	BLASTN
NCBI GI	g4835587
BLAST score	149
E value	7.0e-78
Match length	172
% identity	98
NCBI Description	Oryza sativa ONIT4 mRNA for nitrilase-like protein, complete cds

Seq. No.	385178
Contig ID	110_1.R1084
5'-most EST	LIB3432-037-P1-K1-E3
Method	BLASTX
NCBI GI	g4850330
BLAST score	332
E value	1.0e-30
Match length	63
% identity	100
NCBI Description	(AB027123) cytochrome c oxidase subunit 5c [Oryza sativa]

Seq. No.	385179
Contig ID	111_1.R1084
5'-most EST	g426423
Method	BLASTX
NCBI GI	g2696229
BLAST score	1651
E value	0.0e+00
Match length	304
% identity	100
NCBI Description	(D55712) chitinase [Oryza sativa] >gi_4884494_dbj_BAA77768.1_ (AB027415) class III chitinase homologue (OsChib3H-a)H- [Oryza sativa] >gi_4884496_dbj_BAA77769.1_ (AB027416) class III chitinase homologue (OsChib3H-a) [Oryza sativa] >gi_4884498_dbj_BAA77770.1_ (AB027417) class III chitinase homologue (OsChib3H-a) [Oryza sativa] >gi_4884506_dbj_BAA77771.1_ (AB027418) class III chitinase homologue (OsChib3H-a) [Oryza sativa] >gi_4884508_dbj_BAA77772.1_ (AB027419) class III chitinase homologue (OsChib3H-a) [Oryza sativa] >gi_4884510_dbj_BAA77773.1_ (AB027420) class III chitinase homologue (OsChib3H-a) [Oryza sativa]

Seq. No.	385180
Contig ID	111_2.R1084
5'-most EST	g2312391
Method	BLASTX
NCBI GI	g2696233
BLAST score	1531
E value	1.0e-171
Match length	304
% identity	94
NCBI Description	(D55714) chitinase [Oryza sativa] >gi_4884512_dbj_BAA77774.1_ (AB027421) class III chitinase

homologue (OsChib3H-b) [Oryza sativa]
>gi_4884514_dbj_BAA77775.1_ (AB027422) class III chitinase homologue (OsChib3H-b) [Oryza sativa]

Seq. No.	385181
Contig ID	111_3.R1084
5'-most EST	g2310275
Method	BLASTX
NCBI GI	g2696221
BLAST score	1461
E value	1.0e-163
Match length	292
% identity	94
NCBI Description	(D55708) chitinase [Oryza sativa]

Seq. No.	385182
Contig ID	111_4.R1084
5'-most EST	g5002981
Method	BLASTX
NCBI GI	g2696225
BLAST score	1482
E value	1.0e-165
Match length	289
% identity	96
NCBI Description	(D55710) chitinase [Oryza sativa]

Seq. No.	385183
Contig ID	111_5.R1084
5'-most EST	g426113
Method	BLASTX
NCBI GI	g2696223
BLAST score	1629
E value	0.0e+00
Match length	315
% identity	95
NCBI Description	(D55709) chitinase [Oryza sativa] >gi_4884520_dbj_BAA77778.1_ (AB027425) class III chitinase homologue (OsChib3H-d) [Oryza sativa]

Seq. No.	385184
Contig ID	111_6.R1084
5'-most EST	LIB3434-021-P1-K1-A6
Method	BLASTX
NCBI GI	g2696221
BLAST score	883
E value	6.0e-95
Match length	265
% identity	65
NCBI Description	(D55708) chitinase [Oryza sativa]

Seq. No.	385185
Contig ID	111_7.R1084
5'-most EST	g4884517
Method	BLASTX
NCBI GI	g4884518
BLAST score	1604
E value	1.0e-179

Match length	312
% identity	96
NCBI Description	(AB027424) class III chitinase homologue (OsChib3H-c) [Oryza sativa]

Seq. No.	385186
Contig ID	111_8.R1084
5'-most EST	g2442437
Method	BLASTN
NCBI GI	g5734616
BLAST score	119
E value	6.0e-60
Match length	244
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	385187
Contig ID	111_9.R1084
5'-most EST	g4884523
Method	BLASTX
NCBI GI	g4884524
BLAST score	615
E value	5.0e-64
Match length	147
% identity	81
NCBI Description	(AB027427) class III chitinase homologue (OsChib3H-h) [Oryza sativa]

Seq. No.	385188
Contig ID	122_1.R1084
5'-most EST	g4878226
Method	BLASTX
NCBI GI	g4884522
BLAST score	364
E value	2.0e-55
Match length	122
% identity	90
NCBI Description	(AB027426) class III chitinase homologue (OsChib3H-g) [Oryza sativa]

Seq. No.	385189
Contig ID	124_1.R1084
5'-most EST	g4884525
Method	BLASTX
NCBI GI	g4884526
BLAST score	1519
E value	1.0e-169
Match length	330
% identity	91
NCBI Description	(AB027428) beta 1,3-glucanase [Oryza sativa]

Seq. No.	385190
Contig ID	125_1.R1084
5'-most EST	g4884527
Method	BLASTX
NCBI GI	g4884528
BLAST score	1681

E value	0.0e+00
Match length	338
% identity	96
NCBI Description	(AB027429) beta-1,3-glucanase [Oryza sativa]

Seq. No.	385191
Contig ID	127_1.R1084
5'-most EST	LIB3475-005-P1-K1-A5
Method	BLASTX
NCBI GI	g4884532
BLAST score	1615
E value	0.0e+00
Match length	316
% identity	100
NCBI Description	(AB027431) beta-1,3-glucanase [Oryza sativa] >gi_4884534_dbj_BAA77787.1_ (AB027432) beta-1,3-glucanase [Oryza sativa]

Seq. No.	385192
Contig ID	129_1.R1084
5'-most EST	g569919
Method	BLASTN
NCBI GI	g4958936
BLAST score	195
E value	1.0e-105
Match length	199
% identity	99
NCBI Description	Oryza sativa ICT mRNA, partial cds

Seq. No.	385193
Contig ID	130_1.R1084
5'-most EST	g4996643
Method	BLASTX
NCBI GI	g4996644
BLAST score	1232
E value	1.0e-136
Match length	371
% identity	66
NCBI Description	(AB028131) Dof zinc finger protein [Oryza sativa]

Seq. No.	385194
Contig ID	130_3.R1084
5'-most EST	g4996639
Method	BLASTX
NCBI GI	g4996640
BLAST score	1125
E value	1.0e-123
Match length	370
% identity	60
NCBI Description	(AB028129) Dof zinc finger protein [Oryza sativa]

Seq. No.	385195
Contig ID	130_5.R1084
5'-most EST	g2310616
Method	BLASTX
NCBI GI	g1360088
BLAST score	288

E value	2.0e-25
Match length	50
% identity	92
NCBI Description	(X97947) Zn finger protein [Nicotiana tabacum]

Seq. No.	385196
Contig ID	133_1.R1084
5'-most EST	g2800796
Method	BLASTX
NCBI GI	g4996646
BLAST score	778
E value	1.0e-82
Match length	282
% identity	55
NCBI Description	(AB028132) Dof zinc finger protein [Oryza sativa]

Seq. No.	385197
Contig ID	134_2.R1084
5'-most EST	g2799015
Method	BLASTN
NCBI GI	g4996647
BLAST score	193
E value	1.0e-104
Match length	209
% identity	99
NCBI Description	Oryza sativa mRNA for Dof zinc finger protein, complete cds

Seq. No.	385198
Contig ID	137_1.R1084
5'-most EST	g5103726
Method	BLASTX
NCBI GI	g5103727
BLAST score	1391
E value	1.0e-154
Match length	341
% identity	80
NCBI Description	(AB028884) knotted1-type homeobox protein OSH43 [Oryza sativa]

Seq. No.	385199
Contig ID	140_1.R1084
5'-most EST	g2311992
Method	BLASTX
NCBI GI	g6069671
BLAST score	1452
E value	0.0e+00
Match length	333
% identity	97
NCBI Description	(AP000616) EST C72179(E1153) corresponds to a region of the predicted gene.; similar to Arabidopsis thaliana chromosome II BAC T4C15; hypothetical protein (AC004667) [Oryza sativa]

Seq. No.	385200
Contig ID	141_1.R1084
5'-most EST	uC-osroM202041g05b1
Method	BLASTX

NCBI GI	g1168537
BLAST score	2483
E value	0.0e+00
Match length	496
% identity	95
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa]

Seq. No.	385201
Contig ID	142_1.R1084
5'-most EST	g3767145
Method	BLASTN
NCBI GI	g5106370
BLAST score	482
E value	0.0e+00
Match length	482
% identity	100
NCBI Description	Oryza sativa OsIF1-1 mRNA for F1F0-ATPase inhibitor protein, complete cds

Seq. No.	385202
Contig ID	143_1.R1084
5'-most EST	g3760765
Method	BLASTX
NCBI GI	g5821432
BLAST score	533
E value	4.0e-54
Match length	109
% identity	98
NCBI Description	(AB029060) F1F0-ATPase inhibitor protein [Oryza sativa]

Seq. No.	385203
Contig ID	144_1.R1084
5'-most EST	LIB3434-051-P1-K1-D11
Method	BLASTX
NCBI GI	g3135543
BLAST score	1383
E value	1.0e-153
Match length	290
% identity	92
NCBI Description	(AF062393) aquaporin [Oryza sativa]

Seq. No.	385204
Contig ID	144_2.R1084
5'-most EST	g3061196
Method	BLASTX
NCBI GI	g1657950
BLAST score	1061
E value	1.0e-118
Match length	281
% identity	75
NCBI Description	(U73467) MipE [Mesembryanthemum crystallinum]

Seq. No.	385205
Contig ID	144_3.R1084

5'-most EST	LIB3433-049-P1-K1-D9
Method	BLASTX
NCBI GI	g2662310
BLAST score	672
E value	1.0e-100
Match length	199
% identity	92
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	385206
Contig ID	144_4.R1084
5'-most EST	LIB3431-015-P1-K1-H12
Method	BLASTX
NCBI GI	g2662310
BLAST score	739
E value	2.0e-78
Match length	191
% identity	77
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	385207
Contig ID	144_5.R1084
5'-most EST	g568257
Method	BLASTX
NCBI GI	g2662310
BLAST score	289
E value	5.0e-26
Match length	78
% identity	74
NCBI Description	(AB009307) bpw1 [Hordeum vulgare]

Seq. No.	385208
Contig ID	144_10.R1084
5'-most EST	uC-osroM202023a01b1
Method	BLASTX
NCBI GI	g3135543
BLAST score	703
E value	3.0e-74
Match length	159
% identity	87
NCBI Description	(AF062393) aquaporin [Oryza sativa]

Seq. No.	385209
Contig ID	145_1.R1084
5'-most EST	g3061165
Method	BLASTX
NCBI GI	g5902930
BLAST score	1091
E value	1.0e-119
Match length	214
% identity	98
NCBI Description	(AB029510) small GTP-binding protein OsRac3 [Oryza sativa]

Seq. No.	385210
Contig ID	145_2.R1084
5'-most EST	LIB3474-012-P1-K1-A3
Method	BLASTX

NCBI GI	g5902926
BLAST score	1108
E value	1.0e-121
Match length	214
% identity	100
NCBI Description	(AB029508) small GTP-binding protein OsRac1 [Oryza sativa]

Seq. No.	385211
Contig ID	145_3.R1084
5'-most EST	g5902927
Method	BLASTX
NCBI GI	g5902928
BLAST score	1108
E value	1.0e-121
Match length	214
% identity	100
NCBI Description	(AB029509) small GTP-binding protein OsRac2 [Oryza sativa]

Seq. No.	385212
Contig ID	145_4.R1084
5'-most EST	LIB3434-014-P1-K1-F6
Method	BLASTX
NCBI GI	g4959459
BLAST score	417
E value	2.0e-71
Match length	140
% identity	95
NCBI Description	(AF126052) RACA small GTP binding protein [Zea mays]

Seq. No.	385213
Contig ID	148_1.R1084
5'-most EST	g2429038
Method	BLASTX
NCBI GI	g5931625
BLAST score	975
E value	1.0e-106
Match length	199
% identity	96
NCBI Description	(AB032761) rab5B [Oryza sativa]

Seq. No.	385214
Contig ID	149_1.R1084
5'-most EST	LIB3477-002-P1-K1-D1
Method	BLASTX
NCBI GI	g1215812
BLAST score	811
E value	1.0e-86
Match length	158
% identity	100
NCBI Description	(D38170) probenazole-inducible protein PBZ1 [Oryza sativa] >gi_2780343_dbj_BAA24277_ (D82066) PBZ1 [Oryza sativa]

Seq. No.	385215
Contig ID	150_1.R1084
5'-most EST	g1747293
Method	BLASTX
NCBI GI	g1747294

BLAST score	3445
E value	0.0e+00
Match length	771
% identity	90
NCBI Description	(D45383) vacuolar H+-pyrophosphatase [Oryza sativa]

Seq. No.	385216
Contig ID	151_1.R1084
5'-most EST	uC-osroM202028d02b1
Method	BLASTX
NCBI GI	g1747296
BLAST score	3723
E value	0.0e+00
Match length	767
% identity	96
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	385217
Contig ID	151_2.R1084
5'-most EST	LIB3434-029-P1-K1-B11
Method	BLASTX
NCBI GI	g1747296
BLAST score	1179
E value	1.0e-130
Match length	244
% identity	96
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	385218
Contig ID	151_3.R1084
5'-most EST	g4879002
Method	BLASTX
NCBI GI	g1747296
BLAST score	669
E value	4.0e-70
Match length	190
% identity	73
NCBI Description	(D45384) vacuolar H+-pyrophosphatase [Oryza sativa] >gi_3298476_dbj_BAA31524_ (AB012766) ovp2 [Oryza sativa]

Seq. No.	385219
Contig ID	152_1.R1084
5'-most EST	LIB3474-007-P1-K1-D4
Method	BLASTX
NCBI GI	g1321661
BLAST score	1303
E value	1.0e-144
Match length	250
% identity	100
NCBI Description	(D45423) ascorbate peroxidase [Oryza sativa]

Seq. No.	385220
Contig ID	153_1.R1084
5'-most EST	g2081611
Method	BLASTX

NCBI GI	g2081612
BLAST score	3435
E value	0.0e+00
Match length	716
% identity	96
NCBI Description	(D49714) deltal-pyrroline-5-carboxylate synthetase [Oryza sativa]

Seq. No.	385221
Contig ID	154_1.R1084
5'-most EST	uC-osflcyp061f07b1
Method	BLASTX
NCBI GI	g2627058
BLAST score	2707
E value	0.0e+00
Match length	519
% identity	100
NCBI Description	(D50317) ADP glucose pyrophosphorylase large subunit [Oryza sativa]

Seq. No.	385222
Contig ID	155_1.R1084
5'-most EST	uC-osflm202113e06b1
Method	BLASTX
NCBI GI	g1709129
BLAST score	301
E value	3.0e-27
Match length	101
% identity	61
NCBI Description	GLYCOGEN SYNTHASE KINASE-3 HOMOLOG MSK-3 >gi_481018_pir__S37642 protein kinase MSK-3 (EC 2.7.1.-) - alfalfa >gi_313148_emb_CAA48472_ (X68409) protein kinase [Medicago sativa]

Seq. No.	385223
Contig ID	156_1.R1084
5'-most EST	g4881146
Method	BLASTX
NCBI GI	g626041
BLAST score	523
E value	6.0e-53
Match length	119
% identity	85
NCBI Description	translation initiation factor eIF-1A - wheat (fragment)

Seq. No.	385224
Contig ID	157_1.R1084
5'-most EST	LIB3433-046-P1-K1-A9
Method	BLASTX
NCBI GI	g3747050
BLAST score	520
E value	5.0e-53
Match length	121
% identity	85
NCBI Description	(AF093540) ribosomal protein L26 [Zea mays]

Seq. No.	385225

Contig ID	158_1.R1084
5'-most EST	LIB3432-024-P1-K1-E7
Method	BLASTX
NCBI GI	g5762457
BLAST score	507
E value	2.0e-51
Match length	101
% identity	91
NCBI Description	(AF176040) ubiquitin-conjugating enzyme UBC2 [Mesembryanthemum crystallinum]

Seq. No.	385226
Contig ID	159_1.R1084
5'-most EST	g5005062
Method	BLASTX
NCBI GI	g1084457
BLAST score	864
E value	1.0e-92
Match length	229
% identity	78
NCBI Description	elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa]

Seq. No.	385227
Contig ID	159_2.R1084
5'-most EST	g3763608
Method	BLASTX
NCBI GI	g1084457
BLAST score	448
E value	3.0e-44
Match length	145
% identity	65
NCBI Description	elongation factor 1-beta - Rice >gi_432368_dbj_BAA04903_ (D23674) elongation factor 1 beta [Oryza sativa]

Seq. No.	385228
Contig ID	160_1.R1084
5'-most EST	g1008983
Method	BLASTX
NCBI GI	g2645170
BLAST score	1862
E value	0.0e+00
Match length	389
% identity	93
NCBI Description	(D50576) YY2 protein [Oryza sativa]

Seq. No.	385229
Contig ID	168_1.R1084
5'-most EST	uC-osflcyp093c10b1
Method	BLASTX
NCBI GI	g2662341
BLAST score	2276
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza

sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	385230
Contig ID	168_2.R1084
5'-most EST	uC-osflcyp174d07a1
Method	BLASTX
NCBI GI	g3264767
BLAST score	388
E value	8.0e-37
Match length	265
% identity	40
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	385231
Contig ID	168_3.R1084
5'-most EST	g2662346
Method	BLASTX
NCBI GI	g2662341
BLAST score	2262
E value	0.0e+00
Match length	436
% identity	100
NCBI Description	(D63580) EF-1 alpha [Oryza sativa] >gi_2662345_dbj_BAA23659_ (D63582) EF-1 alpha [Oryza sativa] >gi_2662347_dbj_BAA23660_ (D63583) EF-1 alpha [Oryza sativa]

Seq. No.	385232
Contig ID	168_5.R1084
5'-most EST	g3767139
Method	BLASTX
NCBI GI	g6015059
BLAST score	237
E value	5.0e-23
Match length	61
% identity	97
NCBI Description	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) >gi_2996096 (AF030517) translation elongation factor-1 alpha; EF-1 alpha [Oryza sativa]

Seq. No.	385233
Contig ID	168_6.R1084
5'-most EST	g5003069

Seq. No.	385234
Contig ID	168_12.R1084
5'-most EST	g2800504
Method	BLASTX
NCBI GI	g5917747
BLAST score	160
E value	4.0e-13
Match length	59
% identity	78
NCBI Description	(AF181492) elongation factor-1 alpha 3 [Lilium longiflorum]

Seq. No. 385235

Contig ID	172_1.R1084
5'-most EST	g1841319
Method	BLASTN
NCBI GI	g1841319
BLAST score	431
E value	0.0e+00
Match length	664
% identity	100
NCBI Description	Rice mRNA for EL2 gene, complete cds

Seq. No.	385236
Contig ID	173_1.R1084
5'-most EST	g2696237
Method	BLASTX
NCBI GI	g2696238
BLAST score	588
E value	5.0e-62
Match length	126
% identity	99
NCBI Description	(D67042) aspartate aminotransferase [Oryza sativa]

Seq. No.	385237
Contig ID	174_1.R1084
5'-most EST	uC-osf1M202037c08b1
Method	BLASTX
NCBI GI	g2130067
BLAST score	2172
E value	0.0e+00
Match length	411
% identity	100
NCBI Description	aspartate transaminase (EC 2.6.1.1), mitochondrial - rice >gi_2696240_dbj_BAA23815.1_ (D67043) aspartate aminotransferase [Oryza sativa]

Seq. No.	385238
Contig ID	175_1.R1084
5'-most EST	g3760542
Method	BLASTX
NCBI GI	g1514953
BLAST score	1789
E value	0.0e+00
Match length	370
% identity	91
NCBI Description	(D76415) cysteine proteinase [Oryza sativa]

Seq. No.	385239
Contig ID	175_2.R1084
5'-most EST	LIB3599-001-P1-K6-F9
Method	BLASTX
NCBI GI	g5761329
BLAST score	226
E value	2.0e-18
Match length	44
% identity	98
NCBI Description	(AB004819) cysteine endopeptidase [Oryza sativa]

Seq. No.	385240

Contig ID	176_1.R1084
5'-most EST	g3287493
Method	BLASTX
NCBI GI	g3287494
BLAST score	2394
E value	0.0e+00
Match length	513
% identity	95
NCBI Description	(D78504) similar to yeast SRP1 [Oryza sativa]

Seq. No.	385241
Contig ID	177_1.R1084
5'-most EST	LIB3477-009-P1-K1-G7
Method	BLASTX
NCBI GI	g4107003
BLAST score	2669
E value	0.0e+00
Match length	508
% identity	100
NCBI Description	(D82036) OSK5 [Oryza sativa] >gi_4107007_dbj_BAA36297_ (D82038) OSK3 [Oryza sativa]

Seq. No.	385242
Contig ID	177_2.R1084
5'-most EST	uC-osflcyp140g06b1
Method	BLASTX
NCBI GI	g4107001
BLAST score	1524
E value	1.0e-170
Match length	510
% identity	100
NCBI Description	(D82035) OSK4 [Oryza sativa]

Seq. No.	385243
Contig ID	181_1.R1084
5'-most EST	g4107008
Method	BLASTX
NCBI GI	g4107009
BLAST score	2640
E value	0.0e+00
Match length	501
% identity	100
NCBI Description	(D82039) OSK1 [Oryza sativa]

Seq. No.	385244
Contig ID	182_1.R1084
5'-most EST	g3894215
Method	BLASTX
NCBI GI	g3894214
BLAST score	851
E value	4.0e-91
Match length	226
% identity	77
NCBI Description	(D83726) elongation factor 1 beta 2 [Oryza sativa] >gi_3894216_dbj_BAA34599_ (D83727) elongation factor 1 beta 2 [Oryza sativa]

Seq. No.	385245
Contig ID	183_1.R1084
5'-most EST	LIB3431-044-P1-K1-A4
Method	BLASTX
NCBI GI	g1173275
BLAST score	697
E value	2.0e-73
Match length	156
% identity	91
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_2119068_pir__S58630 ribosomal protein S7 - maize chloroplast >gi_902274_emb_CAA60339_ (X86563) ribosomal protein S7 [Zea mays] >gi_902298_emb_CAA60362_ (X86563) ribosomal protein S7 [Zea mays]

Seq. No.	385246
Contig ID	183_2.R1084
5'-most EST	uC-osflcyp112g05b1
Method	BLASTX
NCBI GI	g1304215
BLAST score	991
E value	1.0e-107
Match length	254
% identity	81
NCBI Description	(D84392) precursor of rice 22 kDa protein of photosystem II (PSII-S) [Oryza sativa]

Seq. No.	385247
Contig ID	183_3.R1084
5'-most EST	g3106718
Method	BLASTX
NCBI GI	g1362086
BLAST score	3512
E value	0.0e+00
Match length	766
% identity	88
NCBI Description	5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_2129919_pir__S65957 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase (EC 2.1.1.14) - Madagascar periwinkle >gi_886471_emb_CAA58474_ (X83499) methionine synthase [Catharanthus roseus]

Seq. No.	385248
Contig ID	183_4.R1084
5'-most EST	LIB3431-063-P1-K1-C12
Method	BLASTX
NCBI GI	g1709846
BLAST score	775
E value	3.0e-82
Match length	268
% identity	65
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_706853 (U04336) 22 kDa component of photosystem II [Lycopersicon esculentum]

Seq. No.	385249
Contig ID	183_5.R1084
5'-most EST	LIB3432-039-P1-K1-E7
Method	BLASTX
NCBI GI	g133999
BLAST score	489
E value	1.0e-48
Match length	99
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S7 >gi_70904_pir__R3RZ7 ribosomal protein S7 - rice chloroplast >gi_12037_emb_CAA33942_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_12065_emb_CAA33919_ (X15901) ribosomal protein S7 [Oryza sativa] >gi_226657_prf__1603356CH ribosomal protein S7 [Oryza sativa]

Seq. No.	385250
Contig ID	183_6.R1084
5'-most EST	LIB3431-006-P1-K1-A3
Method	BLASTX
NCBI GI	g133748
BLAST score	634
E value	3.0e-66
Match length	124
% identity	100
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 >gi_70961_pir__R3RZ12 ribosomal protein S12 - rice chloroplast >gi_1213603_emb_CAA33929_ (X15901) ribosomal protein S12 [Oryza sativa] >gi_226658_prf__1603356CJ ribosomal protein S12 [Oryza sativa]

Seq. No.	385251
Contig ID	183_9.R1084
5'-most EST	g5455601
Method	BLASTN
NCBI GI	g5714761
BLAST score	47
E value	7.0e-17
Match length	63
% identity	94
NCBI Description	Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No.	385252
Contig ID	183_10.R1084
5'-most EST	LIB3432-008-P1-K1-B3
Method	BLASTX
NCBI GI	g400890
BLAST score	298
E value	9.0e-27
Match length	64
% identity	47
NCBI Description	PHOTOSYSTEM II 22 KD PROTEIN PRECURSOR >gi_282837_pir__S26953 photosystem II 22K protein precursor - spinach >gi_21307_emb_CAA48557_ (X68552) 22kD-protein of PSII [Spinacia oleracea] >gi_260917_bbs_119338 (S49864)

photosystem II 22 kda polypeptide [spinach, Peptide, 274 aa] [Spinacia oleracea]

Seq. No.	385253
Contig ID	184_1.R1084
5'-most EST	LIB3434-048-P1-K1-C6
Method	BLASTX
NCBI GI	g3915008
BLAST score	876
E value	3.0e-94
Match length	199
% identity	85
NCBI Description	SUPEROXIDE DISMUTASE [CU-ZN], CHLOROPLAST PRECURSOR >gi_1805502_dbj_BAA12745.1_ (D85239) superoxide dismutase precusor [Oryza sativa]

Seq. No.	385254
Contig ID	185_1.R1084
5'-most EST	g4878192
Method	BLASTX
NCBI GI	g2073375
BLAST score	1815
E value	0.0e+00
Match length	342
% identity	100
NCBI Description	(D85317) farnesyl pyrophosphate synthase [Oryza sativa] >gi_4063829_dbj_BAA36276_ (AB021747) farnesyl diphosphate synthase [Oryza sativa]

Seq. No.	385255
Contig ID	186_1.R1084
5'-most EST	LIB3432-040-P1-K1-G4
Method	BLASTX
NCBI GI	g733454
BLAST score	1260
E value	1.0e-139
Match length	283
% identity	84
NCBI Description	(U23188) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	385256
Contig ID	186_4.R1084
5'-most EST	uC-osflcyp026h05b1
Method	BLASTX
NCBI GI	g100573
BLAST score	428
E value	2.0e-60
Match length	149
% identity	75
NCBI Description	chlorophyll a/b-binding protein CP29 precursor - barley >gi_18958_emb_CAA44777_ (X63052) Precursor of CP29, core chlorophyll a/b binding (CAB) protein of photosystem II (PSII) [Hordeum vulgare] >gi_445122_prf__1908428A chlorophyll a/b-binding protein [Hordeum vulgare]

Seq. No.	385257

Contig ID	186_5.R1084
5'-most EST	LIB3432-024-P1-K1-E12
Method	BLASTX
NCBI GI	g733456
BLAST score	418
E value	9.0e-45
Match length	135
% identity	70
NCBI Description	(U23189) chlorophyll a/b-binding apoprotein CP26 precursor [Zea mays]

Seq. No.	385258
Contig ID	188_1.R1084
5'-most EST	g4106693
Method	BLASTX
NCBI GI	g4106694
BLAST score	2544
E value	0.0e+00
Match length	496
% identity	100
NCBI Description	(D85751) glutathione reductase [Oryza sativa] >gi_4153883_dbj_BAA37092.1_ (AB009592) cytosolic glutathione reductase [Oryza sativa]

Seq. No.	385259
Contig ID	189_1.R1084
5'-most EST	g4666286
Method	BLASTX
NCBI GI	g4666287
BLAST score	2124
E value	0.0e+00
Match length	435
% identity	96
NCBI Description	(D85764) cytosolic monodehydroascorbate reductase [Oryza sativa]

Seq. No.	385260
Contig ID	194_1.R1084
5'-most EST	LIB3434-033-P1-K1-G11
Method	BLASTX
NCBI GI	g3334144
BLAST score	1333
E value	1.0e-147
Match length	257
% identity	100
NCBI Description	G1/S-SPECIFIC CYCLIN C-TYPE >gi_1695698_dbj_BAA13181_ (D86925) C-type cyclin [Oryza sativa]

Seq. No.	385261
Contig ID	196_1.R1084
5'-most EST	g2580439
Method	BLASTX
NCBI GI	g2580440
BLAST score	1457
E value	1.0e-162
Match length	349
% identity	83

NCBI Description	(D87261) PCF2 [Oryza sativa]
Seq. No.	385262
Contig ID	197_1.R1084
5'-most EST	LIB3477-009-P1-K1-G4
Method	BLASTX
NCBI GI	g3913653
BLAST score	1882
E value	0.0e+00
Match length	365
% identity	96
NCBI Description	FERREDOXIN--NADP REDUCTASE, EMBRYO ISOZYME PRECURSOR (FNR) >gi_1778686_dbj_BAA13417_ (D87547) precursor ferredoxin-NADP+ oxidoreductase [Oryza sativa]
Seq. No.	385263
Contig ID	198_1.R1084
5'-most EST	g2443401
Method	BLASTX
NCBI GI	g2443402
BLAST score	4649
E value	0.0e+00
Match length	937
% identity	96
NCBI Description	(D87745) orthophosphate dikinase [Oryza sativa] >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase [Oryza sativa]
Seq. No.	385264
Contig ID	198_2.R1084
5'-most EST	g3550548
Method	BLASTX
NCBI GI	g3550549
BLAST score	4472
E value	0.0e+00
Match length	887
% identity	98
NCBI Description	(AJ004965) cytosolic pyruvate orthophosphate dikinase [Oryza sativa subsp. indica]
Seq. No.	385265
Contig ID	198_5.R1084
5'-most EST	g2312415
Method	BLASTX
NCBI GI	g2443402
BLAST score	336
E value	3.0e-61
Match length	151
% identity	85
NCBI Description	(D87745) orthophosphate dikinase [Oryza sativa] >gi_2443405_dbj_BAA22420_ (D87952) orthophosphate dikinase [Oryza sativa]
Seq. No.	385266
Contig ID	199_1.R1084
5'-most EST	uC-osflcyp011d05b1
Method	BLASTX

NCBI GI	g2723471
BLAST score	2586
E value	0.0e+00
Match length	488
% identity	100
NCBI Description	(D87819) sucrose transporter [Oryza sativa]

Seq. No.	385267
Contig ID	200_1.R1084
5'-most EST	g1669572
Method	BLASTX
NCBI GI	g1669573
BLAST score	1577
E value	1.0e-176
Match length	303
% identity	100
NCBI Description	(D88399) endosperm kinase [Oryza sativa]

Seq. No.	385268
Contig ID	201_1.R1084
5'-most EST	g5038745
Method	BLASTX
NCBI GI	g2605617
BLAST score	901
E value	4.0e-97
Match length	239
% identity	74
NCBI Description	(D88617) OSMYB1 [Oryza sativa]

Seq. No.	385269
Contig ID	201_3.R1084
5'-most EST	uC-osrocyp029e01b1
Method	BLASTX
NCBI GI	g1430846
BLAST score	348
E value	1.0e-32
Match length	129
% identity	38
NCBI Description	(X99210) myb-related transcription factor [Lycopersicon esculentum]

Seq. No.	385270
Contig ID	206_1.R1084
5'-most EST	g2280720
Method	BLASTX
NCBI GI	g6014901
BLAST score	571
E value	1.0e-58
Match length	114
% identity	100
NCBI Description	DEFENDER AGAINST CELL DEATH 1 (DAD-1) (DEFENDER AGAINST APOPTOTIC DEATH 1 PROTEIN) >gi_2723473_dbj_BAA24072_ (D89726) defender against apoptotic death 1 protein [Oryza sativa] >gi_2723883_dbj_BAA24104_ (D89727) defender against apoptotic death 1 protein [Oryza sativa]

Seq. No.	385271

Contig ID	207_1.R1084
5'-most EST	g3762787
Method	BLASTX
NCBI GI	g3868758
BLAST score	806
E value	1.0e-160
Match length	418
% identity	77
NCBI Description	(D89802) elongation factor 1B gamma [Oryza sativa]

Seq. No.	385272
Contig ID	207_2.R1084
5'-most EST	LIB3431-058-P1-K1-D10
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	3.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	385273
Contig ID	207_3.R1084
5'-most EST	LIB3432-015-P1-K1-F2
Method	BLASTX
NCBI GI	g1617206
BLAST score	321
E value	3.0e-29
Match length	73
% identity	77
NCBI Description	(Z72489) CP12 [Pisum sativum]

Seq. No.	385274
Contig ID	207_4.R1084
5'-most EST	LIB3431-047-P1-K1-E12
Method	BLASTX
NCBI GI	g1617197
BLAST score	304
E value	2.0e-27
Match length	76
% identity	76
NCBI Description	(Z72488) CP12 [Nicotiana tabacum]

Seq. No.	385275
Contig ID	207_9.R1084
5'-most EST	LIB3432-050-P1-K1-F12

Seq. No.	385276
Contig ID	208_1.R1084
5'-most EST	g4879418
Method	BLASTX
NCBI GI	g1815660
BLAST score	283
E value	2.0e-50
Match length	155
% identity	73
NCBI Description	(U83669) low molecular mass heat shock protein Oshsp17.3

[Oryza sativa]

Seq. No.	385277
Contig ID	208_2.R1084
5'-most EST	g1213072
Method	BLASTX
NCBI GI	g2119194
BLAST score	281
E value	8.0e-47
Match length	152
% identity	74
NCBI Description	low-molecular-weight heat-shock protein - rice >gi_1815662 (U83670) low molecular mass heat shock protein Oshsp18.0 [Oryza sativa]

Seq. No.	385278
Contig ID	208_3.R1084
5'-most EST	g2801352
Method	BLASTX
NCBI GI	g2119194
BLAST score	606
E value	2.0e-68
Match length	148
% identity	91
NCBI Description	low-molecular-weight heat-shock protein - rice >gi_1815662 (U83670) low molecular mass heat shock protein Oshsp18.0 [Oryza sativa]

Seq. No.	385279
Contig ID	208_4.R1084
5'-most EST	g4311803
Method	BLASTX
NCBI GI	g2119194
BLAST score	350
E value	1.0e-51
Match length	139
% identity	84
NCBI Description	low-molecular-weight heat-shock protein - rice >gi_1815662 (U83670) low molecular mass heat shock protein Oshsp18.0 [Oryza sativa]

Seq. No.	385280
Contig ID	208_5.R1084
5'-most EST	g3760203
Method	BLASTX
NCBI GI	g1815664
BLAST score	393
E value	7.0e-38
Match length	83
% identity	92
NCBI Description	(U83671) low molecular mass heat shock protein Oshsp17.7 [Oryza sativa]

Seq. No.	385281
Contig ID	209_1.R1084
5'-most EST	g1255684
Method	BLASTX

NCBI GI	g2499819
BLAST score	2396
E value	0.0e+00
Match length	509
% identity	91
NCBI Description	ASPARTIC PROTEINASE ORYZASIN 1 PRECURSOR >gi_2130068_pir__S66516 aspartic proteinase 1 precursor - rice >gi_1030715_dbj_BAA06876_ (D32165) aspartic protease [Oryza sativa] >gi_1711289_dbj_BAA06875_ (D32144) aspartic protease [Oryza sativa]

Seq. No.	385282
Contig ID	209_2.R1084
5'-most EST	g2798410
Method	BLASTX
NCBI GI	g169805
BLAST score	613
E value	2.0e-63
Match length	162
% identity	75
NCBI Description	(L12252) [Oryza sativa DNA fragment with a miscellaneous signal and an open reading frame.], gene product [Oryza sativa]

Seq. No.	385283
Contig ID	209_3.R1084
5'-most EST	g2798307
Method	BLASTX
NCBI GI	g232161
BLAST score	653
E value	4.0e-68
Match length	186
% identity	71
NCBI Description	19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN) >gi_68857_pir__WMRZ19 19K globulin precursor - rice >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor [Oryza sativa]

Seq. No.	385284
Contig ID	209_4.R1084
5'-most EST	g2797760
Method	BLASTX
NCBI GI	g232161
BLAST score	209
E value	9.0e-20
Match length	118
% identity	55
NCBI Description	19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN) >gi_68857_pir__WMRZ19 19K globulin precursor - rice >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor [Oryza sativa]

Seq. No.	385285
Contig ID	209_5.R1084
5'-most EST	g2799159
Method	BLASTX
NCBI GI	g232161

BLAST score	294
E value	3.0e-26
Match length	118
% identity	56
NCBI Description	19 KD GLOBULIN PRECURSOR (ALPHA-GLOBULIN) >gi_68857_pir__WMRZ19 19K globulin precursor - rice >gi_20159_emb_CAA45400_ (X63990) 19 kDa globulin precursor [Oryza sativa]

Seq. No.	385286
Contig ID	210_1.R1084
5'-most EST	LIB3434-055-P1-K1-G10
Method	BLASTX
NCBI GI	g2952328
BLAST score	1554
E value	1.0e-173
Match length	318
% identity	93
NCBI Description	(AF049889) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No.	385287
Contig ID	210_2.R1084
5'-most EST	g2280885
Method	BLASTX
NCBI GI	g2492612
BLAST score	1566
E value	1.0e-175
Match length	322
% identity	94
NCBI Description	1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (ACC OXIDASE) (ETHYLENE-FORMING ENZYME) (EFE) >gi_1076734_pir__S52712 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) - rice >gi_755773_emb_CAA59749_ (X85747) 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) [Oryza sativa]

Seq. No.	385288
Contig ID	210_3.R1084
5'-most EST	g569461
Method	BLASTX
NCBI GI	g2952326
BLAST score	1512
E value	1.0e-168
Match length	311
% identity	94
NCBI Description	(AF049888) 1-aminocyclopropane-1-carboxylate oxidase [Oryza sativa]

Seq. No.	385289
Contig ID	210_5.R1084
5'-most EST	g2311847
Method	BLASTN
NCBI GI	g755772
BLAST score	156
E value	3.0e-82
Match length	164

% identity	99
NCBI Description	O.sativa mRNA for 1-aminocyclopropane-1-carboxylate oxidase

Seq. No.	385290
Contig ID	211_1.R1084
5'-most EST	LIB3434-044-P1-K1-B1
Method	BLASTX
NCBI GI	g3915826
BLAST score	1328
E value	1.0e-147
Match length	294
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	385291
Contig ID	211_2.R1084
5'-most EST	g3768108
Method	BLASTX
NCBI GI	g3915826
BLAST score	666
E value	3.0e-77
Match length	168
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	385292
Contig ID	211_3.R1084
5'-most EST	g4879522
Method	BLASTX
NCBI GI	g3915826
BLAST score	283
E value	2.0e-28
Match length	133
% identity	59
NCBI Description	60S RIBOSOMAL PROTEIN L5

Seq. No.	385293
Contig ID	213_1.R1084
5'-most EST	g2310320
Method	BLASTX
NCBI GI	g4158221
BLAST score	1973
E value	0.0e+00
Match length	364
% identity	100
NCBI Description	(Y18624) reversibly glycosylated polypeptide [Oryza sativa]

Seq. No.	385294
Contig ID	214_1.R1084
5'-most EST	g4164415
Method	BLASTX
NCBI GI	g121446
BLAST score	7490
E value	0.0e+00
Match length	1538
% identity	94
NCBI Description	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE PRECURSOR

(FD-GOGAT) >gi_100877_pir__A38596 glutamate synthase (ferredoxin) (EC 1.4.7.1) - maize >gi_168477 (M59190) ferredoxin-dependent glutamate synthase [Zea mays]

Seq. No.	385295
Contig ID	215_1.R1084
5'-most EST	g568570
Method	BLASTX
NCBI GI	g4158219
BLAST score	1831
E value	0.0e+00
Match length	347
% identity	100
NCBI Description	(Y18623) amylogenin [Oryza sativa]

Seq. No.	385296
Contig ID	217_1.R1084
5'-most EST	g4585705
Method	BLASTX
NCBI GI	g4585706
BLAST score	589
E value	1.0e-60
Match length	138
% identity	79
NCBI Description	(AJ238116) putative phospholipase A2 [Oryza sativa]

Seq. No.	385297
Contig ID	218_1.R1084
5'-most EST	g4585707
Method	BLASTX
NCBI GI	g4585708
BLAST score	802
E value	1.0e-85
Match length	153
% identity	96
NCBI Description	(AJ238117) putative phospholipase A2 [Oryza sativa]

Seq. No.	385298
Contig ID	219_1.R1084
5'-most EST	LIB3431-031-P1-K1-B9
Method	BLASTX
NCBI GI	g4138290
BLAST score	815
E value	4.0e-87
Match length	172
% identity	90
NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	385299
Contig ID	219_2.R1084
5'-most EST	g2798536
Method	BLASTX
NCBI GI	g4138290
BLAST score	245
E value	1.0e-20
Match length	49
% identity	100

NCBI Description	(AJ005841) thioredoxin M [Oryza sativa]

Seq. No.	385300
Contig ID	219_3.R1084
5'-most EST	LIB3431-048-P1-N1-C3
Method	BLASTN
NCBI GI	g4138289
BLAST score	203
E value	1.0e-110
Match length	323
% identity	91
NCBI Description	Oryza sativa mRNA for thioredoxin M

Seq. No.	385301
Contig ID	220_1.R1084
5'-most EST	g700466
Method	BLASTX
NCBI GI	g1174598
BLAST score	2189
E value	0.0e+00
Match length	426
% identity	97
NCBI Description	TUBULIN BETA CHAIN >gi_493708_dbj_BAA06381_ (D30716) beta-tubulin [Oryza sativa]

Seq. No.	385302
Contig ID	220_2.R1084
5'-most EST	g303841
Method	BLASTX
NCBI GI	g586078
BLAST score	2178
E value	0.0e+00
Match length	426
% identity	96
NCBI Description	TUBULIN BETA CHAIN >gi_1076736_pir__JC2518 beta-tubulin pTUB22 - rice >gi_303842_dbj_BAA02505_ (D13224) beta-tubulin [Oryza sativa]

Seq. No.	385303
Contig ID	220_3.R1084
5'-most EST	g493709
Method	BLASTX
NCBI GI	g1174600
BLAST score	2148
E value	0.0e+00
Match length	419
% identity	97
NCBI Description	TUBULIN BETA CHAIN >gi_493710_dbj_BAA06382_ (D30717) beta-tubulin [Oryza sativa]

Seq. No.	385304
Contig ID	220_4.R1084
5'-most EST	uC-osflcyp172f05b1
Method	BLASTX
NCBI GI	g398849
BLAST score	2202
E value	0.0e+00

Match length	430
% identity	97
NCBI Description	(X74656) beta-5 tubulin [Zea mays]

Seq. No.	385305
Contig ID	220_5.R1084
5'-most EST	g508575
Method	BLASTX
NCBI GI	g829169
BLAST score	2150
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	(L33263) beta-tubulin [Oryza sativa]

Seq. No.	385306
Contig ID	220_6.R1084
5'-most EST	uC-osflM202039d01b1
Method	BLASTN
NCBI GI	g508575
BLAST score	201
E value	1.0e-109
Match length	315
% identity	97
NCBI Description	Oryza sativa beta-tubulin mRNA

Seq. No.	385307
Contig ID	220_7.R1084
5'-most EST	g3766607
Method	BLASTX
NCBI GI	g4098329
BLAST score	410
E value	8.0e-57
Match length	134
% identity	83
NCBI Description	(U76895) beta-tubulin 4 [Triticum aestivum]

Seq. No.	385308
Contig ID	220_9.R1084
5'-most EST	g3759159
Method	BLASTN
NCBI GI	g460988
BLAST score	251
E value	1.0e-139
Match length	345
% identity	95
NCBI Description	O.sativa (Arborio) Beta Tubulin mRNA, clone OSTB-34

Seq. No.	385309
Contig ID	220_10.R1084
5'-most EST	uC-osflM202049d02b1
Method	BLASTX
NCBI GI	g135449
BLAST score	413
E value	1.0e-51
Match length	104
% identity	98

NCBI Description	TUBULIN BETA-1 CHAIN >gi_100932_pir__S14701 tubulin beta-1 chain - maize >gi_295851_emb_CAA37060_ (X52878) beta 1 tubulin [Zea mays]

Seq. No.	385310
Contig ID	220_15.R1084
5'-most EST	g4879875
Method	BLASTX
NCBI GI	g398845
BLAST score	273
E value	2.0e-24
Match length	54
% identity	91
NCBI Description	(X74654) beta3 tubulin [Zea mays]

Seq. No.	385311
Contig ID	220_16.R1084
5'-most EST	g4880145
Method	BLASTX
NCBI GI	g4415996
BLAST score	301
E value	1.0e-27
Match length	55
% identity	100
NCBI Description	(AF059290) beta-tubulin 4 [Eleusine indica]

Seq. No.	385312
Contig ID	222_1.R1084
5'-most EST	g4878898
Method	BLASTX
NCBI GI	g1419100
BLAST score	1244
E value	1.0e-137
Match length	240
% identity	97
NCBI Description	(Z27242) ACC synthase [Oryza sativa]

Seq. No.	385313
Contig ID	225_1.R1084
5'-most EST	uC-osflm202104e09b1
Method	BLASTX
NCBI GI	g113360
BLAST score	1655
E value	0.0e+00
Match length	365
% identity	91
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_ (X16296) alcohol dehydrogenase 1 [Oryza sativa]

Seq. No.	385314
Contig ID	225_2.R1084
5'-most EST	g3766682
Method	BLASTX
NCBI GI	g113377
BLAST score	1812
E value	0.0e+00

Match length	379
% identity	89
NCBI Description	ALCOHOL DEHYDROGENASE 2 >gi_82671_pir__A23084 alcohol dehydrogenase (EC 1.1.1.1) 2 - maize >gi_22137_emb_CAA26001_ (X01965) Adh2-N (aa 1-379) [Zea mays]

Seq. No.	385315
Contig ID	225_3.R1084
5'-most EST	LIB3434-062-P1-K1-C7
Method	BLASTX
NCBI GI	g899610
BLAST score	260
E value	3.0e-22
Match length	62
% identity	81
NCBI Description	(U29383) acidic ribosomal protein P2 [Zea mays]

Seq. No.	385316
Contig ID	225_4.R1084
5'-most EST	LIB3433-041-P1-K1-B9
Method	BLASTX
NCBI GI	g113360
BLAST score	457
E value	3.0e-45
Match length	161
% identity	86
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_ (X16296) alcohol dehydrogenase 1 [Oryza sativa]

Seq. No.	385317
Contig ID	225_5.R1084
5'-most EST	g2800777
Method	BLASTX
NCBI GI	g113360
BLAST score	212
E value	3.0e-32
Match length	99
% identity	76
NCBI Description	ALCOHOL DEHYDROGENASE 1 >gi_100652_pir__JQ0474 alcohol dehydrogenase (EC 1.1.1.1) 1 - rice >gi_20165_emb_CAA34363_ (X16296) alcohol dehydrogenase 1 [Oryza sativa]

Seq. No.	385318
Contig ID	226_1.R1084
5'-most EST	LIB3431-007-P1-K1-G6
Method	BLASTX
NCBI GI	g2624326
BLAST score	440
E value	3.0e-43
Match length	86
% identity	100
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	385319
Contig ID	226_2.R1084

5'-most EST	g1632373
Method	BLASTX
NCBI GI	g2293480
BLAST score	431
E value	4.0e-42
Match length	85
% identity	98
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385320
Contig ID	226_3.R1084
5'-most EST	g2196541
Method	BLASTX
NCBI GI	g2196542
BLAST score	639
E value	2.0e-66
Match length	121
% identity	100
NCBI Description	(AF001894) glycine-rich protein [Oryza sativa]

Seq. No.	385321
Contig ID	226_4.R1084
5'-most EST	LIB3433-019-P1-K1-C9
Method	BLASTX
NCBI GI	g2624326
BLAST score	318
E value	7.0e-29
Match length	68
% identity	94
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	385322
Contig ID	226_5.R1084
5'-most EST	g2799180
Method	BLASTN
NCBI GI	g2267592
BLAST score	227
E value	1.0e-124
Match length	276
% identity	99
NCBI Description	Oryza sativa glycine-rich RNA-binding protein mRNA, complete cds

Seq. No.	385323
Contig ID	226_6.R1084
5'-most EST	LIB3433-007-Q6-K1-C11
Method	BLASTX
NCBI GI	g2624326
BLAST score	407
E value	2.0e-39
Match length	79
% identity	100
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	385324
Contig ID	226_7.R1084
5'-most EST	uC-osflcyp109d01b1

Method	BLASTX
NCBI GI	g2293480
BLAST score	435
E value	1.0e-42
Match length	86
% identity	98
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385325
Contig ID	226_9.R1084
5'-most EST	uC-osflcyp067b02a1
Method	BLASTN
NCBI GI	g2331130
BLAST score	207
E value	1.0e-112
Match length	238
% identity	99
NCBI Description	Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds

Seq. No.	385326
Contig ID	226_10.R1084
5'-most EST	LIB3434-004-P1-K1-A2
Method	BLASTX
NCBI GI	g2293480
BLAST score	432
E value	9.0e-43
Match length	88
% identity	95
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385327
Contig ID	226_12.R1084
5'-most EST	g4969270
Method	BLASTX
NCBI GI	g2293480
BLAST score	271
E value	2.0e-25
Match length	65
% identity	95
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385328
Contig ID	226_15.R1084
5'-most EST	g1631442
Method	BLASTX
NCBI GI	g2624326
BLAST score	255
E value	8.0e-22
Match length	76
% identity	74
NCBI Description	(AJ002893) OsGRP1 [Oryza sativa]

Seq. No.	385329
Contig ID	226_16.R1084
5'-most EST	uC-osflM202097b01b1
Method	BLASTX

NCBI GI	g2331133
BLAST score	233
E value	3.0e-20
Match length	71
% identity	82
NCBI Description	(AF010580) glycine-rich protein [Oryza sativa]

Seq. No.	385330
Contig ID	226_20.R1084
5'-most EST	LIB3479-004-Q6-K1-H11
Method	BLASTX
NCBI GI	g2293480
BLAST score	220
E value	4.0e-18
Match length	65
% identity	72
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385331
Contig ID	226_21.R1084
5'-most EST	LIB3434-021-P1-K1-C11
Method	BLASTX
NCBI GI	g2293480
BLAST score	199
E value	2.0e-15
Match length	54
% identity	78
NCBI Description	(AF011331) glycine-rich protein [Oryza sativa]

Seq. No.	385332
Contig ID	227_1.R1084
5'-most EST	LIB3431-029-P1-K1-E8
Method	BLASTX
NCBI GI	g2624328
BLAST score	542
E value	4.0e-55
Match length	118
% identity	90
NCBI Description	(AJ002894) OsGRP2 [Oryza sativa]

Seq. No.	385333
Contig ID	229_1.R1084
5'-most EST	g20172
Method	BLASTX
NCBI GI	g113690
BLAST score	2272
E value	0.0e+00
Match length	426
% identity	98
NCBI Description	ALPHA-AMYLASE ISOZYME C2 PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_100658_pir__S19990 alpha-amylase (EC 3.2.1.1) - rice >gi_20173_emb_CAA45903_ (X64619) alpha-amylase [Oryza sativa]

Seq. No.	385334
Contig ID	231_1.R1084
5'-most EST	g1314048

Method	BLASTX
NCBI GI	g2506139
BLAST score	2394
E value	0.0e+00
Match length	518
% identity	92
NCBI Description	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) >gi_1314049_emb_CAA91901_ (Z67962) archain/delta-COP [Oryza sativa]

Seq. No.	385335
Contig ID	234_1.R1084
5'-most EST	LIB3434-024-P1-K1-E11
Method	BLASTX
NCBI GI	g115511
BLAST score	762
E value	6.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN >gi_231682_sp_P29612_CALM_ORYSA CALMODULIN >gi_71682_pir__MCBH calmodulin - barley >gi_100666_pir__S24952 calmodulin 1 (clone lambda DASH) - rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] >gi_506850 (L20691) calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi_1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] >gi_1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestivum] >gi_3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf__1604476A calmodulin [Hordeum vulgare var. distichum] >gi_1583768_prf__2121384B calmodulin [Glycine max]

Seq. No.	385336
Contig ID	234_2.R1084
5'-most EST	g2809480
Method	BLASTX
NCBI GI	g2809481
BLAST score	761
E value	8.0e-81
Match length	149
% identity	100
NCBI Description	(AF042839) calmodulin [Oryza sativa]

Seq. No.	385337
Contig ID	234_3.R1084
5'-most EST	LIB3432-019-P1-K1-E12

Method	BLASTX
NCBI GI	g115511
BLAST score	762
E value	6.0e-81
Match length	149
% identity	100
NCBI Description	CALMODULIN >gi_231682_sp_P29612_CALM_ORYSA CALMODULIN >gi_71682_pir__MCBH calmodulin - barley >gi_100666_pir__S24952 calmodulin 1 (clone lambda DASH) - rice >gi_20188_emb_CAA78287_ (Z12827) calmodulin [Oryza sativa] >gi_167008 (M27303) calmodulin [Hordeum vulgare] >gi_170072 (L01431) calmodulin [Glycine max] >gi_310315 (L18913) calmodulin [Oryza sativa] >gi_506850 (L20691) calmodulin [Vigna radiata] >gi_1478370_bbs_176852 (S81594) auxin-regulated calmodulin, arCaM [Vigna radiata=mung bean, Wilczek, seedling, Peptide, 149 aa] [Vigna radiata] >gi_1742989_emb_CAA70982_ (Y09853) CaM protein [Cicer arietinum] >gi_1754991 (U48242) calmodulin TaCaM1-1 [Triticum aestivum] >gi_1754993 (U48688) calmodulin TaCaM1-2 [Triticum aestivum] >gi_1754995 (U48689) calmodulin TaCaM1-3 [Triticum aestivum] >gi_1755003 (U48693) calmodulin TaCaM3-1 [Triticum aestivum] >gi_1755005 (U49103) calmodulin TaCaM3-2 [Triticum aestivum] >gi_1755007 (U49104) calmodulin TaCaM3-3 [Triticum aestivum] >gi_1755009 (U49105) calmodulin TaCaM4-1 [Triticum aestivum] >gi_3617842 (AF042840) calmodulin [Oryza sativa] >gi_226769_prf__1604476A calmodulin [Hordeum vulgare var. distichum] >gi_1583768_prf__2121384B calmodulin [Glycine max]

Seq. No.	385338
Contig ID	234_4.R1084
5'-most EST	LIB3474-009-P1-K1-E4
Method	BLASTX
NCBI GI	g100665
BLAST score	750
E value	9.0e-80
Match length	147
% identity	99
NCBI Description	calmodulin 2 (clone lambda DASH) - rice >gi_20190_emb_CAA78288_ (Z12828) calmodulin [Oryza sativa] >gi_310313 (L18914) calmodulin [Oryza sativa]

Seq. No.	385339
Contig ID	236_1.R1084
5'-most EST	g20193
Method	BLASTX
NCBI GI	g266410
BLAST score	2217
E value	0.0e+00
Match length	424
% identity	100
NCBI Description	CDC2+/CDC28-RELATED PROTEIN KINASE R2 >gi_82507_pir__S13934 protein kinase (EC 2.7.1.37) chain cdc2/cdc28 homolog - rice >gi_20194_emb_CAA41172_ (X58194) cdc2+/CDC28-related protein kinase [Oryza sativa]

Seq. No.	385340
Contig ID	237_1.R1084
5'-most EST	g587497
Method	BLASTX
NCBI GI	g1705734
BLAST score	2528
E value	0.0e+00
Match length	519
% identity	95
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 2 (CDPK 2) >gi_1362176_pir__S56652 probable calcium-dependent protein kinase (clone OSCPK2) - rice >gi_587498_emb_CAA57157_ (X81394) calcium-dependent protein kinase [Oryza sativa]

Seq. No.	385341
Contig ID	238_1.R1084
5'-most EST	uC-osrocyp032f10b1
Method	BLASTX
NCBI GI	g1705735
BLAST score	2787
E value	0.0e+00
Match length	542
% identity	98
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11) >gi_1362175_pir__S56651 probable calcium-dependent protein kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156_ (X81393) calcium-dependent protein kinase [Oryza sativa]

Seq. No.	385342
Contig ID	238_2.R1084
5'-most EST	LIB3433-011-Q6-K1-C4
Method	BLASTX
NCBI GI	g1705735
BLAST score	397
E value	3.0e-38
Match length	79
% identity	95
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 11 (CDPK 11) >gi_1362175_pir__S56651 probable calcium-dependent protein kinase (clone OSCPK11) - rice >gi_587500_emb_CAA57156_ (X81393) calcium-dependent protein kinase [Oryza sativa]

Seq. No.	385343
Contig ID	240_1.R1084
5'-most EST	g984755
Method	BLASTX
NCBI GI	g984756
BLAST score	1538
E value	1.0e-171
Match length	379
% identity	81
NCBI Description	(Z54153) chilling-inducible protein [Oryza sativa]

Seq. No.	385344
Contig ID	241_1.R1084
5'-most EST	g454268
Method	BLASTX

NCBI GI	g383024
BLAST score	1494
E value	1.0e-166
Match length	303
% identity	90
NCBI Description	chitinase [Oryza sativa]

Seq. No.	385345
Contig ID	245_1.R1084
5'-most EST	g1694891
Method	BLASTX
NCBI GI	g3913236
BLAST score	2067
E value	0.0e+00
Match length	418
% identity	96
NCBI Description	G2/MITOTIC-SPECIFIC CYCLIN 2 (B-LIKE CYCLIN) (CYCOS2) >gi_1694892_emb_CAA57556_ (X82036) cyclin [Oryza sativa]

Seq. No.	385346
Contig ID	248_1.R1084
5'-most EST	g1177319
Method	BLASTX
NCBI GI	g1177320
BLAST score	1201
E value	1.0e-132
Match length	230
% identity	100
NCBI Description	(X89891) EFA27 for EF hand, abscisic acid, 27kD [Oryza sativa]

Seq. No.	385347
Contig ID	250_1.R1084
5'-most EST	g5405277
Method	BLASTX
NCBI GI	g2924247
BLAST score	777
E value	1.0e-143
Match length	261
% identity	95
NCBI Description	(Y07782) expansin [Oryza sativa]

Seq. No.	385348
Contig ID	253_1.R1084
5'-most EST	g427880
Method	BLASTX
NCBI GI	g2130073
BLAST score	1836
E value	0.0e+00
Match length	358
% identity	100
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No. 385349

Contig ID	253_2.R1084
5'-most EST	uC-osroM202036h10b1
Method	BLASTX
NCBI GI	g113622
BLAST score	1828
E value	0.0e+00
Match length	358
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME >gi_68197_pir__ADRZY fructose-bisphosphate aldolase (EC 4.1.2.13), cytosolic - rice >gi_20204_emb_CAA37290_ (X53130) fructose-diphosphate aldolase (AA 1-358) [Oryza sativa]

Seq. No.	385350
Contig ID	253_3.R1084
5'-most EST	uC-osf1cyp009c12b1
Method	BLASTX
NCBI GI	g3023751
BLAST score	1846
E value	0.0e+00
Match length	441
% identity	82
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	385351
Contig ID	253_4.R1084
5'-most EST	LIB3434-026-P1-K1-C9
Method	BLASTX
NCBI GI	g1708032
BLAST score	741
E value	1.0e-78
Match length	139
% identity	100
NCBI Description	GRAVITY SPECIFIC PROTEIN GSC 233 >gi_298743_bbs_127936 (S56877) gravity specific cDNA {clone GSC233} [Oryza sativa, Nipponbare, suspension callus, Peptide, 139 aa] [Oryza sativa] >gi_399662_dbj_BAA01911_ (D11137) This gene product is expressed specifically in callus. [Oryza sativa]

Seq. No.	385352
Contig ID	253_5.R1084
5'-most EST	g3761161
Method	BLASTX
NCBI GI	g218157
BLAST score	271
E value	2.0e-23
Match length	78
% identity	57
NCBI Description	(D13512) cytoplasmic aldolase [Oryza sativa]

Seq. No.	385353
Contig ID	253_6.R1084

5'-most EST	LIB3434-044-P1-K1-E6
Method	BLASTX
NCBI GI	g3023751
BLAST score	1177
E value	1.0e-129
Match length	257
% identity	67
NCBI Description	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) >gi_1076772_pir__S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat >gi_854626_emb_CAA60505_ (X86903) peptidylprolyl isomerase [Triticum aestivum]

Seq. No.	385354
Contig ID	253_7.R1084
5'-most EST	g2800416
Method	BLASTX
NCBI GI	g2130073
BLAST score	194
E value	6.0e-17
Match length	62
% identity	78
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	385355
Contig ID	253_9.R1084
5'-most EST	uC-osf1M202082c12b1
Method	BLASTX
NCBI GI	g2130073
BLAST score	491
E value	2.0e-49
Match length	153
% identity	71
NCBI Description	fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic - rice >gi_786178_dbj_BAA08845_ (D50307) aldolase C-1 [Oryza sativa] >gi_790970_dbj_BAA08830_ (D50301) aldolase C-1 [Oryza sativa]

Seq. No.	385356
Contig ID	254_1.R1084
5'-most EST	g1707639
Method	BLASTX
NCBI GI	g1707640
BLAST score	2818
E value	0.0e+00
Match length	553
% identity	96
NCBI Description	(X98355) transcription factor GAMyb [Oryza sativa]

Seq. No.	385357
Contig ID	255_1.R1084
5'-most EST	LIB3479-006-Q6-K1-B9
Method	BLASTX
NCBI GI	g121475

BLAST score	1337
E value	0.0e+00
Match length	500
% identity	95
NCBI Description	GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin II precursor - rice >gi_20219_emb_CAA29151_ (X05663) glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664) glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza sativa] >gi_556399 (M28156) glutelin [Oryza sativa]

Seq. No.	385358
Contig ID	255_2.R1084
5'-most EST	LIB3479-010-Q6-K1-H3
Method	BLASTX
NCBI GI	g121469
BLAST score	2414
E value	0.0e+00
Match length	499
% identity	94
NCBI Description	GLUTELIN TYPE I PRECURSOR (CLONE PREE 61) >gi_82474_pir__S06350 glutelin type I precursor (clone pREE61) - rice >gi_20215_emb_CAA29149_ (X05661) glutelin [Oryza sativa]

Seq. No.	385359
Contig ID	255_3.R1084
5'-most EST	LIB3479-001-Q6-K1-G7
Method	BLASTX
NCBI GI	g556403
BLAST score	1188
E value	0.0e+00
Match length	493
% identity	73
NCBI Description	(L36819) glutelin [Oryza sativa]

Seq. No.	385360
Contig ID	255_4.R1084
5'-most EST	g2798788
Method	BLASTX
NCBI GI	g225174
BLAST score	502
E value	1.0e-50
Match length	119
% identity	91
NCBI Description	glutelin precursor [Oryza sativa]

Seq. No.	385361
Contig ID	255_6.R1084
5'-most EST	LIB3479-005-Q6-K1-G1
Method	BLASTX
NCBI GI	g100679
BLAST score	675
E value	1.0e-70
Match length	197
% identity	54
NCBI Description	glutelin 2 precursor - rice

Seq. No.	385362
Contig ID	255_8.R1084
5'-most EST	uC-osroM202022b03b1
Method	BLASTX
NCBI GI	g1346804
BLAST score	623
E value	1.0e-64
Match length	128
% identity	86
NCBI Description	PROFILIN 2 >gi_1008443_emb_CAA61944_ (X89826) profilin [Triticum aestivum]

Seq. No.	385363
Contig ID	255_9.R1084
5'-most EST	LIB3479-011-Q6-K1-C6
Method	BLASTX
NCBI GI	g121475
BLAST score	240
E value	3.0e-27
Match length	68
% identity	100
NCBI Description	GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin II precursor - rice >gi_20219_emb_CAA29151_ (X05663) glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664) glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza sativa] >gi_556399 (M28156) glutelin [Oryza sativa]

Seq. No.	385364
Contig ID	255_16.R1084
5'-most EST	g2798888
Method	BLASTX
NCBI GI	g556401
BLAST score	254
E value	1.0e-21
Match length	99
% identity	63
NCBI Description	(M28159) glutelin [Oryza sativa]

Seq. No.	385365
Contig ID	255_17.R1084
5'-most EST	g2798433
Method	BLASTX
NCBI GI	g121475
BLAST score	237
E value	1.0e-19
Match length	80
% identity	65
NCBI Description	GLUTELIN TYPE II PRECURSOR >gi_100678_pir__A34332 glutelin II precursor - rice >gi_20219_emb_CAA29151_ (X05663) glutelin [Oryza sativa] >gi_20221_emb_CAA29152_ (X05664) glutelin [Oryza sativa] >gi_20236_emb_CAA68683_ (Y00687) glutelin [Oryza sativa] >gi_556398 (M28158) glutelin [Oryza sativa] >gi_556399 (M28156) glutelin [Oryza sativa]

Seq. No.	385366

Contig ID	255_18.R1084
5'-most EST	g5005116
Method	BLASTX
NCBI GI	g225174
BLAST score	344
E value	2.0e-32
Match length	67
% identity	100
NCBI Description	glutelin precursor [Oryza sativa]

Seq. No.	385367
Contig ID	255_19.R1084
5'-most EST	LIB3479-012-Q6-K1-A12
Method	BLASTX
NCBI GI	g82473
BLAST score	254
E value	3.0e-35
Match length	140
% identity	37
NCBI Description	glutelin precursor - rice >gi_169791 (M17513) glutelin [Oryza sativa]

Seq. No.	385368
Contig ID	255_40.R1084
5'-most EST	g2797054
Method	BLASTN
NCBI GI	g20205
BLAST score	99
E value	2.0e-48
Match length	152
% identity	98
NCBI Description	Rice mRNA for glutelin (pCSW-321)

Seq. No.	385369
Contig ID	255_41.R1084
5'-most EST	g2798907
Method	BLASTN
NCBI GI	g20216
BLAST score	109
E value	1.0e-54
Match length	136
% identity	94
NCBI Description	Rice mRNA for glutelin type I (clone pREE 103)

Seq. No.	385370
Contig ID	260_1.R1084
5'-most EST	LIB3479-002-Q6-K2-G4
Method	BLASTX
NCBI GI	g121476
BLAST score	2186
E value	0.0e+00
Match length	489
% identity	87
NCBI Description	GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833) precursor (AA -24 to 475) [Oryza sativa]

Seq. No.	385371
Contig ID	260_2.R1084
5'-most EST	LIB3479-002-Q6-K1-G4
Method	BLASTX
NCBI GI	g121477
BLAST score	2426
E value	0.0e+00
Match length	500
% identity	93
NCBI Description	GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]

Seq. No.	385372
Contig ID	260_4.R1084
5'-most EST	g2797580
Method	BLASTX
NCBI GI	g544399
BLAST score	330
E value	2.0e-30
Match length	189
% identity	56
NCBI Description	GLUTELIN TYPE-B 1 PRECURSOR >gi_82472_pir__S04073 glutelin precursor (clone pREEK1) - rice >gi_100677_pir__S17762 glutelin gluB-1 precursor - rice >gi_20210_emb_CAA38212_ (X54314) glutelin [Oryza sativa] >gi_20223_emb_CAA32706_ (X14568) preglutelin [Oryza sativa]

Seq. No.	385373
Contig ID	260_9.R1084
5'-most EST	g2799035
Method	BLASTX
NCBI GI	g121477
BLAST score	355
E value	2.0e-33
Match length	120
% identity	66
NCBI Description	GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]

Seq. No.	385374
Contig ID	260_12.R1084
5'-most EST	g2798376
Method	BLASTX
NCBI GI	g121476
BLAST score	664
E value	2.0e-69
Match length	229
% identity	68
NCBI Description	GLUTELIN PRECURSOR >gi_82470_pir__S07640 glutelin precursor (clone 5b-1) - rice >gi_20232_emb_CAA33838_ (X15833) precursor (AA -24 to 475) [Oryza sativa]

Seq. No.	385375

Contig ID	260_13.R1084
5'-most EST	g2798893
Method	BLASTN
NCBI GI	g20226
BLAST score	133
E value	3.0e-68
Match length	262
% identity	89
NCBI Description	Rice mRNA for preproglutelin

Seq. No.	385376
Contig ID	260_18.R1084
5'-most EST	g2797149
Method	BLASTX
NCBI GI	g121477
BLAST score	392
E value	7.0e-38
Match length	155
% identity	62
NCBI Description	GLUTELIN PRECURSOR >gi_82471_pir__S05443 glutelin precursor (clone lambda-RG21) - rice >gi_20227_emb_CAA32566_ (X14393) preprolglutelin (AA -24 to 476) [Oryza sativa] >gi_226767_prf__1604474A glutelin [Oryza sativa]

Seq. No.	385377
Contig ID	265_1.R1084
5'-most EST	g426712
Method	BLASTN
NCBI GI	g425800
BLAST score	284
E value	1.0e-158
Match length	311
% identity	98
NCBI Description	Rice mRNA for glycine-rich protein (gene name AD489), partial cds

Seq. No.	385378
Contig ID	265_2.R1084
5'-most EST	g3762677
Method	BLASTX
NCBI GI	g3420055
BLAST score	752
E value	1.0e-79
Match length	173
% identity	83
NCBI Description	(AC004680) cyclophilin [Arabidopsis thaliana]

Seq. No.	385379
Contig ID	265_3.R1084
5'-most EST	g871921
Method	BLASTN
NCBI GI	g425800
BLAST score	202
E value	1.0e-109
Match length	245
% identity	96
NCBI Description	Rice mRNA for glycine-rich protein (gene name AD489),

partial cds

Seq. No.	385380
Contig ID	266_1.R1084
5'-most EST	g1841703
Method	BLASTX
NCBI GI	g3915070
BLAST score	2493
E value	0.0e+00
Match length	494
% identity	100
NCBI Description	HISTIDYL-TRNA SYNTHETASE (HISTIDINE--TRNA LIGASE) (HISRS) >gi_1841704_emb_CAB06653_ (Z85984) histidyl tRNA Synthetase [Oryza sativa]

Seq. No.	385381
Contig ID	267_1.R1084
5'-most EST	LIB3431-027-P1-K1-A3
Method	BLASTX
NCBI GI	g417103
BLAST score	636
E value	3.0e-66
Match length	127
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

Seq. No.	385382
Contig ID	267_2.R1084
5'-most EST	uC-osflcyp153e09b1
Method	BLASTX
NCBI GI	g2116601
BLAST score	440
E value	4.0e-47
Match length	126
% identity	82
NCBI Description	(AB003784) Histone H3 [Drosophila simulans]

Seq. No.	385383
Contig ID	267_3.R1084
5'-most EST	g2326783
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	385384
Contig ID	267_4.R1084
5'-most EST	g568549
Method	BLASTX
NCBI GI	g122085
BLAST score	546
E value	9.0e-56
Match length	127
% identity	87
NCBI Description	HISTONE H3 >gi_81641_pir__S06250 histone H3 - Arabidopsis thaliana >gi_82482_pir__S04099 histone H3 (variant H3R-21) - rice >gi_1362194_pir__S57626 histone H3 - maize >gi_20251_emb_CAA31969_ (X13678) histone H3 (AA 1-136) [Oryza sativa] >gi_20253_emb_CAA31970_ (X13680) histone H3 (AA 1-136) [Oryza sativa] >gi_168493 (M36658) histone H3 (H3C3) [Zea mays] >gi_168495 (M13378) histone H3 [Zea mays] >gi_168497 (M13379) histone H3 [Zea mays] >gi_168506 (M35388) histone H3 [Zea mays] >gi_169655 (M77493) histone H3 [Petroselinum crispum] >gi_169657 (M77494) histone H3 [Petroselinum crispum] >gi_169659 (M77495) histone H3 [Petroselinum crispum] >gi_387565 (M17130) histone H3 [Arabidopsis thaliana] >gi_387567 (M17131) histone H3 [Arabidopsis thaliana] >gi_886738_emb_CAA59111_ (X84377) histone 3 [Zea mays] >gi_1040764 (M35387) histone H3 [Arabidopsis thaliana] >gi_1314779 (U54827) histone H3 homolog [Brassica napus] >gi_1531754_emb_CAA57811_ (X82414) Histone H3 [Asparagus officinalis] >gi_1667592 (U77296) histone 3 [Oryza sativa] >gi_3249101 (AC003114) Match to histone H3 gene gb_M17131 and gb_M35387 from A. thaliana. ESTs gb_H76511 gb_H76255, gb_AA712452, gb_N65260 and gb_T42306 come from this gene. [Arabidopsis thaliana] >gi_5295939_dbj_BAA81840.1_ (AB026295) ESTs C74053(E30274),D15300(C0425),AU030134(E50667) correspond to a region of the predicted gene.; Similar to Asparagus officinalis mRNA for Histone H3.(X82414) [Oryza sativa] >gi_5295940_dbj_BAA81841.1_ (AB026295) ESTs C74053(E30274),D15300(C0425),AU030134(E50667) correspond to a region of the predicted gene.; Similar to Asparagus

officinalis mRNA for Histone H3.(X82414) [Oryza sativa] >gi_225459_prf__1303352A histone H3 [Helicoverpa zea] >gi_225839_prf__1314298B histone H3 [Arabidopsis thaliana]

Seq. No.	385385
Contig ID	267_5.R1084
5'-most EST	LIB3434-010-P1-K1-B8
Method	BLASTX
NCBI GI	g122087
BLAST score	589
E value	8.0e-61
Match length	136
% identity	88
NCBI Description	HISTONE H3 >gi_81849_pir__S04520 histone H3 (clone pH3c-1) - alfalfa >gi_82609_pir__A26014 histone H3 - wheat >gi_19607_emb_CAA31964_ (X13673) histone H3 (AA 1-136) [Medicago sativa] >gi_19609_emb_CAA31965_ (X13674) histone H3 (AA 1-136) [Medicago sativa] >gi_21797_emb_CAA25451_ (X00937) H3 histone [Triticum aestivum] >gi_488565 (U09459) histone H3.1 [Medicago sativa] >gi_2565419 (AF026803) histone H3 [Onobrychis viciifolia]

Seq. No.	385386
Contig ID	267_8.R1084
5'-most EST	uC-osflcyp153a07a1
Method	BLASTX
NCBI GI	g70748
BLAST score	154
E value	3.0e-10
Match length	34
% identity	88
NCBI Description	histone H3, embryonic - sea urchin (Strongylocentrotus purpuratus)

Seq. No.	385387
Contig ID	268_1.R1084
5'-most EST	g5006848
Method	BLASTX
NCBI GI	g5006849
BLAST score	900
E value	6.0e-97
Match length	269
% identity	66
NCBI Description	(AF145726) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	385388
Contig ID	268_2.R1084
5'-most EST	g6634482
Method	BLASTX
NCBI GI	g1235565
BLAST score	907
E value	9.0e-98
Match length	285
% identity	64
NCBI Description	(X96681) DNA-binding protein [Oryza sativa]

Seq. No.	385389
Contig ID	269_1.R1084
5'-most EST	uC-osf1cyp039f03b1
Method	BLASTX
NCBI GI	g417154
BLAST score	2117
E value	0.0e+00
Match length	444
% identity	93
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	385390
Contig ID	269_2.R1084
5'-most EST	uC-osrocyp012b01b1
Method	BLASTX
NCBI GI	g417154
BLAST score	492
E value	1.0e-78
Match length	194
% identity	87
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	385391
Contig ID	269_4.R1084
5'-most EST	g2798797
Method	BLASTN
NCBI GI	g425794
BLAST score	277
E value	1.0e-154
Match length	335
% identity	97
NCBI Description	Rice mRNA for heat shock protein 82 (gene name AD167), partial cds

Seq. No.	385392
Contig ID	269_5.R1084
5'-most EST	g3760353
Method	BLASTX
NCBI GI	g417154
BLAST score	468
E value	1.0e-59
Match length	153
% identity	81
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]

Seq. No.	385393
Contig ID	269_9.R1084
5'-most EST	g2800623

Method	BLASTN
NCBI GI	g425794
BLAST score	186
E value	1.0e-100
Match length	332
% identity	91
NCBI Description	Rice mRNA for heat shock protein 82 (gene name AD167), partial cds

Seq. No.	385394
Contig ID	269_10.R1084
5'-most EST	g2798611
Method	BLASTX
NCBI GI	g547683
BLAST score	418
E value	1.0e-50
Match length	132
% identity	84
NCBI Description	HEAT SHOCK COGNATE PROTEIN 80 >gi_170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] >gi_445601_prf__1909348A heat shock protein hsp80 [Lycopersicon esculentum]

Seq. No.	385395
Contig ID	270_1.R1084
5'-most EST	g2182028
Method	BLASTX
NCBI GI	g2182029
BLAST score	1986
E value	0.0e+00
Match length	373
% identity	100
NCBI Description	(Y13437) shaggy-like kinase etha (OSKetha) [Oryza sativa]

Seq. No.	385396
Contig ID	271_1.R1084
5'-most EST	g1235566
Method	BLASTX
NCBI GI	g1486503
BLAST score	690
E value	2.0e-72
Match length	200
% identity	72
NCBI Description	(U57641) LEA-like protein [Oryza sativa]

Seq. No.	385397
Contig ID	272_1.R1084
5'-most EST	g4716644
Method	BLASTX
NCBI GI	g2114207
BLAST score	504
E value	8.0e-51
Match length	98
% identity	100
NCBI Description	(D86744) glutaredoxin [Oryza sativa]

Seq. No.	385398

Contig ID	273_1.R1084
5'-most EST	LIB3431-031-P1-K1-A4
Method	BLASTX
NCBI GI	g417260
BLAST score	421
E value	8.0e-41
Match length	128
% identity	66
NCBI Description	LIGHT REGULATED PROTEIN PRECURSOR >gi_422003_pir__S33632 lir1 protein - rice >gi_20263_emb_CAA48706_ (X68807) light-regulated gene [Oryza sativa]

Seq. No.	385399
Contig ID	273_5.R1084
5'-most EST	g2799997
Method	BLASTN
NCBI GI	g20262
BLAST score	459
E value	0.0e+00
Match length	571
% identity	96
NCBI Description	O.sativa light-induced mRNA

Seq. No.	385400
Contig ID	273_10.R1084
5'-most EST	LIB3431-028-P1-K1-B3
Method	BLASTN
NCBI GI	g20262
BLAST score	268
E value	1.0e-148
Match length	397
% identity	96
NCBI Description	O.sativa light-induced mRNA

Seq. No.	385401
Contig ID	273_15.R1084
5'-most EST	LIB3431-047-P1-K1-A12
Method	BLASTN
NCBI GI	g20262
BLAST score	374
E value	0.0e+00
Match length	574
% identity	92
NCBI Description	O.sativa light-induced mRNA

Seq. No.	385402
Contig ID	273_16.R1084
5'-most EST	LIB3431-011-P1-K1-H12
Method	BLASTN
NCBI GI	g3273244
BLAST score	58
E value	7.0e-24
Match length	74
% identity	95
NCBI Description	Oryza sativa DNA for NLS receptor, complete cds

Seq. No.	385403

Contig ID	274_1.R1084
5'-most EST	g2427876
Method	BLASTX
NCBI GI	g479696
BLAST score	551
E value	6.0e-56
Match length	127
% identity	89
NCBI Description	oxidase lip19 - rice >gi_394736_emb_CAA40596_ (X57325) basic/leucine zipper protein [Oryza sativa]

Seq. No.	385404
Contig ID	275_1.R1084
5'-most EST	LIB3434-056-P1-K1-D7
Method	BLASTX
NCBI GI	g1076740
BLAST score	1427
E value	1.0e-158
Match length	340
% identity	76
NCBI Description	chitinase (EC 3.2.1.14) - rice >gi_407472_emb_CAA40107_ (X56787) chitinase [Oryza sativa] >gi_500616_dbj_BAA03750_ (D16222) endochitinase [Oryza sativa] >gi_742301_prf__2009354A chitinase [Oryza sativa]

Seq. No.	385405
Contig ID	275_2.R1084
5'-most EST	g561872
Method	BLASTX
NCBI GI	g561873
BLAST score	1324
E value	1.0e-146
Match length	310
% identity	79
NCBI Description	(L37289) chitinase [Oryza sativa]

Seq. No.	385406
Contig ID	276_1.R1084
5'-most EST	g2312812
Method	BLASTX
NCBI GI	g123543
BLAST score	573
E value	8.0e-59
Match length	143
% identity	80
NCBI Description	16.9 KD CLASS I HEAT SHOCK PROTEIN >gi_82480_pir__S20874 heat shock protein - rice >gi_20265_emb_CAA43210_ (X60820) 16.9 KD low molecular weight heat shock protein [Oryza sativa] >gi_169797 (M80938) 16.9 kDa heat shock protein [Oryza sativa] >gi_445139_prf__1908439A heat shock protein 16.9A [Oryza sativa]

Seq. No.	385407
Contig ID	276_2.R1084
5'-most EST	g2312819
Method	BLASTX
NCBI GI	g123543

BLAST score	320
E value	2.0e-29
Match length	118
% identity	58
NCBI Description	16.9 KD CLASS I HEAT SHOCK PROTEIN >gi_82480_pir__S20874 heat shock protein - rice >gi_20265_emb_CAA43210_ (X60820) 16.9 KD low molecular weight heat shock protein [Oryza sativa] >gi_169797 (M80938) 16.9 kDa heat shock protein [Oryza sativa] >gi_445139_prf__1908439A heat shock protein 16.9A [Oryza sativa]

Seq. No.	385408
Contig ID	277_1.R1084
5'-most EST	g20266
Method	BLASTX
NCBI GI	g126401
BLAST score	4351
E value	0.0e+00
Match length	858
% identity	97
NCBI Description	LIPOXYGENASE L-2 >gi_100690_pir__S23454 lipoxygenase (EC 1.13.11.12) L-2 - rice >gi_20267_emb_CAA45738_ (X64396) lipoxygenase [Oryza sativa]

Seq. No.	385409
Contig ID	278_1.R1084
5'-most EST	g5005321
Method	BLASTX
NCBI GI	g2497746
BLAST score	304
E value	3.0e-37
Match length	96
% identity	85
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa]

Seq. No.	385410
Contig ID	278_2.R1084
5'-most EST	LIB3432-052-P1-K1-C11
Method	BLASTX
NCBI GI	g68843
BLAST score	326
E value	8.0e-30
Match length	91
% identity	71
NCBI Description	phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures

Seq. No.	385411
Contig ID	278_3.R1084
5'-most EST	g4969102
Method	BLASTX
NCBI GI	g2497746
BLAST score	380

E value	3.0e-36
Match length	99
% identity	76
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 2 PRECURSOR (LTP 2) >gi_951334 (U31766) lipid transfer protein precursor [Oryza sativa]

Seq. No.	385412
Contig ID	278_4.R1084
5'-most EST	LIB3432-052-P1-K1-E7
Method	BLASTX
NCBI GI	g68843
BLAST score	326
E value	8.0e-30
Match length	91
% identity	71
NCBI Description	phospholipid transfer protein homolog - rice >gi_4139635_pdb_1RZL_ Rice Nonspecific Lipid Transfer Protein >gi_5107522_pdb_1BV2_ Lipid Transfer Protein From Rice Seeds, Nmr, 14 Structures

Seq. No.	385413
Contig ID	280_1.R1084
5'-most EST	g5005232
Method	BLASTX
NCBI GI	g2497748
BLAST score	254
E value	7.0e-34
Match length	88
% identity	90
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 4 PRECURSOR (LTP 4) >gi_902058 (U29176) lipid transfer protein precursor [Oryza sativa]

Seq. No.	385414
Contig ID	281_1.R1084
5'-most EST	g5455563
Method	BLASTN
NCBI GI	g4097337
BLAST score	512
E value	0.0e+00
Match length	573
% identity	100
NCBI Description	Oryza sativa metallothionein-like protein mRNA, complete cds

Seq. No.	385415
Contig ID	281_2.R1084
5'-most EST	g2800458
Method	BLASTN
NCBI GI	g4105602
BLAST score	294
E value	1.0e-164
Match length	375
% identity	98
NCBI Description	Oryza sativa metallothionein (MTe) gene, complete cds

Seq. No.	385416
Contig ID	281_3.R1084
5'-most EST	g1632710
Method	BLASTX
NCBI GI	g2497904
BLAST score	224
E value	3.0e-18
Match length	42
% identity	100
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 2 >gi_1667588 (U77294) metallothionein-like protein [Oryza sativa] >gi_2326785_emb_CAA69845_ (Y08529) metallothionein-like protein [Oryza sativa] >gi_4097338 (U57638) metallothionein-like protein [Oryza sativa] >gi_4105603 (AF048750) metallothionein [Oryza sativa]

Seq. No.	385417
Contig ID	283_1.R1084
5'-most EST	LIB3475-005-P1-K1-C12
Method	BLASTX
NCBI GI	g1946265
BLAST score	1060
E value	1.0e-115
Match length	257
% identity	77
NCBI Description	(Y11414) myb [Oryza sativa]

Seq. No.	385418
Contig ID	288_1.R1084
5'-most EST	g1658312
Method	BLASTX
NCBI GI	g1658313
BLAST score	1245
E value	0.0e+00
Match length	411
% identity	42
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385419
Contig ID	288_2.R1084
5'-most EST	LIB3475-001-P1-K2-H1
Method	BLASTX
NCBI GI	g1296955
BLAST score	1704
E value	0.0e+00
Match length	319
% identity	65
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]

Seq. No.	385420
Contig ID	288_3.R1084
5'-most EST	g1658314
Method	BLASTX
NCBI GI	g1658315
BLAST score	443
E value	8.0e-96
Match length	205

% identity	88
NCBI Description	(Y08988) osr40g3 [Oryza sativa]

Seq. No.	385421
Contig ID	288_4.R1084
5'-most EST	LIB3431-039-P1-K2-G10
Method	BLASTX
NCBI GI	g1296955
BLAST score	639
E value	2.0e-66
Match length	191
% identity	35
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]

Seq. No.	385422
Contig ID	288_5.R1084
5'-most EST	LIB3432-008-P1-K1-E7
Method	BLASTX
NCBI GI	g1658315
BLAST score	888
E value	1.0e-106
Match length	204
% identity	90
NCBI Description	(Y08988) osr40g3 [Oryza sativa]

Seq. No.	385423
Contig ID	288_6.R1084
5'-most EST	LIB3433-027-P1-K1-A2
Method	BLASTX
NCBI GI	g1658315
BLAST score	447
E value	1.0e-74
Match length	206
% identity	68
NCBI Description	(Y08988) osr40g3 [Oryza sativa]

Seq. No.	385424
Contig ID	288_7.R1084
5'-most EST	g2800477
Method	BLASTX
NCBI GI	g1658313
BLAST score	275
E value	6.0e-24
Match length	79
% identity	32
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385425
Contig ID	288_8.R1084
5'-most EST	uC-osf1M202081b09b1
Method	BLASTX
NCBI GI	g1658315
BLAST score	351
E value	9.0e-51
Match length	158
% identity	47
NCBI Description	(Y08988) osr40g3 [Oryza sativa]

Seq. No.	385426
Contig ID	288_9.R1084
5'-most EST	LIB3479-006-Q6-K1-D4
Method	BLASTX
NCBI GI	g1658313
BLAST score	945
E value	1.0e-102
Match length	213
% identity	48
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385427
Contig ID	288_10.R1084
5'-most EST	g2799956
Method	BLASTX
NCBI GI	g1296955
BLAST score	474
E value	1.0e-59
Match length	114
% identity	50
NCBI Description	(X95402) duplicated domain structure protein [Oryza sativa]

Seq. No.	385428
Contig ID	288_14.R1084
5'-most EST	uC-osflcyp077h12b1
Method	BLASTX
NCBI GI	g1658313
BLAST score	1047
E value	1.0e-114
Match length	256
% identity	39
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385429
Contig ID	288_16.R1084
5'-most EST	g2431131
Method	BLASTX
NCBI GI	g1658313
BLAST score	224
E value	4.0e-18
Match length	133
% identity	15
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385430
Contig ID	288_18.R1084
5'-most EST	g4881105
Method	BLASTX
NCBI GI	g1658313
BLAST score	529
E value	5.0e-54
Match length	132
% identity	33
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385431

Contig ID	288_20.R1084
5'-most EST	uC-osflm202111a12b1
Method	BLASTX
NCBI GI	g1658313
BLAST score	225
E value	9.0e-38
Match length	84
% identity	49
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385432
Contig ID	288_21.R1084
5'-most EST	uC-osflm202111a06b1
Method	BLASTX
NCBI GI	g1658313
BLAST score	585
E value	1.0e-60
Match length	125
% identity	47
NCBI Description	(Y08987) osr40g2 [Oryza sativa]

Seq. No.	385433
Contig ID	290_1.R1084
5'-most EST	LIB3475-001-P1-K2-H6
Method	BLASTX
NCBI GI	g1419090
BLAST score	1252
E value	1.0e-138
Match length	279
% identity	82
NCBI Description	(X94968) 37kDa chloroplast inner envelope membrane polypeptide precursor [Nicotiana tabacum]

Seq. No.	385434
Contig ID	291_1.R1084
5'-most EST	g426582
Method	BLASTX
NCBI GI	g1706325
BLAST score	2956
E value	0.0e+00
Match length	600
% identity	97
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 1 (PDC) >gi_476286 (U07339) pyruvate decarboxylase 1 [Oryza sativa] >gi_1098559 (U26660) pyruvate decarboxylase [Oryza sativa]

Seq. No.	385435
Contig ID	291_2.R1084
5'-most EST	g1054820
Method	BLASTX
NCBI GI	g1054821
BLAST score	976
E value	1.0e-106
Match length	196
% identity	92
NCBI Description	(X92743) pyruvate decarboxylase [Oryza sativa]

Seq. No.	385436
Contig ID	291_5.R1084
5'-most EST	uC-osflm202108a02b1
Method	BLASTX
NCBI GI	g1706331
BLAST score	717
E value	4.0e-81
Match length	179
% identity	87
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 3 (PDC) >gi_476284 (U07338) pyruvate decarboxylase [Oryza sativa]

Seq. No.	385437
Contig ID	292_1.R1084
5'-most EST	LIB3431-005-P1-K1-G3
Method	BLASTX
NCBI GI	g2429290
BLAST score	1404
E value	1.0e-156
Match length	292
% identity	95
NCBI Description	(AF014469) peroxidase [Oryza sativa]

Seq. No.	385438
Contig ID	292_2.R1084
5'-most EST	LIB3477-001-P1-K1-B2
Method	BLASTX
NCBI GI	g100694
BLAST score	1383
E value	1.0e-153
Match length	288
% identity	94
NCBI Description	peroxidase (EC 1.11.1.7) precursor - rice >gi_20286_emb_CAA46916_ (X66125) peroxidase [Oryza sativa] >gi_445620_prf__1909367A peroxidase [Oryza sativa]

Seq. No.	385439
Contig ID	292_3.R1084
5'-most EST	g428922
Method	BLASTX
NCBI GI	g585662
BLAST score	1388
E value	1.0e-154
Match length	287
% identity	94
NCBI Description	PEROXIDASE PRECURSOR >gi_303851_dbj_BAA03911_ (D16442) peroxidase [Oryza sativa]

Seq. No.	385440
Contig ID	292_4.R1084
5'-most EST	uC-osroM202010h03b1
Method	BLASTX
NCBI GI	g2429288
BLAST score	1424
E value	1.0e-158
Match length	293
% identity	94

NCBI Description	(AF014468) peroxidase [Oryza sativa]

Seq. No.	385441
Contig ID	292_5.R1084
5'-most EST	LIB3477-003-P1-K1-B1
Method	BLASTX
NCBI GI	g585662
BLAST score	150
E value	2.0e-09
Match length	51
% identity	57
NCBI Description	PEROXIDASE PRECURSOR >gi_303851_dbj_BAA03911_ (D16442) peroxidase [Oryza sativa]

Seq. No.	385442
Contig ID	292_6.R1084
5'-most EST	LIB3433-021-P1-K1-H12
Method	BLASTX
NCBI GI	g2117619
BLAST score	677
E value	4.0e-71
Match length	163
% identity	78
NCBI Description	peroxidase (EC 1.11.1.7) 4 precursor - wheat >gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum aestivum]

Seq. No.	385443
Contig ID	292_8.R1084
5'-most EST	LIB3434-030-P1-K1-E2
Method	BLASTX
NCBI GI	g2117619
BLAST score	753
E value	5.0e-80
Match length	186
% identity	79
NCBI Description	peroxidase (EC 1.11.1.7) 4 precursor - wheat >gi_732976_emb_CAA59487_ (X85230) peroxidase [Triticum aestivum]

Seq. No.	385444
Contig ID	294_2.R1084
5'-most EST	jC-osleLIB3474037b11a1
Method	BLASTX
NCBI GI	g100598
BLAST score	618
E value	3.0e-64
Match length	155
% identity	79
NCBI Description	ubiquitin / ribosomal protein S27a-1 - barley >gi_167073 (M60175) ubiquitin [Hordeum vulgare]

Seq. No.	385445
Contig ID	294_3.R1084
5'-most EST	g2310822
Method	BLASTX
NCBI GI	g70654

BLAST score	337
E value	2.0e-37
Match length	121
% identity	74
NCBI Description	ubiquitin / ribosomal protein CEP52 - Chlamydomonas reinhardtii >gi_18244_emb_CAA43216_ (X60826) ubiquitin extension protein (UbCEP52) [Chlamydomonas reinhardtii] >gi_18246_emb_CAA33466_ (X15427) ubiquitin/ribosomal protein [Chlamydomonas reinhardtii]

Seq. No.	385446
Contig ID	294_4.R1084
5'-most EST	uC-osf1M202039a11b1
Method	BLASTX
NCBI GI	g100934
BLAST score	932
E value	1.0e-100
Match length	385
% identity	9
NCBI Description	ubiquitin precursor Ubi-1 - maize >gi_422037_pir__S20926 ubiquitin precursor Ubi-2 - maize >gi_248337_bbs_94465 (S94464) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays] >gi_248339_bbs_94467 (S94466) polyubiquitin(ubiquitin) [maize, Peptide, 533 aa] [Zea mays]

Seq. No.	385447
Contig ID	294_5.R1084
5'-most EST	uC-osf1cyp064b12b1
Method	BLASTX
NCBI GI	g82733
BLAST score	465
E value	4.0e-46
Match length	156
% identity	67
NCBI Description	ubiquitin fusion protein UBF9 - maize >gi_168651 (M68937) ubiquitin fusion protein [Zea mays] >gi_902527 (U29161) ubiquitin fusion protein [Zea mays] >gi_1589388_prf__2211240B ubiquitin fusion protein [Zea mays]

Seq. No.	385448
Contig ID	294_6.R1084
5'-most EST	LIB3477-011-P1-K1-B8
Method	BLASTX
NCBI GI	g541546
BLAST score	456
E value	2.0e-55
Match length	373
% identity	8
NCBI Description	ubiquitin precursor - Volvox carteri >gi_395295_emb_CAA52290_ (X74214) polyubiquitin [Volvox carteri]

Seq. No.	385449
Contig ID	294_7.R1084
5'-most EST	g1944227

Method	BLASTX
NCBI GI	g468272
BLAST score	191
E value	3.0e-25
Match length	94
% identity	72
NCBI Description	(L31492) ubiquitin/ribosomal fusion protein [Caenorhabditis elegans] >gi_3881474_emb_CAB04967.1_ (Z82083) UBQ-2 ubiquitin; cDNA EST EMBL:C08020 comes from this gene; cDNA EST EMBL:C09601 comes from this gene; cDNA EST EMBL:C13305 comes from this gene; cDNA EST EMBL:C11253 comes from this gene; cDNA EST EMBL:C13403 comes

Seq. No.	385450
Contig ID	294_8.R1084
5'-most EST	g4716886
Method	BLASTX
NCBI GI	g1332579
BLAST score	719
E value	3.0e-75
Match length	869
% identity	6
NCBI Description	(X98063) polyubiquitin [Pinus sylvestris]

Seq. No.	385451
Contig ID	300_1.R1084
5'-most EST	g2798179
Method	BLASTX
NCBI GI	g130946
BLAST score	389
E value	3.0e-37
Match length	134
% identity	59
NCBI Description	10 KD PROLAMIN PRECURSOR >gi_82451_pir__S08219 prolamin, 10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074) prolamin (AA 1-134) [Oryza sativa] >gi_20308_emb_CAA33301_ (X15231) 10 kD prolamin [Oryza sativa] >gi_551659_emb_CAA57495_ (X81970) 10KD prolamin [Oryza sativa] >gi_556405 (L36604) prolamin [Oryza sativa] >gi_556407 (L36605) prolamin [Oryza sativa] >gi_226932_prf__1611458A prolamin 10kD [Oryza sativa]

Seq. No.	385452
Contig ID	300_2.R1084
5'-most EST	g2799047
Method	BLASTX
NCBI GI	g130946
BLAST score	328
E value	3.0e-30
Match length	115
% identity	62
NCBI Description	10 KD PROLAMIN PRECURSOR >gi_82451_pir__S08219 prolamin, 10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074) prolamin (AA 1-134) [Oryza sativa] >gi_20308_emb_CAA33301_ (X15231) 10 kD prolamin [Oryza sativa] >gi_551659_emb_CAA57495_ (X81970) 10KD prolamin [Oryza sativa] >gi_556405 (L36604) prolamin [Oryza sativa]

>gi_556407 (L36605) prolamin [Oryza sativa]
>gi_226932_prf__1611458A prolamin 10kD [Oryza sativa]

Seq. No.	385453
Contig ID	300_4.R1084
5'-most EST	g2799073
Method	BLASTN
NCBI GI	g20295
BLAST score	287
E value	1.0e-160
Match length	445
% identity	93
NCBI Description	Rice DNA for 10kDa prolamin

Seq. No.	385454
Contig ID	300_8.R1084
5'-most EST	g2799185
Method	BLASTX
NCBI GI	g130946
BLAST score	162
E value	1.0e-10
Match length	110
% identity	35
NCBI Description	10 KD PROLAMIN PRECURSOR >gi_82451_pir__S08219 prolamin, 10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074) prolamin (AA 1-134) [Oryza sativa] >gi_20308_emb_CAA33301_ (X15231) 10 kD prolamin [Oryza sativa] >gi_551659_emb_CAA57495_ (X81970) 10KD prolamin [Oryza sativa] >gi_556405 (L36604) prolamin [Oryza sativa] >gi_556407 (L36605) prolamin [Oryza sativa] >gi_226932_prf__1611458A prolamin 10kD [Oryza sativa]

Seq. No.	385455
Contig ID	300_11.R1084
5'-most EST	g2798442
Method	BLASTX
NCBI GI	g130946
BLAST score	222
E value	1.0e-28
Match length	113
% identity	65
NCBI Description	10 KD PROLAMIN PRECURSOR >gi_82451_pir__S08219 prolamin, 10K, precursor - rice >gi_20296_emb_CAA34926_ (X17074) prolamin (AA 1-134) [Oryza sativa] >gi_20308_emb_CAA33301_ (X15231) 10 kD prolamin [Oryza sativa] >gi_551659_emb_CAA57495_ (X81970) 10KD prolamin [Oryza sativa] >gi_556405 (L36604) prolamin [Oryza sativa] >gi_556407 (L36605) prolamin [Oryza sativa] >gi_226932_prf__1611458A prolamin 10kD [Oryza sativa]

Seq. No.	385456
Contig ID	301_1.R1084
5'-most EST	g20311
Method	BLASTX
NCBI GI	g100689
BLAST score	724
E value	1.0e-76

Match length	137
% identity	100
NCBI Description	ribosomal protein L10.e, cytosolic - rice (fragment) >gi_20312_emb_CAA45905_ (X64621) unknown [Oryza sativa]

Seq. No.	385457
Contig ID	304_1.R1084
5'-most EST	g1631965
Method	BLASTX
NCBI GI	g231984
BLAST score	624
E value	1.0e-64
Match length	187
% identity	66
NCBI Description	DEHYDRIN RAB25 >gi_100709_pir__S19132 rab25 protein - rice >gi_20320_emb_CAA40604_ (X57327) rab25 product [Oryza sativa]

Seq. No.	385458
Contig ID	305_1.R1084
5'-most EST	g20321
Method	BLASTX
NCBI GI	g113222
BLAST score	1937
E value	0.0e+00
Match length	377
% identity	99
NCBI Description	ACTIN 1 >gi_295885_emb_CAA33874_ (X15865) actin [Oryza sativa]

Seq. No.	385459
Contig ID	305_2.R1084
5'-most EST	LIB3599-001-P1-K6-D4
Method	BLASTX
NCBI GI	g4139264
BLAST score	786
E value	1.0e-83
Match length	175
% identity	86
NCBI Description	(AF111812) actin [Brassica napus]

Seq. No.	385460
Contig ID	305_3.R1084
5'-most EST	g2428949
Method	BLASTX
NCBI GI	g1531674
BLAST score	769
E value	1.0e-97
Match length	194
% identity	93
NCBI Description	(U68462) actin [Striga asiatica]

Seq. No.	385461
Contig ID	305_5.R1084
5'-most EST	uC-osrocyp002f01b1
Method	BLASTX
NCBI GI	g1498388

BLAST score 287
E value 7.0e-26
Match length 100
% identity 62
NCBI Description (U60510) actin [Zea mays]

Seq. No. 385462
Contig ID 306_1.R1084
5'-most EST g1632222
Method BLASTX
NCBI GI g2118429
BLAST score 573
E value 7.0e-59
Match length 160
% identity 68
NCBI Description allergen RA5B precursor - rice >gi_1398918_dbj_BAA07713_ (D42142) allergenic protein [Oryza sativa]

Seq. No. 385463
Contig ID 306_2.R1084
5'-most EST LIB3479-007-Q6-K1-A12
Method BLASTX
NCBI GI g2118427
BLAST score 775
E value 1.0e-82
Match length 166
% identity 85
NCBI Description allergen RA14B precursor - rice >gi_1398913_dbj_BAA07710_ (D42139) allergenic protein [Oryza sativa]

Seq. No. 385464
Contig ID 306_3.R1084
5'-most EST g2798996
Method BLASTX
NCBI GI g2118429
BLAST score 430
E value 3.0e-42
Match length 113
% identity 79
NCBI Description allergen RA5B precursor - rice >gi_1398918_dbj_BAA07713_ (D42142) allergenic protein [Oryza sativa]

Seq. No. 385465
Contig ID 306_4.R1084
5'-most EST g1632061
Method BLASTX
NCBI GI g2118430
BLAST score 735
E value 7.0e-78
Match length 157
% identity 85
NCBI Description allergen RA16 precursor - rice >gi_1398916_dbj_BAA07712_ (D42141) allergenic protein [Oryza sativa]

Seq. No. 385466
Contig ID 306_5.R1084
5'-most EST LIB3479-007-Q6-K1-H8

Method	BLASTX
NCBI GI	g548660
BLAST score	419
E value	1.0e-73
Match length	161
% identity	79
NCBI Description	SEED ALLERGENIC PROTEIN RA17 PRECURSOR >gi_100691_pir__S21157 seed allergen RA17 - rice >gi_2130064_pir__JC4887 allergenic protein - rice >gi_218195_dbj_BAA01997_ (D11431) allergenic protein [Oryza sativa] >gi_311893_emb_CAA46983_ (X66257) major allergenic protein (RAP) [Oryza sativa]

Seq. No.	385467
Contig ID	306_6.R1084
5'-most EST	g572410
Method	BLASTX
NCBI GI	g3695403
BLAST score	599
E value	6.0e-62
Match length	136
% identity	85
NCBI Description	(AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1_ (AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No.	385468
Contig ID	306_8.R1084
5'-most EST	LIB3475-007-P1-K1-D11
Method	BLASTX
NCBI GI	g3695403
BLAST score	1016
E value	1.0e-110
Match length	260
% identity	75
NCBI Description	(AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana] >gi_4538955_emb_CAB39779.1_ (AL049488) fructokinase-like protein [Arabidopsis thaliana]

Seq. No.	385469
Contig ID	306_9.R1084
5'-most EST	g2798687
Method	BLASTN
NCBI GI	g11957
BLAST score	908
E value	0.0e+00
Match length	1082
% identity	53
NCBI Description	Rice complete chloroplast genome

Seq. No.	385470
Contig ID	306_12.R1084
5'-most EST	g2800284
Method	BLASTN
NCBI GI	g11957

BLAST score	364
E value	0.0e+00
Match length	424
% identity	49
NCBI Description	Rice complete chloroplast genome

Seq. No.	385471
Contig ID	306_13.R1084
5'-most EST	g2799155
Method	BLASTX
NCBI GI	g2827316
BLAST score	194
E value	2.0e-14
Match length	129
% identity	30
NCBI Description	(AF042200) allergenic protein [Oryza sativa]

Seq. No.	385472
Contig ID	306_14.R1084
5'-most EST	g2799032
Method	BLASTX
NCBI GI	g2118429
BLAST score	426
E value	4.0e-44
Match length	126
% identity	76
NCBI Description	allergen RA5B precursor - rice >gi_1398918_dbj_BAA07713_ (D42142) allergenic protein [Oryza sativa]

Seq. No.	385473
Contig ID	308_1.R1084
5'-most EST	g2654869
Method	BLASTX
NCBI GI	g2654870
BLAST score	3821
E value	0.0e+00
Match length	745
% identity	97
NCBI Description	(AF015302) RbohAOsp [Oryza sativa]

Seq. No.	385474
Contig ID	309_1.R1084
5'-most EST	g428619
Method	BLASTX
NCBI GI	g231706
BLAST score	1539
E value	1.0e-172
Match length	294
% identity	100
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 1 >gi_100667_pir__S22440 protein kinase (EC 2.7.1.37) cdc2 homolog 1 - rice >gi_20343_emb_CAA42922_ (X60374) Rcdc2-1 [Oryza sativa] >gi_228924_prf__1814443A cdc2 protein:ISOTYPE=cdc2Os-1 [Oryza sativa]

Seq. No.	385475
Contig ID	310_1.R1084

5'-most EST	LIB3433-053-P1-K1-F5
Method	BLASTX
NCBI GI	g231707
BLAST score	1530
E value	1.0e-171
Match length	292
% identity	100
NCBI Description	CELL DIVISION CONTROL PROTEIN 2 HOMOLOG 2 >gi_100668_pir__S22441 protein kinase (EC 2.7.1.37) cdc2 homolog 2 - rice >gi_20345_emb_CAA42923_ (X60375) Rcdc2-2 [Oryza sativa] >gi_228925_prf__1814443B cdc2 protein:ISOTYPE=cdc2Os-2 [Oryza sativa]

Seq. No.	385476
Contig ID	311_1.R1084
5'-most EST	g20355
Method	BLASTX
NCBI GI	g132521
BLAST score	1090
E value	1.0e-119
Match length	217
% identity	100
NCBI Description	RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY PROTEIN RGP1) >gi_100684_pir__S16554 GTP-binding protein rgp1 - rice >gi_20356_emb_CAA41966_ (X59276) GTP-binding protein [Oryza sativa] >gi_228209_prf__1718315A GTP-binding protein [Oryza sativa]

Seq. No.	385477
Contig ID	313_1.R1084
5'-most EST	g3746580
Method	BLASTX
NCBI GI	g3746581
BLAST score	1046
E value	1.0e-114
Match length	215
% identity	92
NCBI Description	(AF062403) glutathione S-transferase II [Oryza sativa]

Seq. No.	385478
Contig ID	313_3.R1084
5'-most EST	g2442797
Method	BLASTX
NCBI GI	g3746581
BLAST score	330
E value	1.0e-30
Match length	82
% identity	84
NCBI Description	(AF062403) glutathione S-transferase II [Oryza sativa]

Seq. No.	385479
Contig ID	314_1.R1084
5'-most EST	g2310529
Method	BLASTX
NCBI GI	g121349
BLAST score	1910
E value	0.0e+00

Match length	353
% identity	100
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_ (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza sativa]

Seq. No.	385480
Contig ID	314_2.R1084
5'-most EST	g700941
Method	BLASTX
NCBI GI	g121332
BLAST score	1929
E value	0.0e+00
Match length	357
% identity	100
NCBI Description	GLUTAMINE SYNTHETASE ROOT ISOZYME (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS8) >gi_68590_pir__AJRZQB glutamate--ammonia ligase (EC 6.3.1.2) beta, cytosolic - rice >gi_20358_emb_CAA32460_ (X14244) cytosolic glutamine syntethase (AA 1-357) [Oryza sativa]

Seq. No.	385481
Contig ID	314_3.R1084
5'-most EST	uC-osroM202013b12b1
Method	BLASTX
NCBI GI	g543867
BLAST score	1244
E value	1.0e-137
Match length	324
% identity	77
NCBI Description	ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR >gi_1076684_pir__A47493 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor - sweet potato >gi_303626_dbj_BAA03526_ (D14699) F1-ATPase gammma subunit [Ipomoea batatas]

Seq. No.	385482
Contig ID	314_8.R1084
5'-most EST	g3761791
Method	BLASTX
NCBI GI	g121349
BLAST score	748
E value	2.0e-79
Match length	185
% identity	79
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS28) >gi_20368_emb_CAA32461_ (X14245) cytosolic glutamine synthetase (AA 1-356) [Oryza sativa]

Seq. No.	385483
Contig ID	315_1.R1084
5'-most EST	g556408
Method	BLASTX
NCBI GI	g556409
BLAST score	1319

E value	1.0e-146
Match length	296
% identity	86
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	385484
Contig ID	315_2.R1084
5'-most EST	LIB3434-024-P1-K1-F11
Method	BLASTX
NCBI GI	g556409
BLAST score	953
E value	1.0e-103
Match length	257
% identity	79
NCBI Description	(L34551) transcriptional activator protein [Oryza sativa]

Seq. No.	385485
Contig ID	316_1.R1084
5'-most EST	g2428430
Method	BLASTX
NCBI GI	g1362172
BLAST score	2044
E value	0.0e+00
Match length	520
% identity	80
NCBI Description	hook-containing protein AT1 - rice >gi_871496_emb_CAA61276_ (X88798) putative [Oryza sativa]

Seq. No.	385486
Contig ID	318_1.R1084
5'-most EST	uC-osrocyp027c09b1
Method	BLASTX
NCBI GI	g1345881
BLAST score	715
E value	2.0e-75
Match length	137
% identity	99
NCBI Description	CYTOCHROME B5 >gi_1076743_pir__S46307 cytochrome b5 - rice >gi_414705_emb_CAA53366_ (X75670) cytochrome b5 [Oryza sativa]

Seq. No.	385487
Contig ID	321_1.R1084
5'-most EST	uC-osflM202089c12b1
Method	BLASTX
NCBI GI	g3929545
BLAST score	1471
E value	1.0e-163
Match length	398
% identity	95
NCBI Description	(AF067194) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No.	385488
Contig ID	321_2.R1084
5'-most EST	uC-osflcyp161b01b1
Method	BLASTX

NCBI GI	g1881585
BLAST score	330
E value	4.0e-30
Match length	150
% identity	50
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	385489
Contig ID	321_6.R1084
5'-most EST	LIB3432-006-P1-K1-C11
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	5.0e-11
Match length	37
% identity	60
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	385490
Contig ID	322_1.R1084
5'-most EST	LIB3433-009-Q6-K1-A5
Method	BLASTX
NCBI GI	g1172811
BLAST score	1104
E value	1.0e-121
Match length	217
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L10-1 (PUTATIVE TUMOR SUPRESSOR SC34) >gi_1076751_pir__S49575 ribosomal protein L10.e, cytosolic - rice >gi_575355_emb_CAA57339_ (X81691) putative tumor suppresser [Oryza sativa]

Seq. No.	385491
Contig ID	322_2.R1084
5'-most EST	g2311309
Method	BLASTX
NCBI GI	g2500353
BLAST score	364
E value	1.0e-50
Match length	101
% identity	94
NCBI Description	60S RIBOSOMAL PROTEIN L10-3 (QM/R22) >gi_1293784 (U55048) similar to human QM protein, a putative tumor supressor, and to maize ubiquinol-cytochrome C reductase complex subunit VI requiring protein SC34 [Oryza sativa]

Seq. No.	385492
Contig ID	323_1.R1084
5'-most EST	g2326786
Method	BLASTX
NCBI GI	g3047118
BLAST score	646
E value	4.0e-67
Match length	227
% identity	59
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	385493
Contig ID	325_1.R1084
5'-most EST	LIB3431-016-P1-K1-A9
Method	BLASTX
NCBI GI	g121343
BLAST score	1952
E value	0.0e+00
Match length	413
% identity	90
NCBI Description	GLUTAMINE SYNTHETASE SHOOT ISOZYME, CHLOROPLAST PRECURSOR (GLUTAMATE--AMMONIA LIGASE) (CLONE LAMBDA-GS31) >gi_68598_pir__AJRZQD glutamate--ammonia ligase (EC 6.3.1.2) delta precursor, chloroplast - rice >gi_20370_emb_CAA32462_ (X14246) precursor chloroplastic glutamine synthetase (AA -46 to 382) [Oryza sativa]

Seq. No.	385494
Contig ID	326_1.R1084
5'-most EST	LIB3433-003-Q6-K6-A6
Method	BLASTX
NCBI GI	g2501449
BLAST score	508
E value	3.0e-51
Match length	96
% identity	100
NCBI Description	UBIQUITIN-LIKE PROTEIN SMT3 >gi_1668773_emb_CAA67922_ (X99608) ubiquitin-like protein [Oryza sativa]

Seq. No.	385495
Contig ID	327_1.R1084
5'-most EST	g2208961
Method	BLASTX
NCBI GI	g6094345
BLAST score	473
E value	4.0e-47
Match length	93
% identity	100
NCBI Description	SIGNAL RECOGNITION PARTICLE 14 KD PROTEIN (SRP14) >gi_2208962_emb_CAA71204_ (Y10118) signal recognition particle subunit 14 [Oryza sativa]

Seq. No.	385496
Contig ID	328_1.R1084
5'-most EST	g1877392
Method	BLASTX
NCBI GI	g1877393
BLAST score	1142
E value	1.0e-125
Match length	211
% identity	100
NCBI Description	(Y11527) serine/threonine protein kinase [Oryza sativa]

Seq. No.	385497
Contig ID	329_1.R1084
5'-most EST	uC-osroM202021h04b1
Method	BLASTX
NCBI GI	g267056

BLAST score	4070
E value	0.0e+00
Match length	808
% identity	96
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) >gi_100710_pir__S25526 sucrose synthase (EC 2.4.1.13) - rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase [Oryza sativa]

Seq. No.	385498
Contig ID	329_2.R1084
5'-most EST	LIB3433-059-P1-K1-A8
Method	BLASTX
NCBI GI	g267056
BLAST score	649
E value	7.0e-68
Match length	123
% identity	99
NCBI Description	SUCROSE SYNTHASE 1 (SUCROSE-UDP GLUCOSYLTRANSFERASE 1) >gi_100710_pir__S25526 sucrose synthase (EC 2.4.1.13) - rice >gi_20374_emb_CAA78747_ (Z15028) sucrose synthase [Oryza sativa]

Seq. No.	385499
Contig ID	329_5.R1084
5'-most EST	g2443051
Method	BLASTX
NCBI GI	g283008
BLAST score	422
E value	2.0e-43
Match length	105
% identity	90
NCBI Description	sucrose synthase (EC 2.4.1.13) - rice >gi_20366_emb_CAA46017_ (X64770) sucrose synthase [Oryza sativa]

Seq. No.	385500
Contig ID	330_1.R1084
5'-most EST	LIB3431-017-P1-K1-D9
Method	BLASTX
NCBI GI	g3341648
BLAST score	562
E value	2.0e-57
Match length	115
% identity	90
NCBI Description	(AJ005343) DNA directed RNA polymerase [Zea mays]

Seq. No.	385501
Contig ID	331_1.R1084
5'-most EST	uC-osrocyp011b04b1
Method	BLASTX
NCBI GI	g1136122
BLAST score	2158
E value	0.0e+00
Match length	432
% identity	95
NCBI Description	(X91807) alfa-tubulin [Oryza sativa]

Seq. No.	385502
Contig ID	331_2.R1084
5'-most EST	uC-osflm202112e04b1
Method	BLASTX
NCBI GI	g1136120
BLAST score	2189
E value	0.0e+00
Match length	437
% identity	96
NCBI Description	(X91806) alpha-tubulin [Oryza sativa]

Seq. No.	385503
Contig ID	331_3.R1084
5'-most EST	g2427251
Method	BLASTX
NCBI GI	g129916
BLAST score	1671
E value	0.0e+00
Match length	402
% identity	84
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	385504
Contig ID	331_4.R1084
5'-most EST	g4715112
Method	BLASTX
NCBI GI	g6094430
BLAST score	806
E value	3.0e-86
Match length	156
% identity	96
NCBI Description	TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi_2511533 (AF008121) alpha-tubulin 2 [Eleusine indica]

Seq. No.	385505
Contig ID	331_5.R1084
5'-most EST	g2799045
Method	BLASTX
NCBI GI	g1223784
BLAST score	98
E value	2.0e-09
Match length	65
% identity	69
NCBI Description	(X96475) alpha-tubulin [Reticulomyxa filosa]

Seq. No.	385506
Contig ID	331_6.R1084
5'-most EST	g3760318
Method	BLASTX
NCBI GI	g1136122
BLAST score	500
E value	2.0e-50
Match length	116

% identity	84
NCBI Description	(X91807) alfa-tubulin [Oryza sativa]

Seq. No.	385507
Contig ID	331_7.R1084
5'-most EST	g4879406
Method	BLASTX
NCBI GI	g129916
BLAST score	156
E value	5.0e-10
Match length	87
% identity	74
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	385508
Contig ID	331_10.R1084
5'-most EST	g2428814
Method	BLASTX
NCBI GI	g3915102
BLAST score	155
E value	7.0e-10
Match length	50
% identity	50
NCBI Description	GAMMA-THIONIN HOMOLOG PPT PRECURSOR >gi_1076652_pir__S52634 gamma-thionin - Petunia inflata >gi_499655 (L27173) gamma-thionin homolog [Petunia inflata]

Seq. No.	385509
Contig ID	331_14.R1084
5'-most EST	LIB3434-055-P1-K1-D7
Method	BLASTN
NCBI GI	g1136121
BLAST score	188
E value	1.0e-101
Match length	327
% identity	98
NCBI Description	O.sativa mRNA for alpha-tubulin (clone OSTA-136)

Seq. No.	385510
Contig ID	333_1.R1084
5'-most EST	g571747
Method	BLASTX
NCBI GI	g135399
BLAST score	2082
E value	0.0e+00
Match length	427
% identity	93
NCBI Description	TUBULIN ALPHA-1 CHAIN >gi_100716_pir__S20758 tubulin alpha-1 chain - rice >gi_20379_emb_CAA77988_ (Z11931) alpha 1 tubulin [Oryza sativa] >gi_1136124_emb_CAA62918_ (X91808) alfa-tubulin [Oryza sativa]

Seq. No.	385511
Contig ID	334_1.R1084

5'-most EST	LIB3477-010-P1-K1-A12
Method	BLASTX
NCBI GI	g401190
BLAST score	772
E value	4.0e-82
Match length	153
% identity	92
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir__S25551 thaumatin-like protein - rice >gi_20376_emb_CAA48278_ (X68197) thaumatin-like protein [Oryza sativa]

Seq. No.	385512
Contig ID	334_2.R1084
5'-most EST	LIB3433-034-P1-K1-E5
Method	BLASTX
NCBI GI	g401190
BLAST score	281
E value	5.0e-25
Match length	75
% identity	69
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir__S25551 thaumatin-like protein - rice >gi_20376_emb_CAA48278_ (X68197) thaumatin-like protein [Oryza sativa]

Seq. No.	385513
Contig ID	334_3.R1084
5'-most EST	LIB3432-012-P1-K1-C5
Method	BLASTX
NCBI GI	g401190
BLAST score	424
E value	1.0e-42
Match length	84
% identity	91
NCBI Description	THAUMATIN-LIKE PROTEIN PRECURSOR >gi_100715_pir__S25551 thaumatin-like protein - rice >gi_20376_emb_CAA48278_ (X68197) thaumatin-like protein [Oryza sativa]

Seq. No.	385514
Contig ID	335_1.R1084
5'-most EST	g572087
Method	BLASTX
NCBI GI	g1707642
BLAST score	4336
E value	0.0e+00
Match length	962
% identity	88
NCBI Description	(Y07748) TMK [Oryza sativa]

Seq. No.	385515
Contig ID	340_1.R1084
5'-most EST	LIB3431-013-P1-K1-E12
Method	BLASTX
NCBI GI	g3345477
BLAST score	1191
E value	1.0e-131
Match length	272
% identity	84

NCBI Description	(AB016283) carbonic anhydrase [Oryza sativa]

Seq. No.	385516
Contig ID	340_2.R1084
5'-most EST	LIB3431-004-P1-K1-D5
Method	BLASTX
NCBI GI	g606817
BLAST score	603
E value	2.0e-62
Match length	116
% identity	99
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No.	385517
Contig ID	340_5.R1084
5'-most EST	LIB3431-056-P1-K1-H1
Method	BLASTX
NCBI GI	g606817
BLAST score	516
E value	2.0e-68
Match length	195
% identity	84
NCBI Description	(U08404) carbonic anhydrase [Oryza sativa] >gi_5917783_gb_AAD56038.1_AF182806_1 (AF182806) carbonic anhydrase 3 [Oryza sativa]

Seq. No.	385518
Contig ID	340_6.R1084
5'-most EST	g3764121
Method	BLASTX
NCBI GI	g1684629
BLAST score	151
E value	2.0e-10
Match length	37
% identity	79
NCBI Description	(Y09374) lacZ-PhoC [synthetic construct]

Seq. No.	385519
Contig ID	341_1.R1084
5'-most EST	g571505
Method	BLASTN
NCBI GI	g571505
BLAST score	385
E value	0.0e+00
Match length	428
% identity	98
NCBI Description	Oryza sativa clone SI2 sucrose-regulated mRNA sequence

Seq. No.	385520
Contig ID	342_1.R1084
5'-most EST	g4574405
Method	BLASTX
NCBI GI	g4574406
BLAST score	3837
E value	0.0e+00

Match length	724
% identity	98
NCBI Description	(AF121139) RIM2 protein [Oryza sativa]

Seq. No.	385521
Contig ID	343_1.R1084
5'-most EST	g818848
Method	BLASTX
NCBI GI	g818849
BLAST score	2174
E value	0.0e+00
Match length	415
% identity	97
NCBI Description	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]

Seq. No.	385522
Contig ID	344_1.R1084
5'-most EST	LIB3433-032-P1-K1-B6
Method	BLASTX
NCBI GI	g2493147
BLAST score	669
E value	5.0e-70
Match length	165
% identity	84
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574 (U27098) H+-ATPase [Oryza sativa]

Seq. No.	385523
Contig ID	344_3.R1084
5'-most EST	LIB3434-046-P1-K1-H10
Method	BLASTX
NCBI GI	g2493147
BLAST score	472
E value	3.0e-47
Match length	95
% identity	58
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574 (U27098) H+-ATPase [Oryza sativa]

Seq. No.	385524
Contig ID	344_4.R1084
5'-most EST	g2442992
Method	BLASTX
NCBI GI	g2493147
BLAST score	494
E value	7.0e-50
Match length	100
% identity	59
NCBI Description	VACUOLAR ATP SYNTHASE 16 KD PROTEOLIPID SUBUNIT >gi_857574 (U27098) H+-ATPase [Oryza sativa]

Seq. No.	385525
Contig ID	345_1.R1084
5'-most EST	uC-osrocyp008b02b1
Method	BLASTX
NCBI GI	g1706328

BLAST score	2764
E value	0.0e+00
Match length	586
% identity	95
NCBI Description	PYRUVATE DECARBOXYLASE ISOZYME 2 (PDC) >gi_1009710 (U27350) pyruvate decarboxylase 2 [Oryza sativa] >gi_1777455 (U38199) pyruvate decarboxylase 2 [Oryza sativa]

Seq. No.	385526
Contig ID	346_1.R1084
5'-most EST	g2312953
Method	BLASTX
NCBI GI	g1143864
BLAST score	1762
E value	0.0e+00
Match length	325
% identity	100
NCBI Description	(U28047) beta glucosidase [Oryza sativa]

Seq. No.	385527
Contig ID	348_1.R1084
5'-most EST	g5003435
Method	BLASTX
NCBI GI	g3023816
BLAST score	1643
E value	0.0e+00
Match length	337
% identity	96
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	385528
Contig ID	348_2.R1084
5'-most EST	LIB3432-013-P1-K1-C5
Method	BLASTX
NCBI GI	g3023816
BLAST score	362
E value	2.0e-34
Match length	87
% identity	82
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa]

Seq. No.	385529
Contig ID	350_1.R1084
5'-most EST	g1173556
Method	BLASTX
NCBI GI	g2498586
BLAST score	1093
E value	1.0e-135
Match length	241
% identity	95
NCBI Description	MAJOR POLLEN ALLERGEN ORY S 1 PRECURSOR (ORY S I) >gi_1173557 (U31771) Ory s 1 [Oryza sativa]

Seq. No.	385530
Contig ID	351_1.R1084
5'-most EST	g1236333
Method	BLASTX
NCBI GI	g1236334
BLAST score	881
E value	3.0e-95
Match length	167
% identity	100
NCBI Description	(U34283) T3/T7-like RNA polymerase [Oryza sativa]

Seq. No.	385531
Contig ID	352_1.R1084
5'-most EST	LIB3433-035-P1-K1-F12
Method	BLASTX
NCBI GI	g1184112
BLAST score	419
E value	5.0e-56
Match length	170
% identity	69
NCBI Description	(U46138) Zn-induced protein [Oryza sativa]

Seq. No.	385532
Contig ID	352_2.R1084
5'-most EST	uC-osflcyp065c01b1
Method	BLASTX
NCBI GI	g2129579
BLAST score	987
E value	1.0e-174
Match length	353
% identity	81
NCBI Description	Dwarf1 protein - Arabidopsis thaliana >gi_516043 (U12400) Dwarf1 [Arabidopsis thaliana]

Seq. No.	385533
Contig ID	352_4.R1084
5'-most EST	g2442231
Method	BLASTX
NCBI GI	g6016873
BLAST score	239
E value	2.0e-30
Match length	90
% identity	81
NCBI Description	(AP000570) EST AU078346(E30133) corresponds to a region of the predicted gene.; Similar to zinc inducible protein. (AF022734) [Oryza sativa]

Seq. No.	385534
Contig ID	352_5.R1084
5'-most EST	g2800621
Method	BLASTX
NCBI GI	g1184112
BLAST score	412
E value	4.0e-40
Match length	149
% identity	60
NCBI Description	(U46138) Zn-induced protein [Oryza sativa]

Seq. No.	385535
Contig ID	352_8.R1084
5'-most EST	g425861
Method	BLASTN
NCBI GI	g6016845
BLAST score	293
E value	1.0e-164
Match length	334
% identity	98
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	385536
Contig ID	355_1.R1084
5'-most EST	g1432053
Method	BLASTX
NCBI GI	g3182921
BLAST score	2963
E value	0.0e+00
Match length	591
% identity	95
NCBI Description	ASPARAGINE SYNTHETASE [GLUTAMINE-HYDROLYZING] (GLUTAMINE-DEPENDENT ASPARAGINE SYNTHETASE) >gi_1432054 (U55873) asparagine synthetase [Oryza sativa] >gi_1902992_dbj_BAA18951_ (D83378) asparagine synthetase [Oryza sativa]

Seq. No.	385537
Contig ID	356_1.R1084
5'-most EST	g6631115
Method	BLASTX
NCBI GI	g1399913
BLAST score	435
E value	1.0e-42
Match length	165
% identity	53
NCBI Description	(U60097) Oryza sativa dehydrin mRNA, complete cds [Oryza sativa]

Seq. No.	385538
Contig ID	356_2.R1084
5'-most EST	g2801366
Method	BLASTX
NCBI GI	g1169279
BLAST score	161
E value	3.0e-18
Match length	75
% identity	89
NCBI Description	WATER-STRESS INDUCIBLE PROTEIN RAB21 >gi_82508_pir__S01152 RAB21 protein - rice >gi_295826_emb_CAA68765_ (Y00842) RAB21 protein [Oryza sativa]

Seq. No.	385539
Contig ID	357_1.R1084
5'-most EST	uC-osflm202112g07b1
Method	BLASTX
NCBI GI	g1519249

BLAST score	1280
E value	1.0e-141
Match length	256
% identity	100
NCBI Description	(U65956) GF14-b protein [Oryza sativa]

Seq. No.	385540
Contig ID	358_1.R1084
5'-most EST	g3090456
Method	BLASTX
NCBI GI	g1519251
BLAST score	1290
E value	1.0e-142
Match length	256
% identity	100
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	385541
Contig ID	358_2.R1084
5'-most EST	uC-osflcyp143f11b1
Method	BLASTX
NCBI GI	g1519251
BLAST score	633
E value	1.0e-119
Match length	249
% identity	88
NCBI Description	(U65957) GF14-c protein [Oryza sativa]

Seq. No.	385542
Contig ID	358_4.R1084
5'-most EST	g3763816
Method	BLASTX
NCBI GI	g2492487
BLAST score	710
E value	4.0e-75
Match length	153
% identity	92
NCBI Description	14-3-3-LIKE PROTEIN B (14-3-3B) >gi_1070354_emb_CAA63658_ (X93170) Hv14-3-3b [Hordeum vulgare]

Seq. No.	385543
Contig ID	359_1.R1084
5'-most EST	uC-osflcyp032a09b1
Method	BLASTX
NCBI GI	g1519253
BLAST score	1201
E value	1.0e-132
Match length	265
% identity	91
NCBI Description	(U65958) GF14-d protein [Oryza sativa]

Seq. No.	385544
Contig ID	360_4.R1084
5'-most EST	uC-osflcyp111e12b1
Method	BLASTN
NCBI GI	g5295936
BLAST score	511

E value	0.0e+00
Match length	523
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	385545
Contig ID	360_5.R1084
5'-most EST	uC-osflcyp115h05a1
Method	BLASTX
NCBI GI	g115772
BLAST score	246
E value	8.0e-21
Match length	69
% identity	81
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN 1 PRECURSOR (LHCII TYPE I CAB-1) (LHCP) >gi_82460_pir__S03705 chlorophyll a/b-binding protein 1R precursor - rice >gi_20178_emb_CAA32108_ (X13908) chlorophyll a/b-binding preprotein (AA -31 to 235) [Oryza sativa]

Seq. No.	385546
Contig ID	360_6.R1084
5'-most EST	g4714851
Method	BLASTX
NCBI GI	g1076746
BLAST score	993
E value	1.0e-108
Match length	253
% identity	67
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	385547
Contig ID	360_7.R1084
5'-most EST	g5004401
Method	BLASTX
NCBI GI	g2119719
BLAST score	424
E value	2.0e-82
Match length	185
% identity	90
NCBI Description	heat-shock cognate protein 70-3 - tomato >gi_762844 (L41253) Hsc70 [Lycopersicon esculentum]

Seq. No.	385548
Contig ID	360_8.R1084
5'-most EST	g3766780
Method	BLASTX
NCBI GI	g4522007
BLAST score	166
E value	7.0e-21
Match length	97
% identity	57
NCBI Description	(AC007069) unknown protein [Arabidopsis thaliana]

Seq. No.	385549
Contig ID	360_9.R1084
5'-most EST	g570040
Method	BLASTX
NCBI GI	g2827002
BLAST score	664
E value	1.0e-69
Match length	142
% identity	91
NCBI Description	(AF005993) HSP70 [Triticum aestivum]

Seq. No.	385550
Contig ID	360_10.R1084
5'-most EST	g4878151
Method	BLASTX
NCBI GI	g2495346
BLAST score	222
E value	2.0e-31
Match length	201
% identity	46
NCBI Description	HEAT SHOCK 70 KD PROTEIN (HSP70) >gi_1006833 (U35064) heat shock protein 70 [Oncorhynchus tschawytscha]

Seq. No.	385551
Contig ID	360_11.R1084
5'-most EST	g2312515
Method	BLASTX
NCBI GI	g3962377
BLAST score	657
E value	1.0e-108
Match length	351
% identity	66
NCBI Description	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]

Seq. No.	385552
Contig ID	360_12.R1084
5'-most EST	LIB3474-008-P1-K1-G11
Method	BLASTX
NCBI GI	g640324
BLAST score	443
E value	3.0e-68
Match length	284
% identity	55
NCBI Description	Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal Fragment) (E.C.3.6.1.3) Mutant With Glu 175 Replaced By Ser (E175s)

Seq. No.	385553
Contig ID	360_13.R1084
5'-most EST	LIB3431-039-P1-K2-D7
Method	BLASTX
NCBI GI	g1661160
BLAST score	270
E value	6.0e-29
Match length	263
% identity	30
NCBI Description	(U74295) chlorophyll a/b binding protein [Oryza sativa]

Seq. No.	385554
Contig ID	360_14.R1084
5'-most EST	LIB3431-025-P1-K1-H7
Method	BLASTX
NCBI GI	g320618
BLAST score	356
E value	2.0e-46
Match length	268
% identity	43
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	385555
Contig ID	360_15.R1084
5'-most EST	LIB3431-035-P1-K1-B3
Method	BLASTX
NCBI GI	g320618
BLAST score	263
E value	3.0e-34
Match length	256
% identity	29
NCBI Description	chlorophyll a/b-binding protein I precursor - rice >gi_218172_dbj_BAA00536_ (D00641) type I light-harvesting chlorophyll a/b-binding protein [Oryza sativa] >gi_227611_prf__1707316A chlorophyll a/b binding protein 1 [Oryza sativa]

Seq. No.	385556
Contig ID	360_16.R1084
5'-most EST	LIB3432-030-P1-K1-G7
Method	BLASTX
NCBI GI	g2570513
BLAST score	219
E value	4.0e-17
Match length	255
% identity	22
NCBI Description	(AF022739) chlorophyll a-b binding protein [Oryza sativa]

Seq. No.	385557
Contig ID	361_1.R1084
5'-most EST	LIB3431-033-P1-K1-C2
Method	BLASTX
NCBI GI	g6006363
BLAST score	366
E value	2.0e-34
Match length	71
% identity	100
NCBI Description	(AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No.	385558
Contig ID	361_2.R1084

5'-most EST	g2427762
Method	BLASTX
NCBI GI	g6006363
BLAST score	330
E value	3.0e-30
Match length	62
% identity	100
NCBI Description	(AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No.	385559
Contig ID	361_5.R1084
5'-most EST	uC-osroM202023f04b1
Method	BLASTN
NCBI GI	g6006355
BLAST score	185
E value	2.0e-99
Match length	352
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	385560
Contig ID	361_8.R1084
5'-most EST	uC-osflcyp108e11b1
Method	BLASTX
NCBI GI	g6006363
BLAST score	413
E value	1.0e-40
Match length	82
% identity	96
NCBI Description	(AP000559) ESTs AU078183(C62904),C73912(E21020) correspond to a region of the predicted gene.; Similar to water stress inducible protein (U74296) [Oryza sativa]

Seq. No.	385561
Contig ID	366_1.R1084
5'-most EST	g20402
Method	BLASTX
NCBI GI	g136758
BLAST score	3058
E value	0.0e+00
Match length	595
% identity	98
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_82479_pir__S22519 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) precursor - rice >gi_421998_pir__S30485 ADP(UDP)-glucose starch glycosyl transferase - rice >gi_626033_pir__JQ2224 waxy protein - rice >gi_1084459_pir__S11481 UDPglucose--starch glucosyltransferase (EC 2.4.1.11) - rice >gi_20401_emb_CAA41186_ (X58228) ADP(UDP)-glucose starch glycosyl transferase [Oryza sativa] >gi_20403_emb_CAA44065_ (X62134) starch (bacterial glycogen) synthase [Oryza sativa] >gi_577599_emb_CAA37732_ (X53694) starch synthase [Oryza sativa]

Seq. No.	385562
Contig ID	366_2.R1084
5'-most EST	g2799205
Method	BLASTX
NCBI GI	g2833382
BLAST score	304
E value	2.0e-27
Match length	83
% identity	73
NCBI Description	GRANULE-BOUND GLYCOGEN (STARCH) SYNTHASE PRECURSOR >gi_532287_dbj_BAA01272_ (D10472) glucosyl transferase [Oryza glaberrima]

Seq. No.	385563
Contig ID	366_4.R1084
5'-most EST	LIB3479-004-Q6-K2-F3
Method	BLASTN
NCBI GI	g20402
BLAST score	92
E value	5.0e-44
Match length	112
% identity	96
NCBI Description	O.sativa Waxy mRNA

Seq. No.	385564
Contig ID	367_1.R1084
5'-most EST	LIB3475-010-P1-K1-G11
Method	BLASTX
NCBI GI	g2584803
BLAST score	333
E value	3.0e-31
Match length	107
% identity	63
NCBI Description	(Y14825) RIR1a protein [Oryza sativa]

Seq. No.	385565
Contig ID	368_1.R1084
5'-most EST	g2286110
Method	BLASTX
NCBI GI	g2286111
BLAST score	1332
E value	1.0e-147
Match length	259
% identity	98
NCBI Description	(U78891) MADS box protein [Oryza sativa]

Seq. No.	385566
Contig ID	368_2.R1084
5'-most EST	g2286112
Method	BLASTX
NCBI GI	g2286113
BLAST score	1253
E value	1.0e-138
Match length	241
% identity	100
NCBI Description	(U78892) MADS box protein [Oryza sativa]

Seq. No.	385567
Contig ID	369_1.R1084
5'-most EST	LIB3433-013-Q6-K1-C11
Method	BLASTX
NCBI GI	g3123270
BLAST score	1000
E value	1.0e-133
Match length	254
% identity	94
NCBI Description	40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620) >gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4 [Oryza sativa]

Seq. No.	385568
Contig ID	369_2.R1084
5'-most EST	LIB3477-007-P1-K1-A7
Method	BLASTX
NCBI GI	g3914899
BLAST score	1095
E value	1.0e-120
Match length	239
% identity	87
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No.	385569
Contig ID	369_3.R1084
5'-most EST	LIB3433-033-P1-K1-B6
Method	BLASTX
NCBI GI	g3914899
BLAST score	621
E value	1.0e-127
Match length	256
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No.	385570
Contig ID	369_4.R1084
5'-most EST	LIB3477-005-P1-K1-B11
Method	BLASTX
NCBI GI	g3123270
BLAST score	589
E value	6.0e-61
Match length	144
% identity	83
NCBI Description	40S RIBOSOMAL PROTEIN S4 (SCAR PROTEIN SS620) >gi_2463335_emb_CAA75242_ (Y15009) ribosomal protein S4 [Oryza sativa]

Seq. No.	385571
Contig ID	369_5.R1084
5'-most EST	uC-osflM202082d03b1
Method	BLASTX
NCBI GI	g3914899
BLAST score	367
E value	6.0e-76

Match length	246
% identity	67
NCBI Description	40S RIBOSOMAL PROTEIN S4 >gi_2331301 (AF013487) ribosomal protein S4 type I [Zea mays]

Seq. No.	385572
Contig ID	370_1.R1084
5'-most EST	g1375074
Method	BLASTX
NCBI GI	g3183079
BLAST score	1730
E value	0.0e+00
Match length	341
% identity	100
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	385573
Contig ID	371_1.R1084
5'-most EST	LIB3477-002-P1-K1-F11
Method	BLASTX
NCBI GI	g549063
BLAST score	811
E value	1.0e-86
Match length	168
% identity	93
NCBI Description	TRANSLATIONALLY CONTROLLED TUMOR PROTEIN HOMOLOG (TCTP) >gi_1072464_pir__A38958 IgE-dependent histamine-releasing factor homolog - rice >gi_303835_dbj_BAA02151_ (D12626) 21kd polypeptide [Oryza sativa]

Seq. No.	385574
Contig ID	372_1.R1084
5'-most EST	LIB3475-003-P1-K2-E9
Method	BLASTX
NCBI GI	g3789948
BLAST score	793
E value	1.0e-84
Match length	160
% identity	94
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	385575
Contig ID	372_2.R1084
5'-most EST	LIB3431-008-P1-K1-E11
Method	BLASTX
NCBI GI	g3789948
BLAST score	809
E value	2.0e-86
Match length	160
% identity	96
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	385576
Contig ID	373_1.R1084
5'-most EST	uC-osflm202100d01b1

Method	BLASTX
NCBI GI	g730510
BLAST score	979
E value	1.0e-106
Match length	197
% identity	98
NCBI Description	RAS-RELATED PROTEIN RIC1 >gi_542150_pir__S38740 GTP-binding protein - rice >gi_432607_gb_AAB28535_ (S66160) ras-related GTP binding protein possessing GTPase activity=ric1 [Oryza sativa=rice, var. Yamahoushi, callus, Peptide, 202 aa] [Oryza sativa]

Seq. No.	385577
Contig ID	374_1.R1084
5'-most EST	g4716741
Method	BLASTX
NCBI GI	g2459420
BLAST score	714
E value	2.0e-75
Match length	140
% identity	97
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	385578
Contig ID	375_1.R1084
5'-most EST	LIB3432-035-P2-K1-E1
Method	BLASTX
NCBI GI	g729252
BLAST score	529
E value	1.0e-53
Match length	134
% identity	74
NCBI Description	CYTOCHROME B5 >gi_167140 (M87514) cytochrome b-5 [Brassica oleracea] >gi_384338_prf__1905426A cytochrome b5 [Brassica oleracea]

Seq. No.	385579
Contig ID	376_1.R1084
5'-most EST	g2312778
Method	BLASTX
NCBI GI	g3868754
BLAST score	2692
E value	0.0e+00
Match length	492
% identity	100
NCBI Description	(D64013) catalase [Oryza sativa]

Seq. No.	385580
Contig ID	376_2.R1084
5'-most EST	g218097
Method	BLASTX
NCBI GI	g3868754
BLAST score	463
E value	4.0e-46
Match length	89
% identity	97

NCBI Description	(D64013) catalase [Oryza sativa]

Seq. No.	385581
Contig ID	377_1.R1084
5'-most EST	LIB3434-046-P1-K1-G12
Method	BLASTX
NCBI GI	g1173187
BLAST score	632
E value	5.0e-66
Match length	136
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S23 (S12) >gi_1362041_pir__S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry >gi_643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]

Seq. No.	385582
Contig ID	378_1.R1084
5'-most EST	g2311164
Method	BLASTX
NCBI GI	g3914140
BLAST score	435
E value	1.0e-42
Match length	92
% identity	90
NCBI Description	NONSPECIFIC LIPID-TRANSFER PROTEIN 5 PRECURSOR (LTP 5) >gi_3172343 (AF051369) lipid transfer protein [Oryza sativa]

Seq. No.	385583
Contig ID	378_6.R1084
5'-most EST	g4878589
Method	BLASTN
NCBI GI	g218106
BLAST score	137
E value	7.0e-71
Match length	225
% identity	91
NCBI Description	Rice mRNA for Phospholipid transfer protein

Seq. No.	385584
Contig ID	379_1.R1084
5'-most EST	g3462564
Method	BLASTX
NCBI GI	g3021713
BLAST score	759
E value	1.0e-80
Match length	145
% identity	100
NCBI Description	(AB012605) MRL [Oryza sativa]

Seq. No.	385585
Contig ID	380_1.R1084
5'-most EST	LIB3431-013-P1-K1-B12
Method	BLASTX
NCBI GI	g1169797
BLAST score	2131

E value	0.0e+00
Match length	567
% identity	92
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC A (GPI-A) (PHOSPHOGLUCOSE ISOMERASE A) (PGI-A) (PHOSPHOHEXOSE ISOMERASE A) (PHI-A) >gi_639684_dbj_BAA08148_ (D45217) phosphoglucose isomerase (Pgi-a) [Oryza sativa]

Seq. No.	385586
Contig ID	380_2.R1084
5'-most EST	uC-osroM202014e06b1
Method	BLASTX
NCBI GI	g1169798
BLAST score	2762
E value	0.0e+00
Match length	568
% identity	95
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B) (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218) phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No.	385587
Contig ID	380_3.R1084
5'-most EST	g2312242
Method	BLASTX
NCBI GI	g1169798
BLAST score	430
E value	8.0e-53
Match length	119
% identity	97
NCBI Description	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC B (GPI-B) (PHOSPHOGLUCOSE ISOMERASE B) (PGI-B) (PHOSPHOHEXOSE ISOMERASE B) (PHI-B) >gi_639686_dbj_BAA08149_ (D45218) phosphoglucose isomerase (Pgi-b) [Oryza sativa]

Seq. No.	385588
Contig ID	381_1.R1084
5'-most EST	g426872
Method	BLASTX
NCBI GI	g2500380
BLAST score	508
E value	2.0e-51
Match length	105
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L44 >gi_2119128_pir__JC4923 ribosomal protein RL44 - upland cotton >gi_1553129 (U64677) ribosomal protein L44 isoform a [Gossypium hirsutum] >gi_1553131 (U64678) ribosomal protein L44 isoform b [Gossypium hirsutum]

Seq. No.	385589
Contig ID	382_1.R1084
5'-most EST	uC-osrocyp011a05b1
Method	BLASTX
NCBI GI	g3290022
BLAST score	590

E value	9.0e-61
Match length	168
% identity	65
NCBI Description	(AF044173) cysteine synthase; CS-B; O-acetylserine (thiol) lyase; plastidic isoform [Solanum tuberosum]

Seq. No.	385590
Contig ID	382_2.R1084
5'-most EST	uC-osflcyp121e08b1
Method	BLASTX
NCBI GI	g416869
BLAST score	516
E value	1.0e-91
Match length	232
% identity	74
NCBI Description	CYSTEINE SYNTHASE, CHLOROPLAST PRECURSOR (O-ACETYLSERINE SULFHYDRYLASE) (O-ACETYLSERINE (THIOL)-LYASE) (CSASE) >gi_303902_dbj_BAA03542_ (D14722) cysteine synthase [Spinacia oleracea]

Seq. No.	385591
Contig ID	383_1.R1084
5'-most EST	g3767705
Method	BLASTX
NCBI GI	g421960
BLAST score	353
E value	4.0e-33
Match length	80
% identity	85
NCBI Description	small nuclear ribonucleoprotein U2B'' - potato >gi_169589 (M72892) spliceosomal protein [Solanum tuberosum]

Seq. No.	385592
Contig ID	383_2.R1084
5'-most EST	g2442259
Method	BLASTX
NCBI GI	g421960
BLAST score	607
E value	9.0e-63
Match length	233
% identity	56
NCBI Description	small nuclear ribonucleoprotein U2B'' - potato >gi_169589 (M72892) spliceosomal protein [Solanum tuberosum]

Seq. No.	385593
Contig ID	384_1.R1084
5'-most EST	LIB3433-053-P1-K1-D1
Method	BLASTX
NCBI GI	g462195
BLAST score	524
E value	5.0e-53
Match length	115
% identity	89
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza

sativa]

Seq. No.	385594
Contig ID	384_2.R1084
5'-most EST	uC-osroM202020b07b1

Seq. No.	385595
Contig ID	384_9.R1084
5'-most EST	g286474
Method	BLASTX
NCBI GI	g462195
BLAST score	309
E value	3.0e-33
Match length	109
% identity	80
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	385596
Contig ID	385_1.R1084
5'-most EST	uC-osflcyp171f01b1
Method	BLASTX
NCBI GI	g1706260
BLAST score	1723
E value	0.0e+00
Match length	348
% identity	91
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	385597
Contig ID	385_2.R1084
5'-most EST	uC-osroM202023e02b1
Method	BLASTX
NCBI GI	g1706260
BLAST score	1428
E value	1.0e-159
Match length	347
% identity	76
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	385598
Contig ID	385_5.R1084
5'-most EST	LIB3433-058-P1-K1-G7
Method	BLASTX
NCBI GI	g1706260
BLAST score	464
E value	2.0e-50
Match length	125

% identity	86
NCBI Description	CYSTEINE PROTEINASE 1 PRECURSOR >gi_2118131_pir__S59597 cysteine proteinase 1 precursor - maize >gi_643597_dbj_BAA08244_ (D45402) cysteine proteinase [Zea mays]

Seq. No.	385599
Contig ID	386_1.R1084
5'-most EST	g391874
Method	BLASTX
NCBI GI	g548851
BLAST score	590
E value	6.0e-61
Match length	117
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S20 >gi_481226_pir__S38356 ribosomal protein S20 - rice >gi_391875_dbj_BAA02157_ (D12632) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	385600
Contig ID	387_1.R1084
5'-most EST	g2801167
Method	BLASTX
NCBI GI	g548852
BLAST score	425
E value	1.0e-41
Match length	82
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S21 >gi_481227_pir__S38357 ribosomal protein S21 - rice >gi_303839_dbj_BAA02158_ (D12633) 40S subunit ribosomal protein [Oryza sativa]

Seq. No.	385601
Contig ID	387_2.R1084
5'-most EST	LIB3433-038-P1-K1-H8
Method	BLASTN
NCBI GI	g303838
BLAST score	75
E value	9.0e-34
Match length	75
% identity	100
NCBI Description	Rice mRNA for 40S subunit ribosomal protein, complete cds

Seq. No.	385602
Contig ID	388_1.R1084
5'-most EST	uC-osflcyp106c10b1
Method	BLASTX
NCBI GI	g455399
BLAST score	483
E value	4.0e-48
Match length	94
% identity	99
NCBI Description	(D21068) dihydrolipoamide acetyltransferase [Oryza sativa]

Seq. No.	385603
Contig ID	388_2.R1084
5'-most EST	g3107150

Method	BLASTX
NCBI GI	g455399
BLAST score	483
E value	1.0e-48
Match length	94
% identity	100
NCBI Description	(D21068) dihydrolipoamide acetyltransferase [Oryza sativa]

Seq. No.	385604
Contig ID	390_1.R1084
5'-most EST	g5002874
Method	BLASTX
NCBI GI	g3660467
BLAST score	616
E value	6.0e-64
Match length	238
% identity	52
NCBI Description	(AJ001807) succinyl-CoA-ligase alpha subunit [Arabidopsis thaliana]

Seq. No.	385605
Contig ID	391_1.R1084
5'-most EST	g569348
Method	BLASTX
NCBI GI	g4774163
BLAST score	604
E value	3.0e-62
Match length	202
% identity	60
NCBI Description	(AB026909) F1-ATP synthase delta subunit [Ipomoea batatas]

Seq. No.	385606
Contig ID	392_1.R1084
5'-most EST	g4716302
Method	BLASTX
NCBI GI	g2982268
BLAST score	669
E value	4.0e-70
Match length	139
% identity	91
NCBI Description	(AF051217) probable 40S ribosomal protein S15 [Picea mariana]

Seq. No.	385607
Contig ID	392_3.R1084
5'-most EST	LIB3433-020-P1-K1-G5
Method	BLASTX
NCBI GI	g401043
BLAST score	288
E value	1.0e-50
Match length	126
% identity	84
NCBI Description	40S RIBOSOMAL PROTEIN S15 >gi_218131_dbj_BAA01746_ (D10962) unnamed protein product [Oryza sativa]

Seq. No.	385608
Contig ID	394_1.R1084

5'-most EST	g426432
Method	BLASTX
NCBI GI	g113682
BLAST score	1885
E value	0.0e+00
Match length	434
% identity	92
NCBI Description	ALPHA-AMYLASE ISOZYME 3D PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_82457_pir__S12625 alpha-amylase (EC 3.2.1.1) 3D - rice >gi_169771 (M59351) alpha-amylase [Oryza sativa]

Seq. No.	385609
Contig ID	394_2.R1084
5'-most EST	g3759673
Method	BLASTX
NCBI GI	g113683
BLAST score	546
E value	1.0e-55
Match length	146
% identity	77
NCBI Description	ALPHA-AMYLASE ISOZYME 3E PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_100663_pir__JT0946 alpha-amylase 3E - rice >gi_169773 (M59352) alpha-amylase [Oryza sativa]

Seq. No.	385610
Contig ID	394_3.R1084
5'-most EST	g2800783
Method	BLASTX
NCBI GI	g113683
BLAST score	453
E value	2.0e-62
Match length	118
% identity	97
NCBI Description	ALPHA-AMYLASE ISOZYME 3E PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_100663_pir__JT0946 alpha-amylase 3E - rice >gi_169773 (M59352) alpha-amylase [Oryza sativa]

Seq. No.	385611
Contig ID	394_4.R1084
5'-most EST	g169752
Method	BLASTX
NCBI GI	g100654
BLAST score	2296
E value	0.0e+00
Match length	434
% identity	96
NCBI Description	alpha-amylase (EC 3.2.1.1) precursor (clone pOS103) - rice >gi_169753 (M24286) alpha-amylase (EC 3.2.1.1) [Oryza sativa]

Seq. No.	385612
Contig ID	394_9.R1084
5'-most EST	g5004996
Method	BLASTX
NCBI GI	g113683
BLAST score	756

E value	1.0e-117
Match length	272
% identity	77
NCBI Description	ALPHA-AMYLASE ISOZYME 3E PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE) >gi_100663_pir__JT0946 alpha-amylase 3E - rice >gi_169773 (M59352) alpha-amylase [Oryza sativa]

Seq. No.	385613
Contig ID	396_1.R1084
5'-most EST	uC-osrocyp006b07b1
Method	BLASTX
NCBI GI	g584706
BLAST score	2092
E value	0.0e+00
Match length	407
% identity	100
NCBI Description	ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (TRANSAMINASE A) >gi_2130066_pir__JC5124 aspartate transaminase (EC 2.6.1.1), cytoplasmic - rice >gi_287298_dbj_BAA03504_ (D14673) aspartate aminotransferase [Oryza sativa]

Seq. No.	385614
Contig ID	396_2.R1084
5'-most EST	LIB3432-048-P2-K1-D11
Method	BLASTX
NCBI GI	g3540201
BLAST score	330
E value	1.0e-30
Match length	137
% identity	49
NCBI Description	(AC004260) Putative nuclear protein [Arabidopsis thaliana]

Seq. No.	385615
Contig ID	396_3.R1084
5'-most EST	uC-osflcyp007a12b1
Method	BLASTX
NCBI GI	g2500813
BLAST score	161
E value	6.0e-11
Match length	57
% identity	58
NCBI Description	NUCLEAR PROTEIN SKIP (SNW1 PROTEIN) >gi_1236986 (U51432) nuclear protein Skip [Homo sapiens] >gi_3417599 (AF045184) nuclear receptor coactivator NCoA-62 [Homo sapiens]

Seq. No.	385616
Contig ID	403_1.R1084
5'-most EST	uC-osroM202026h12b1
Method	BLASTX
NCBI GI	g2497538
BLAST score	1419
E value	1.0e-157
Match length	326
% identity	86
NCBI Description	PYRUVATE KINASE, CYTOSOLIC ISOZYME >gi_466350 (L08632) pyruvate kinase [Glycine max]

Seq. No.	385617
Contig ID	407_1.R1084
5'-most EST	LIB3434-042-P1-K1-H12
Method	BLASTX
NCBI GI	g1184774
BLAST score	1537
E value	1.0e-171
Match length	337
% identity	88
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No.	385618
Contig ID	407_2.R1084
5'-most EST	g5003524
Method	BLASTX
NCBI GI	g120668
BLAST score	716
E value	1.0e-75
Match length	150
% identity	92
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No.	385619
Contig ID	407_3.R1084
5'-most EST	g5003122
Method	BLASTX
NCBI GI	g120668
BLAST score	339
E value	2.0e-31
Match length	120
% identity	51
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_82399_pir__A24159 glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12), cytosolic - barley (fragment) >gi_167044 (M36650) glyceraldehyde-3-phosphate dehydrogenase [Hordeum vulgare] >gi_225347_prf__1301218A dehydrogenase,glyceraldehydephosphate [Hordeum vulgare var. distichum]

Seq. No.	385620
Contig ID	407_4.R1084
5'-most EST	g3445020
Method	BLASTX
NCBI GI	g3023816
BLAST score	155
E value	6.0e-11
Match length	66
% identity	62
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_968996 (U31676) glyceraldehyde-3-phosphate

dehydrogenase [Oryza sativa]

Seq. No.	385621
Contig ID	407_7.R1084
5'-most EST	LIB3431-063-P1-K1-G1
Method	BLASTX
NCBI GI	g1184774
BLAST score	716
E value	1.0e-75
Match length	170
% identity	82
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No.	385622
Contig ID	407_11.R1084
5'-most EST	LIB3434-065-P1-K1-A4
Method	BLASTX
NCBI GI	g1184774
BLAST score	245
E value	3.0e-27
Match length	89
% identity	79
NCBI Description	(U45856) cytosolic glyceroldehyde-3-phosphate dehydrogenase GAPC3 [Zea mays]

Seq. No.	385623
Contig ID	408_1.R1084
5'-most EST	g3767496
Method	BLASTX
NCBI GI	g2196672
BLAST score	374
E value	4.0e-37
Match length	109
% identity	76
NCBI Description	(Y08807) HMGd1 [Zea mays]

Seq. No.	385624
Contig ID	411_1.R1084
5'-most EST	g3761442
Method	BLASTX
NCBI GI	g480450
BLAST score	2235
E value	0.0e+00
Match length	512
% identity	85
NCBI Description	ketol-acid reductoisomerase (EC 1.1.1.86) - Arabidopsis thaliana >gi_402552_emb_CAA49506_ (X69880) ketol-acid reductoisomerase [Arabidopsis thaliana]

Seq. No.	385625
Contig ID	412_1.R1084
5'-most EST	g2310966
Method	BLASTX
NCBI GI	g2398679
BLAST score	1347
E value	1.0e-155

Match length	300
% identity	90
NCBI Description	(Y14797) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]

Seq. No.	385626
Contig ID	413_1.R1084
5'-most EST	g2427548
Method	BLASTX
NCBI GI	g349104
BLAST score	1146
E value	1.0e-126
Match length	231
% identity	94
NCBI Description	(L19436) manganese-superoxide dismutase [Oryza sativa]

Seq. No.	385627
Contig ID	413_2.R1084
5'-most EST	LIB3431-009-P1-K1-A7
Method	BLASTX
NCBI GI	g601869
BLAST score	1147
E value	1.0e-126
Match length	231
% identity	94
NCBI Description	(L34038) manganese superoxide dismutase [Oryza sativa]

Seq. No.	385628
Contig ID	413_3.R1084
5'-most EST	LIB3431-014-P1-K1-G5
Method	BLASTX
NCBI GI	g2754849
BLAST score	1213
E value	1.0e-133
Match length	259
% identity	88
NCBI Description	(AF039000) putative serine-glyoxylate aminotransferase [Fritillaria agrestis]

Seq. No.	385629
Contig ID	415_1.R1084
5'-most EST	g2312439
Method	BLASTX
NCBI GI	g3021357
BLAST score	287
E value	1.0e-25
Match length	83
% identity	70
NCBI Description	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]

Seq. No.	385630
Contig ID	416_1.R1084
5'-most EST	g3760981
Method	BLASTX
NCBI GI	g2982289
BLAST score	440

E value	2.0e-49
Match length	132
% identity	80
NCBI Description	(AF051229) 60S ribosomal protein L17 [Picea mariana]

Seq. No.	385631
Contig ID	416_2.R1084
5'-most EST	uC-osflcyp095c02b1
Method	BLASTX
NCBI GI	g2459420
BLAST score	714
E value	2.0e-75
Match length	140
% identity	97
NCBI Description	(AC002332) putative ribosomal protein L17 [Arabidopsis thaliana]

Seq. No.	385632
Contig ID	416_3.R1084
5'-most EST	LIB3433-014-Q6-K1-E12
Method	BLASTX
NCBI GI	g2341028
BLAST score	374
E value	1.0e-56
Match length	119
% identity	97
NCBI Description	(AC000104) Strong similarity to 60S ribosomal protein L17 (gb_X01694). EST gb_AA042332 comes from this gene. [Arabidopsis thaliana]

Seq. No.	385633
Contig ID	421_1.R1084
5'-most EST	uC-osflcyp177d01b1
Method	BLASTX
NCBI GI	g1076746
BLAST score	1983
E value	0.0e+00
Match length	446
% identity	88
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	385634
Contig ID	421_2.R1084
5'-most EST	g2312434
Method	BLASTX
NCBI GI	g3986110
BLAST score	1227
E value	1.0e-147
Match length	335
% identity	80
NCBI Description	(AB012716) heat shock protein 70 cognate [Salix gilgiana]

Seq. No.	385635
Contig ID	421_3.R1084
5'-most EST	g5056007

Method	BLASTX
NCBI GI	g2290780
BLAST score	453
E value	1.0e-48
Match length	149
% identity	71
NCBI Description	(AF002667) heat shock cognate protein [Solanum commersonii]

Seq. No.	385636
Contig ID	421_4.R1084
5'-most EST	g2312690
Method	BLASTX
NCBI GI	g123650
BLAST score	233
E value	1.0e-22
Match length	79
% identity	70
NCBI Description	HEAT SHOCK COGNATE 70 KD PROTEIN >gi_82245_pir__S03250 heat shock protein 70 (clone pMON9743) - garden petunia >gi_20557_emb_CAA30018_ (X06932) heat shock protein 70 [Petunia x hybrida]

Seq. No.	385637
Contig ID	421_5.R1084
5'-most EST	uC-osroM202029b09a1
Method	BLASTX
NCBI GI	g861170
BLAST score	311
E value	2.0e-28
Match length	64
% identity	92
NCBI Description	(X03697) heat shock protein 70 [Zea mays]

Seq. No.	385638
Contig ID	421_6.R1084
5'-most EST	g3760100
Method	BLASTX
NCBI GI	g1076746
BLAST score	230
E value	2.0e-33
Match length	134
% identity	66
NCBI Description	heat shock protein 70 - rice (fragment) >gi_763160_emb_CAA47948_ (X67711) heat shock protein 70 [Oryza sativa]

Seq. No.	385639
Contig ID	422_1.R1084
5'-most EST	uC-osroM202008e01a1
Method	BLASTX
NCBI GI	g1518540
BLAST score	924
E value	1.0e-156
Match length	301
% identity	87
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	385640
Contig ID	422_2.R1084
5'-most EST	LIB3434-033-P1-K1-E12
Method	BLASTX
NCBI GI	g1518540
BLAST score	760
E value	9.0e-81
Match length	155
% identity	88
NCBI Description	(U53418) UDP-glucose dehydrogenase [Glycine max]

Seq. No.	385641
Contig ID	422_4.R1084
5'-most EST	LIB3477-001-P1-K1-D12
Method	BLASTX
NCBI GI	g2911148
BLAST score	2559
E value	0.0e+00
Match length	593
% identity	83
NCBI Description	(AB005808) NADP-malic enzyme [Aloe arborescens]

Seq. No.	385642
Contig ID	423_1.R1084
5'-most EST	g425804
Method	BLASTX
NCBI GI	g2642640
BLAST score	243
E value	8.0e-21
Match length	92
% identity	54
NCBI Description	(AF032473) ADP-glucose pyrophosphorylase large subunit 2 [Citrullus lanatus]

Seq. No.	385643
Contig ID	424_1.R1084
5'-most EST	LIB3434-007-P1-K1-G7
Method	BLASTX
NCBI GI	g1351270
BLAST score	1261
E value	1.0e-139
Match length	253
% identity	98
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CYTOSOLIC (TIM) >gi_478410_pir__JQ2255 triose-phosphate isomerase (EC 5.3.1.1) - rice >gi_169821 (M87064) triosephosphate isomerase [Oryza sativa]

Seq. No.	385644
Contig ID	425_1.R1084
5'-most EST	g2310069
Method	BLASTX
NCBI GI	g6056373
BLAST score	3335
E value	0.0e+00
Match length	693
% identity	91

NCBI Description	(AC009894) elongation factor EF-2 [Arabidopsis thaliana]

Seq. No.	385645
Contig ID	425_2.R1084
5'-most EST	uC-osrocyp033c02a1

Seq. No.	385646
Contig ID	425_3.R1084
5'-most EST	LIB3479-006-Q6-K1-A4
Method	BLASTX
NCBI GI	g6015065
BLAST score	988
E value	1.0e-107
Match length	207
% identity	90
NCBI Description	ELONGATION FACTOR 2 (EF-2) >gi_2369714_emb_CAB09900_ (Z97178) elongation factor 2 [Beta vulgaris]

Seq. No.	385647
Contig ID	425_4.R1084
5'-most EST	g427180
Method	BLASTX
NCBI GI	g549060
BLAST score	683
E value	8.0e-72
Match length	233
% identity	58
NCBI Description	T-COMPLEX PROTEIN 1, ETA SUBUNIT (TCP-1-ETA) (CCT-ETA) >gi_631656_pir__S43058 CCTeta protein eta chain - mouse >gi_468504_emb_CAA83274_ (Z31399) CCTeta, eta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus] >gi_5295935_dbj_BAA81878.1_ (AB022160) chaperonin containing TCP-1 eta subunit [Mus musculus]

Seq. No.	385648
Contig ID	426_1.R1084
5'-most EST	g568134
Method	BLASTX
NCBI GI	g3023713
BLAST score	2208
E value	0.0e+00
Match length	446
% identity	97
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa]

Seq. No.	385649
Contig ID	426_2.R1084
5'-most EST	LIB3432-005-P1-K1-F12
Method	BLASTX
NCBI GI	g2661039
BLAST score	491
E value	5.0e-49
Match length	282
% identity	54
NCBI Description	(AF035286) alpha enolase [Homo sapiens]

Seq. No.	385650
Contig ID	426_3.R1084
5'-most EST	g5900716
Method	BLASTX
NCBI GI	g1169528
BLAST score	860
E value	2.0e-92
Match length	172
% identity	98
NCBI Description	ENOLASE 2 (2-PHOSPHOGLYCERATE DEHYDRATASE 2) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE 2) >gi_602253 (U17973) enolase [Zea mays]

Seq. No.	385651
Contig ID	426_4.R1084
5'-most EST	g2798885
Method	BLASTX
NCBI GI	g3023683
BLAST score	99
E value	1.0e-09
Match length	49
% identity	55
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) >gi_2118302_pir__JC4542 6beta-hydroxyhyoscyamine epoxidase (EC 1.14.11.14) - Aspergillus oryzae >gi_1217828_dbj_BAA09973_ (D63941) enolase [Aspergillus oryzae] >gi_2665456_dbj_BAA23760_ (D64113) enolase [Aspergillus oryzae] >gi_1586931_prf__2205241A enolase [Aspergillus oryzae]

Seq. No.	385652
Contig ID	426_5.R1084
5'-most EST	g3767866
Method	BLASTN
NCBI GI	g780371
BLAST score	159
E value	1.0e-83
Match length	364
% identity	95
NCBI Description	Oryza sativa enolase mRNA, complete cds

Seq. No.	385653
Contig ID	426_7.R1084
5'-most EST	g2800360
Method	BLASTX
NCBI GI	g3023713
BLAST score	212
E value	1.0e-16
Match length	45
% identity	93
NCBI Description	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (OSE1) >gi_780372 (U09450) enolase [Oryza sativa]

Seq. No.	385654
Contig ID	431_1.R1084

5'-most EST	g2311138
Method	BLASTX
NCBI GI	g2160314
BLAST score	497
E value	3.0e-50
Match length	141
% identity	79
NCBI Description	(D25236) possible 1-3,1-4-beta-glucanase coding sequence [Oryza sativa]

Seq. No.	385655
Contig ID	434_1.R1084
5'-most EST	g2800570
Method	BLASTX
NCBI GI	g488571
BLAST score	312
E value	2.0e-28
Match length	64
% identity	98
NCBI Description	(U09462) histone H3.2 [Medicago sativa]

Seq. No.	385656
Contig ID	434_2.R1084
5'-most EST	LIB3432-026-P1-K1-E10
Method	BLASTX
NCBI GI	g417103
BLAST score	679
E value	3.0e-71
Match length	136
% identity	100
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to histone H3 (AB015760) [Oryza sativa]

Seq. No.	385657
Contig ID	435_1.R1084
5'-most EST	g1631722
Method	BLASTX

NCBI GI	g585338
BLAST score	1224
E value	1.0e-135
Match length	238
% identity	100
NCBI Description	ADENYLATE KINASE B (ATP-AMP TRANSPHOSPHORYLASE) >gi_391879_dbj_BAA01181_ (D10335) adenylate kinase-b [Oryza sativa]

Seq. No.	385658
Contig ID	435_2.R1084
5'-most EST	g391876
Method	BLASTX
NCBI GI	g585337
BLAST score	1225
E value	1.0e-135
Match length	238
% identity	100
NCBI Description	ADENYLATE KINASE A (ATP-AMP TRANSPHOSPHORYLASE) >gi_391877_dbj_BAA01180_ (D10334) adenylate kinase-a [Oryza sativa]

Seq. No.	385659
Contig ID	435_3.R1084
5'-most EST	g5455346
Method	BLASTN
NCBI GI	g391878
BLAST score	339
E value	0.0e+00
Match length	360
% identity	98
NCBI Description	Oryza sativa mRNA for adenylate kinase-b, complete cds

Seq. No.	385660
Contig ID	437_1.R1084
5'-most EST	LIB3479-003-Q6-K2-G2
Method	BLASTX
NCBI GI	g100675
BLAST score	2377
E value	0.0e+00
Match length	483
% identity	96
NCBI Description	glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) precursor - rice >gi_169759 (J04960) ADP-glucose pyrophosphorylase 51kD subunit (EC 2.7.7.27) [Oryza sativa]

Seq. No.	385661
Contig ID	438_1.R1084
5'-most EST	uC-osflcyp173f03b1
Method	BLASTX
NCBI GI	g417154
BLAST score	1545
E value	1.0e-172
Match length	395
% identity	78
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One)

	>gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
Seq. No.	385662
Contig ID	438_2.R1084
5'-most EST	LIB3474-007-P1-K1-F3
Method	BLASTX
NCBI GI	g417154
BLAST score	1067
E value	1.0e-116
Match length	266
% identity	82
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
Seq. No.	385663
Contig ID	438_3.R1084
5'-most EST	g3090539
Method	BLASTX
NCBI GI	g1515105
BLAST score	282
E value	3.0e-30
Match length	94
% identity	87
NCBI Description	(Y07613) heat shock protein 90A [Arabidopsis thaliana]
Seq. No.	385664
Contig ID	438_4.R1084
5'-most EST	g570030
Method	BLASTX
NCBI GI	g417154
BLAST score	395
E value	7.0e-45
Match length	113
% identity	90
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
Seq. No.	385665
Contig ID	438_6.R1084
5'-most EST	g5004406
Method	BLASTX
NCBI GI	g417154
BLAST score	408
E value	8.0e-40
Match length	109
% identity	85
NCBI Description	HEAT SHOCK PROTEIN 82 >gi_100685_pir__S25541 heat shock protein 82 - rice (strain Taichung Native One) >gi_20256_emb_CAA77978_ (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
Seq. No.	385666

Contig ID	440_1.R1084
5'-most EST	g218137
Method	BLASTX
NCBI GI	g3024122
BLAST score	125
E value	2.0e-10
Match length	41
% identity	75
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	385667
Contig ID	444_1.R1084
5'-most EST	g426577
Method	BLASTX
NCBI GI	g5007084
BLAST score	2147
E value	0.0e+00
Match length	410
% identity	100
NCBI Description	(AF155333) NADP-specific isocitrate dehydrogenase [Oryza sativa]

Seq. No.	385668
Contig ID	445_1.R1084
5'-most EST	uC-osroM202029b11b1
Method	BLASTX
NCBI GI	g2499489
BLAST score	2323
E value	0.0e+00
Match length	547
% identity	80
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE BETA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483536_emb_CAA83683_ (Z32850) pyrophosphate-dependent phosphofructokinase beta subunit [Ricinus communis]

Seq. No.	385669
Contig ID	446_1.R1084
5'-most EST	g1107460
Method	BLASTX
NCBI GI	g1777375
BLAST score	4424
E value	0.0e+00
Match length	890
% identity	98
NCBI Description	(D78573) aspartate kinase-homoserine dehydrogenase [Oryza sativa]

Seq. No.	385670
Contig ID	450_1.R1084
5'-most EST	uC-osf1M202089f01b1
Method	BLASTX
NCBI GI	g283006

BLAST score	385
E value	9.0e-37
Match length	74
% identity	100
NCBI Description	osc6 protein - rice

Seq. No.	385671
Contig ID	452_1.R1084
5'-most EST	LIB3475-010-P1-K1-A12
Method	BLASTX
NCBI GI	g1703380
BLAST score	939
E value	1.0e-101
Match length	181
% identity	100
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	385672
Contig ID	452_2.R1084
5'-most EST	g4878937
Method	BLASTX
NCBI GI	g2293566
BLAST score	937
E value	1.0e-101
Match length	181
% identity	100
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No.	385673
Contig ID	452_3.R1084
5'-most EST	uC-osrocyp009e11b1
Method	BLASTX
NCBI GI	g2293566
BLAST score	925
E value	1.0e-100
Match length	181
% identity	99
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No.	385674
Contig ID	452_4.R1084
5'-most EST	LIB3434-005-P1-K1-C1
Method	BLASTX
NCBI GI	g1703380
BLAST score	934
E value	1.0e-101
Match length	181
% identity	99
NCBI Description	ADP-RIBOSYLATION FACTOR >gi_1132483_dbj_BAA04607_ (D17760) ADP-ribosylation factor [Oryza sativa]

Seq. No.	385675
Contig ID	452_5.R1084
5'-most EST	LIB3433-030-P1-K1-H6
Method	BLASTX
NCBI GI	g2293566

BLAST score	937
E value	1.0e-101
Match length	181
% identity	100
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No.	385676
Contig ID	452_7.R1084
5'-most EST	uC-osflcyp178d11b1
Method	BLASTX
NCBI GI	g2293566
BLAST score	446
E value	4.0e-84
Match length	180
% identity	88
NCBI Description	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]

Seq. No.	385677
Contig ID	452_10.R1084
5'-most EST	LIB3475-011-P1-K1-D4
Method	BLASTN
NCBI GI	g287394
BLAST score	45
E value	3.0e-16
Match length	106
% identity	96
NCBI Description	Oryza sativa mRNA for chilling tolerance related protein, complete cds, clone:pBC121

Seq. No.	385678
Contig ID	455_1.R1084
5'-most EST	g2428652
Method	BLASTX
NCBI GI	g399015
BLAST score	1927
E value	0.0e+00
Match length	382
% identity	97
NCBI Description	ADP,ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator [Oryza sativa]

Seq. No.	385679
Contig ID	455_2.R1084
5'-most EST	g4879574
Method	BLASTX
NCBI GI	g485517
BLAST score	709
E value	5.0e-75
Match length	140
% identity	99
NCBI Description	ADP,ATP carrier protein - rice

Seq. No.	385680
Contig ID	455_3.R1084
5'-most EST	g4879515

Method	BLASTX
NCBI GI	g2129636
BLAST score	185
E value	5.0e-23
Match length	150
% identity	43
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	385681
Contig ID	457_1.R1084
5'-most EST	g4704817
Method	BLASTX
NCBI GI	g283000
BLAST score	4096
E value	0.0e+00
Match length	795
% identity	95
NCBI Description	1,4-alpha-glucan branching enzyme (EC 2.4.1.18) I precursor - rice >gi_218151_dbj_BAA01855_ (D11082) branching enzyme-I precursor [Oryza sativa] >gi_4704818_gb_AAD28284.1_AF136268_1 (AF136268) starch-branching enzyme I [Oryza sativa subsp. japonica]

Seq. No.	385682
Contig ID	463_1.R1084
5'-most EST	g2310386
Method	BLASTX
NCBI GI	g1783305
BLAST score	1576
E value	1.0e-176
Match length	425
% identity	75
NCBI Description	(D78609) bZIP protein [Oryza sativa]

Seq. No.	385683
Contig ID	464_1.R1084
5'-most EST	uC-osflM202082g12b1
Method	BLASTX
NCBI GI	g1705667
BLAST score	2302
E value	0.0e+00
Match length	429
% identity	100
NCBI Description	SERINE CARBOXYPEPTIDASE-LIKE PRECURSOR >gi_409582_dbj_BAA04511_ (D17587) serine carboxypeptidase-like protein [Oryza sativa]

Seq. No.	385684
Contig ID	465_1.R1084
5'-most EST	g435465
Method	BLASTX
NCBI GI	g1705733
BLAST score	2723
E value	0.0e+00
Match length	534
% identity	98

NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1) >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC 2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436) calcium-dependent protein kinase [Oryza sativa]
Seq. No.	385685
Contig ID	465_3.R1084
5'-most EST	g2317488
Method	BLASTX
NCBI GI	g1705733
BLAST score	517
E value	2.0e-52
Match length	108
% identity	88
NCBI Description	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 1 (CDPK 1) >gi_542156_pir__JC1515 calcium-dependent protein kinase (EC 2.7.1.-) - rice >gi_435466_dbj_BAA02698_ (D13436) calcium-dependent protein kinase [Oryza sativa]
Seq. No.	385686
Contig ID	467_1.R1084
5'-most EST	LIB3432-017-P1-K1-D11
Method	BLASTX
NCBI GI	g118170
BLAST score	429
E value	8.0e-42
Match length	102
% identity	85
NCBI Description	CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I) >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259) oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967) oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin [Oryza sativa]
Seq. No.	385687
Contig ID	467_4.R1084
5'-most EST	g2428823
Method	BLASTX
NCBI GI	g118170
BLAST score	310
E value	3.0e-28
Match length	100
% identity	74
NCBI Description	CYSTEINE PROTEINASE INHIBITOR-I (ORYZACYSTATIN-I) >gi_82491_pir__A28464 oryzacystatin - rice >gi_169784 (J03469) oryzacystatin [Oryza sativa] >gi_169807 (M29259) oryzastatin [Oryza sativa] >gi_259137_bbs_120195 (S49967) oryzacystatin=cysteine protease inhibitor [Oryza=rice, Peptide, 102 aa] [Oryza] >gi_1280613 (U54702) oryzacystatin [Oryza sativa]
Seq. No.	385688
Contig ID	468_1.R1084
5'-most EST	LIB3433-014-Q6-K1-G3
Method	BLASTX

NCBI GI	g1084454
BLAST score	448
E value	1.0e-87
Match length	176
% identity	93
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp1 - rice >gi_600765 (L29471) cyclophilin 1 [Oryza sativa]

Seq. No.	385689
Contig ID	469_1.R1084
5'-most EST	LIB3433-026-P1-K1-G8
Method	BLASTX
NCBI GI	g1084455
BLAST score	840
E value	5.0e-90
Match length	172
% identity	93
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	385690
Contig ID	469_2.R1084
5'-most EST	uC-osflcyp152f04b1
Method	BLASTX
NCBI GI	g1084455
BLAST score	768
E value	2.0e-81
Match length	172
% identity	87
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	385691
Contig ID	469_4.R1084
5'-most EST	uC-osflcyp078f07b1
Method	BLASTX
NCBI GI	g1084455
BLAST score	471
E value	5.0e-50
Match length	126
% identity	83
NCBI Description	peptidylprolyl isomerase (EC 5.2.1.8) Cyp2 - rice >gi_600767 (L29469) cyclophilin 2 [Oryza sativa]

Seq. No.	385692
Contig ID	470_1.R1084
5'-most EST	LIB3434-065-P1-K1-C5
Method	BLASTX
NCBI GI	g232031
BLAST score	769
E value	1.0e-81
Match length	224
% identity	71
NCBI Description	ELONGATION FACTOR 1-BETA' (EF-1-BETA') >gi_322851_pir__S29224 translation elongation factor eEF-1 beta' chain - rice >gi_218161_dbj_BAA02253_ (D12821) elongation factor 1 beta' [Oryza sativa]

Seq. No.	385693
Contig ID	472_1.R1084
5'-most EST	g5004606
Method	BLASTX
NCBI GI	g547712
BLAST score	2098
E value	0.0e+00
Match length	412
% identity	100
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	385694
Contig ID	472_2.R1084
5'-most EST	LIB3433-044-P1-K1-A3
Method	BLASTX
NCBI GI	g547712
BLAST score	607
E value	6.0e-63
Match length	120
% identity	98
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A (EIF-4A) >gi_542153_pir__S38358 translation initiation factor eIF-4A - rice >gi_303844_dbj_BAA02152_ (D12627) eukaryotic initiation factor 4A [Oryza sativa]

Seq. No.	385695
Contig ID	473_1.R1084
5'-most EST	g3766815
Method	BLASTX
NCBI GI	g1841391
BLAST score	1297
E value	1.0e-143
Match length	315
% identity	79
NCBI Description	(D64039) EL3 [Oryza sativa]

Seq. No.	385696
Contig ID	473_2.R1084
5'-most EST	uC-osroM202037e06b1
Method	BLASTN
NCBI GI	g984040
BLAST score	252
E value	1.0e-139
Match length	331
% identity	96
NCBI Description	Rice mRNA for EL3 gene, complete cds

Seq. No.	385697
Contig ID	473_3.R1084
5'-most EST	uC-osf1cyp127d05a1
Method	BLASTX
NCBI GI	g3894178
BLAST score	127

E value	4.0e-13
Match length	41
% identity	67
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	385698
Contig ID	480_1.R1084
5'-most EST	LIB3433-045-P1-K1-E12
Method	BLASTX
NCBI GI	g3122703
BLAST score	451
E value	2.0e-44
Match length	142
% identity	68
NCBI Description	60S RIBOSOMAL PROTEIN L23A >gi_2641201 (AF031542) ribosomal protein L23a [Fritillaria agrestis]

Seq. No.	385699
Contig ID	480_2.R1084
5'-most EST	g2311766
Method	BLASTX
NCBI GI	g585876
BLAST score	482
E value	3.0e-48
Match length	125
% identity	76
NCBI Description	60S RIBOSOMAL PROTEIN L23A (L25) >gi_1084424_pir__S48026 ribosomal protein L25 - common tobacco >gi_310935 (L18908) 60S ribosomal protein L25 [Nicotiana tabacum]

Seq. No.	385700
Contig ID	481_1.R1084
5'-most EST	LIB3431-028-P1-K1-F2
Method	BLASTX
NCBI GI	g132672
BLAST score	418
E value	6.0e-57
Match length	122
% identity	98
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L14 >gi_71224_pir__R5RZ14 ribosomal protein L14 - rice chloroplast >gi_12023_emb_CAA33932_ (X15901) ribosomal protein L14 [Oryza sativa] >gi_226644_prf__1603356BU ribosomal protein L14 [Oryza sativa]

Seq. No.	385701
Contig ID	482_1.R1084
5'-most EST	g6012867
Method	BLASTX
NCBI GI	g1173218
BLAST score	650
E value	6.0e-68
Match length	130
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN S15A >gi_440824 (L27461) ribosomal protein S15 [Arabidopsis thaliana] >gi_2150130 (AF001412)

cytoplasmic ribosomal protein S15a [Arabidopsis thaliana]

Seq. No.	385702
Contig ID	483_1.R1084
5'-most EST	LIB3432-012-P1-K1-E5
Method	BLASTX
NCBI GI	g3122386
BLAST score	648
E value	1.0e-92
Match length	203
% identity	51
NCBI Description	WD-40 REPEAT PROTEIN MSI1 >gi_2394227 (AF016845) WD-40 repeat protein [Lycopersicon esculentum]

Seq. No.	385703
Contig ID	484_1.R1084
5'-most EST	LIB3433-034-P1-K1-D5
Method	BLASTN
NCBI GI	g487295
BLAST score	220
E value	1.0e-120
Match length	310
% identity	95
NCBI Description	Rice mRNA EN242, partial sequence

Seq. No.	385704
Contig ID	485_1.R1084
5'-most EST	LIB3434-044-P1-K1-E7
Method	BLASTX
NCBI GI	g445613
BLAST score	839
E value	7.0e-90
Match length	234
% identity	68
NCBI Description	ribosomal protein L7 [Solanum tuberosum]

Seq. No.	385705
Contig ID	490_1.R1084
5'-most EST	g426326
Method	BLASTX
NCBI GI	g2286153
BLAST score	1580
E value	1.0e-176
Match length	331
% identity	92
NCBI Description	(AF007581) cytoplasmic malate dehydrogenase [Zea mays]

Seq. No.	385706
Contig ID	492_1.R1084
5'-most EST	g3767489
Method	BLASTX
NCBI GI	g4996105
BLAST score	885
E value	2.0e-95
Match length	194
% identity	83
NCBI Description	(AB014076) histidine decarboxylase [Brassica napus]

Seq. No.	385707
Contig ID	494_1.R1084
5'-most EST	LIB3434-027-P1-K1-D11
Method	BLASTX
NCBI GI	g480669
BLAST score	191
E value	5.0e-16
Match length	130
% identity	30
NCBI Description	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - Jerusalem artichoke (fragment) >gi_1359894_emb_CAA81210_ (Z26251) NADPH-ferrihemoprotein reductase [Helianthus tuberosus]

Seq. No.	385708
Contig ID	500_1.R1084
5'-most EST	g4880769
Method	BLASTX
NCBI GI	g1174853
BLAST score	753
E value	6.0e-80
Match length	153
% identity	86
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-18 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42) >gi_481811_pir__S39483 ubiquitin-conjugating enzyme UBC2-1 - Arabidopsis thaliana >gi_22658_emb_CAA48378_ (X68306) ubiquitin-conjugating enzyme [Arabidopsis thaliana]

Seq. No.	385709
Contig ID	501_1.R1084
5'-most EST	g286656
Method	BLASTX
NCBI GI	g3914685
BLAST score	757
E value	2.0e-80
Match length	170
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	385710
Contig ID	501_2.R1084
5'-most EST	g3763292
Method	BLASTX
NCBI GI	g3914685
BLAST score	177
E value	2.0e-12
Match length	36
% identity	92
NCBI Description	60S RIBOSOMAL PROTEIN L17 >gi_2668748 (AF034948) ribosomal protein L17 [Zea mays]

Seq. No.	385711
Contig ID	503_1.R1084
5'-most EST	g487314
Method	BLASTX

NCBI GI	g2129754
BLAST score	466
E value	3.0e-46
Match length	132
% identity	73
NCBI Description	translation elongation factor Tu precursor - Arabidopsis thaliana >gi_1149571_emb_CAA61511_ (X89227) mitochondrial elongation factor Tu [Arabidopsis thaliana]

Seq. No.	385712
Contig ID	504_1.R1084
5'-most EST	g487315
Method	BLASTX
NCBI GI	g3142294
BLAST score	394
E value	2.0e-70
Match length	178
% identity	82
NCBI Description	(AC002411) Strong similarity to initiation factor eIF-2, gb_U37354 from S. pombe. ESTs gb_T41979, gb_N37284 and gb_N37529 come from this gene. [Arabidopsis thaliana]

Seq. No.	385713
Contig ID	506_1.R1084
5'-most EST	LIB3434-030-P1-K1-E11
Method	BLASTX
NCBI GI	g113169
BLAST score	416
E value	2.0e-40
Match length	115
% identity	76
NCBI Description	ACYL CARRIER PROTEIN II PRECURSOR (ACP II) >gi_166969 (M63799) acyl carrier protein II [Hordeum vulgare] >gi_228694_prf__1808324A acyl carrier protein II [Hordeum vulgare]

Seq. No.	385714
Contig ID	507_1.R1084
5'-most EST	uC-osf1cyp065d09b1
Method	BLASTX
NCBI GI	g1346764
BLAST score	1569
E value	1.0e-175
Match length	307
% identity	95
NCBI Description	SERINE/THREONINE PROTEIN PHOSPHATASE PP1 >gi_951336_gb_AAA74625_ (U31773) protein phosphatase 1 [Oryza sativa]

Seq. No.	385715
Contig ID	508_1.R1084
5'-most EST	g487320
Method	BLASTX
NCBI GI	g3915054
BLAST score	600
E value	1.0e-63
Match length	124

% identity	98
NCBI Description	SUCROSE SYNTHASE 3 (SUCROSE-UDP GLUCOSYLTRANSFERASE 3) >gi_1196837 (L03366) sucrose synthase 3 [Oryza sativa] >gi_1587663_prf__2207194B sucrose synthase:ISOTYPE=3 [Oryza sativa]

Seq. No.	385716
Contig ID	509_1.R1084
5'-most EST	uC-osflcyp169a01b1
Method	BLASTX
NCBI GI	g3335333
BLAST score	355
E value	2.0e-82
Match length	290
% identity	66
NCBI Description	(AC004512) Similar to chloroplast membrane-associated 30KD protein precursor (IM30) gb_M73744 from Pisum sativum. ESTs gb_N37557, gb_W43887 and gb_AA042479 come from this gene. [Arabidopsis thaliana]

Seq. No.	385717
Contig ID	511_1.R1084
5'-most EST	LIB3431-053-P1-K1-A1
Method	BLASTX
NCBI GI	g871931
BLAST score	526
E value	3.0e-53
Match length	131
% identity	82
NCBI Description	(D30763) ferredoxin [Oryza sativa]

Seq. No.	385718
Contig ID	511_3.R1084
5'-most EST	LIB3431-061-P1-K1-D6
Method	BLASTN
NCBI GI	g505134
BLAST score	170
E value	2.0e-90
Match length	250
% identity	92
NCBI Description	Rice mRNA for ferredoxin, complete cds

Seq. No.	385719
Contig ID	512_1.R1084
5'-most EST	LIB3475-009-P1-K1-F1
Method	BLASTX
NCBI GI	g729480
BLAST score	1948
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	FERREDOXIN--NADP REDUCTASE, ROOT ISOZYME PRECURSOR (FNR) >gi_435647_dbj_BAA04232_ (D17410) ferredoxin-NADP+ reductase [Oryza sativa] >gi_902936_dbj_BAA07479.1_ (D38445) root ferredoxin-NADP+ reductase [Oryza sativa] >gi_1096932_prf__2113196A ferredoxin-NADP oxidoreductase [Oryza sativa]

Seq. No.	385720
Contig ID	513_1.R1084
5'-most EST	g409782
Method	BLASTX
NCBI GI	g729478
BLAST score	1686
E value	0.0e+00
Match length	337
% identity	94
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	385721
Contig ID	513_2.R1084
5'-most EST	LIB3431-054-P1-K1-G7
Method	BLASTX
NCBI GI	g729478
BLAST score	798
E value	2.0e-85
Match length	153
% identity	99
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	385722
Contig ID	514_1.R1084
5'-most EST	uC-osroM202023b03b1
Method	BLASTX
NCBI GI	g2130072
BLAST score	2949
E value	0.0e+00
Match length	581
% identity	97
NCBI Description	ferredoxin--nitrite reductase (EC 1.7.7.1) - rice >gi_809514_dbj_BAA09122_ (D50556) ferredoxin-nitrite reductase [Oryza sativa]

Seq. No.	385723
Contig ID	514_2.R1084
5'-most EST	LIB3431-008-P1-K1-E6
Method	BLASTX
NCBI GI	g2459417
BLAST score	740
E value	3.0e-78
Match length	197
% identity	71
NCBI Description	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]

Seq. No.	385724
Contig ID	516_1.R1084
5'-most EST	g836661
Method	BLASTX
NCBI GI	g1783306
BLAST score	4960
E value	0.0e+00
Match length	986
% identity	96
NCBI Description	(D50602) starch debranching enzyme precursor [Oryza sativa]

Seq. No.	385725
Contig ID	518_1.R1084
5'-most EST	g1208445
Method	BLASTX
NCBI GI	g2058273
BLAST score	886
E value	2.0e-95
Match length	188
% identity	94
NCBI Description	(D83527) YK426 [Oryza sativa]

Seq. No.	385726
Contig ID	518_2.R1084
5'-most EST	g3767012
Method	BLASTX
NCBI GI	g3107903
BLAST score	251
E value	8.0e-21
Match length	154
% identity	52
NCBI Description	(D83719) polycomb-like protein [Daucus carota]

Seq. No.	385727
Contig ID	518_3.R1084
5'-most EST	g2801012
Method	BLASTX
NCBI GI	g2058273
BLAST score	237
E value	1.0e-19
Match length	61
% identity	84
NCBI Description	(D83527) YK426 [Oryza sativa]

Seq. No.	385728
Contig ID	518_5.R1084
5'-most EST	LIB3434-041-P1-K1-F2
Method	BLASTX
NCBI GI	g2058273
BLAST score	467
E value	8.0e-47
Match length	115
% identity	83
NCBI Description	(D83527) YK426 [Oryza sativa]

Seq. No.	385729

Contig ID	523_1.R1084
5'-most EST	LIB3477-005-P1-K1-C12
Method	BLASTX
NCBI GI	g1346109
BLAST score	1704
E value	0.0e+00
Match length	334
% identity	96
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]

Seq. No.	385730
Contig ID	523_2.R1084
5'-most EST	uC-osf1cyp081a09b1
Method	BLASTX
NCBI GI	g1346109
BLAST score	798
E value	2.0e-93
Match length	205
% identity	38
NCBI Description	GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (GPB-LR) (RWD) >gi_540535_dbj_BAA07404_ (D38231) RWD [Oryza sativa]

Seq. No.	385731
Contig ID	526_1.R1084
5'-most EST	g642120
Method	BLASTX
NCBI GI	g642121
BLAST score	1100
E value	1.0e-120
Match length	223
% identity	96
NCBI Description	(L35845) small GTP-binding protein [Oryza sativa]

Seq. No.	385732
Contig ID	526_2.R1084
5'-most EST	g3768641
Method	BLASTX
NCBI GI	g1346957
BLAST score	466
E value	5.0e-73
Match length	146
% identity	95
NCBI Description	RAS-RELATED PROTEIN RAB-2-B >gi_722328 (U22433) GTP binding protein [Zea mays]

Seq. No.	385733
Contig ID	527_1.R1084
5'-most EST	uC-osroM202025e09b1
Method	BLASTX
NCBI GI	g1172635
BLAST score	2027
E value	0.0e+00
Match length	417
% identity	97

NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	385734
Contig ID	527_2.R1084
5'-most EST	LIB3433-037-P1-K1-D2
Method	BLASTX
NCBI GI	g1172635
BLAST score	971
E value	1.0e-105
Match length	209
% identity	94
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 4 HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 2) >gi_556558_dbj_BAA04615_ (D17789) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	385735
Contig ID	528_1.R1084
5'-most EST	uC-osflm202101b12b1
Method	BLASTX
NCBI GI	g1174613
BLAST score	1937
E value	0.0e+00
Match length	403
% identity	96
NCBI Description	26S PROTEASE REGULATORY SUBUNIT 6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) >gi_556560_dbj_BAA04614_ (D17788) rice homologue of Tat binding protein [Oryza sativa]

Seq. No.	385736
Contig ID	532_1.R1084
5'-most EST	LIB3434-044-P1-K1-B5
Method	BLASTX
NCBI GI	g135535
BLAST score	711
E value	5.0e-75
Match length	262
% identity	48
NCBI Description	T-COMPLEX PROTEIN 1, ALPHA SUBUNIT (TCP-1-ALPHA) (CCT-ALPHA) >gi_322602_pir__JN0448 t-complex polypeptide Tcp-1 - Arabidopsis thaliana >gi_217871_dbj_BAA01955_ (D11351) t-complex polypeptide 1 homologue [Arabidopsis thaliana] >gi_2326265_dbj_BAA21772_ (D11352) CCT alpha/TCP-1 [Arabidopsis thaliana]

Seq. No.	385737
Contig ID	533_1.R1084
5'-most EST	g4716224
Method	BLASTX
NCBI GI	g113172
BLAST score	513
E value	9.0e-52
Match length	122
% identity	83
NCBI Description	ACYL CARRIER PROTEIN III PRECURSOR (ACP III)

>gi_100561_pir__S17928 acyl carrier protein 3 - barley
>gi_166971 (M58754) acyl carrier protein III [Hordeum vulgare]

Seq. No.	385738
Contig ID	535_1.R1084
5'-most EST	LIB3434-018-P1-K1-D3
Method	BLASTX
NCBI GI	g464981
BLAST score	563
E value	9.0e-58
Match length	112
% identity	93
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_388207 (L23762) ubiquitin carrier protein [Lycopersicon esculentum]

Seq. No.	385739
Contig ID	535_2.R1084
5'-most EST	uC-osf1M202031h07a1
Method	BLASTX
NCBI GI	g2104681
BLAST score	325
E value	2.0e-29
Match length	321
% identity	34
NCBI Description	(X97907) transcription factor [Vicia faba]

Seq. No.	385740
Contig ID	535_3.R1084
5'-most EST	g5005399
Method	BLASTX
NCBI GI	g2245037
BLAST score	172
E value	4.0e-21
Match length	212
% identity	42
NCBI Description	(Z97342) nuclear antigen homolog [Arabidopsis thaliana]

Seq. No.	385741
Contig ID	536_1.R1084
5'-most EST	g468491
Method	BLASTX
NCBI GI	g5070257
BLAST score	2427
E value	0.0e+00
Match length	822
% identity	95
NCBI Description	(AF095895) lipoxygenase [Oryza sativa]

Seq. No.	385742
Contig ID	537_1.R1084
5'-most EST	g427592
Method	BLASTX
NCBI GI	g433214
BLAST score	1653
E value	0.0e+00

Match length	349
% identity	96
NCBI Description	(D13817) lactate dehydrogenase [Oryza sativa]

Seq. No.	385743
Contig ID	537_2.R1084
5'-most EST	g2311093
Method	BLASTX
NCBI GI	g433214
BLAST score	389
E value	2.0e-38
Match length	92
% identity	98
NCBI Description	(D13817) lactate dehydrogenase [Oryza sativa]

Seq. No.	385744
Contig ID	538_1.R1084
5'-most EST	g530789
Method	BLASTX
NCBI GI	g4689404
BLAST score	817
E value	3.0e-87
Match length	199
% identity	74
NCBI Description	(AF140681) lectin [Oryza sativa subsp. indica] >gi_4689406_gb_AAD27890.1_ (AF140682) lectin [Oryza sativa subsp. japonica]

Seq. No.	385745
Contig ID	541_1.R1084
5'-most EST	g169802
Method	BLASTX
NCBI GI	g118171
BLAST score	395
E value	4.0e-38
Match length	95
% identity	84
NCBI Description	CYSTEINE PROTEINASE INHIBITOR-II (ORYZACYSTATIN-II) >gi_100692_pir__A38375 oryzacystatin II - rice >gi_169803 (J05595) oryzacystatin-II [Oryza sativa]

Seq. No.	385746
Contig ID	542_1.R1084
5'-most EST	g5003428
Method	BLASTX
NCBI GI	g1076739
BLAST score	1131
E value	1.0e-124
Match length	250
% identity	90
NCBI Description	box protein - rice >gi_508577 (L34271) box protein [Oryza sativa]

Seq. No.	385747
Contig ID	543_1.R1084
5'-most EST	g415314
Method	BLASTX

NCBI GI	g1170871
BLAST score	2774
E value	0.0e+00
Match length	555
% identity	97
NCBI Description	MALATE OXIDOREDUCTASE, CHLOROPLAST PRECURSOR (MALIC ENZYME) (ME) (NADP-DEPENDENT MALIC ENZYME) (NADP-ME) >gi_1076749_pir__S46499 NADP-dependent malic enzyme - rice >gi_415315_dbj_BAA03949_ (D16499) NADP-dependent malic enzyme [Oryza sativa]

Seq. No.	385748
Contig ID	544_1.R1084
5'-most EST	LIB3433-045-P1-K1-F6
Method	BLASTX
NCBI GI	g544359
BLAST score	482
E value	3.0e-74
Match length	145
% identity	91
NCBI Description	G10 PROTEIN HOMOLOG >gi_303847_dbj_BAA02153_ (D12628) Maternal G10 like protein [Oryza sativa]

Seq. No.	385749
Contig ID	544_2.R1084
5'-most EST	g3106694
Method	BLASTX
NCBI GI	g544359
BLAST score	392
E value	4.0e-38
Match length	92
% identity	88
NCBI Description	G10 PROTEIN HOMOLOG >gi_303847_dbj_BAA02153_ (D12628) Maternal G10 like protein [Oryza sativa]

Seq. No.	385750
Contig ID	546_1.R1084
5'-most EST	LIB3434-010-P1-K1-E4
Method	BLASTX
NCBI GI	g585551
BLAST score	793
E value	1.0e-84
Match length	149
% identity	100
NCBI Description	NUCLEOSIDE DIPHOSPHATE KINASE I (NDK I) (NDP KINASE I) >gi_629798_pir__S43330 nucleoside-diphosphate kinase (EC 2.7.4.6) - rice >gi_303849_dbj_BAA03798_ (D16292) nucleoside diphosphate kinase [Oryza sativa]

Seq. No.	385751
Contig ID	549_1.R1084
5'-most EST	g5455549
Method	BLASTX
NCBI GI	g3355468
BLAST score	412
E value	2.0e-42
Match length	111

% identity	86
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	385752
Contig ID	549_2.R1084
5'-most EST	g5455536
Method	BLASTX
NCBI GI	g3355468
BLAST score	365
E value	1.0e-34
Match length	118
% identity	69
NCBI Description	(AC004218) putative ribosomal protein L35 [Arabidopsis thaliana]

Seq. No.	385753
Contig ID	551_1.R1084
5'-most EST	g441056
Method	BLASTX
NCBI GI	g729205
BLAST score	870
E value	1.0e-93
Match length	156
% identity	100
NCBI Description	18 KD COLD-INDUCED PROTEIN >gi_287397_dbj_BAA01631_ (D10860) chilling tolerance related protein [Oryza sativa] >gi_445132_prf__1908434B chilling tolerance-related protein:ISOTYPE=pBC442 [Oryza sativa]

Seq. No.	385754
Contig ID	552_1.R1084
5'-most EST	g2310153
Method	BLASTX
NCBI GI	g729206
BLAST score	504
E value	1.0e-50
Match length	259
% identity	58
NCBI Description	PROBABLE GLUTATHIONE S-TRANSFERASE (28 KD COLD-INDUCED PROTEIN) >gi_287399_dbj_BAA01632_ (D10861) chilling tolerance related protein [Oryza sativa] >gi_445133_prf__1908434C chilling tolerance-related protein:ISOTYPE=pBC591 [Oryza sativa]

Seq. No.	385755
Contig ID	552_2.R1084
5'-most EST	uC-osf1M202035f09b1
Method	BLASTX
NCBI GI	g4127350
BLAST score	143
E value	5.0e-15
Match length	124
% identity	42
NCBI Description	(AJ010450) glutathione transferase [Alopecurus myosuroides]

Seq. No.	385756

Contig ID	553_1.R1084
5'-most EST	uC-osf1M202123c04b1
Method	BLASTX
NCBI GI	g218179
BLAST score	4324
E value	0.0e+00
Match length	956
% identity	89
NCBI Description	(D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H ATPase [Oryza sativa]

Seq. No.	385757
Contig ID	553_2.R1084
5'-most EST	g3760931
Method	BLASTX
NCBI GI	g114332
BLAST score	269
E value	2.0e-23
Match length	117
% identity	54
NCBI Description	PLASMA MEMBRANE ATPASE 1 (PROTON PUMP) >gi_482389_pir__A45506 H+-transporting ATPase (EC 3.6.1.35) LHA1 - tomato >gi_170464 (M60166) H+-ATPase [Lycopersicon esculentum] >gi_228405_prf__1803518A H ATPase [Lycopersicon esculentum]

Seq. No.	385758
Contig ID	554_1.R1084
5'-most EST	g633109
Method	BLASTX
NCBI GI	g633110
BLAST score	4383
E value	0.0e+00
Match length	957
% identity	91
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	385759
Contig ID	555_1.R1084
5'-most EST	LIB3431-012-P1-K1-C3
Method	BLASTX
NCBI GI	g4079798
BLAST score	1108
E value	1.0e-121
Match length	245
% identity	89
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	385760
Contig ID	555_3.R1084
5'-most EST	LIB3431-028-P1-K1-H3
Method	BLASTX
NCBI GI	g4079798
BLAST score	480
E value	2.0e-89
Match length	171

% identity	99
NCBI Description	(AF052203) 23 kDa polypeptide of photosystem II [Oryza sativa]

Seq. No.	385761
Contig ID	556_1.R1084
5'-most EST	g452235
Method	BLASTX
NCBI GI	g1171924
BLAST score	1344
E value	1.0e-148
Match length	327
% identity	81
NCBI Description	HOMEOBOX PROTEIN OSH1 >gi_540536_dbj_BAA03959_ (D16507) homeobox protein [Oryza sativa]

Seq. No.	385762
Contig ID	557_1.R1084
5'-most EST	g886404
Method	BLASTX
NCBI GI	g2130078
BLAST score	1115
E value	1.0e-122
Match length	236
% identity	94
NCBI Description	MADS-box protein 3 - rice >gi_886405 (L37528) MADS box protein [Oryza sativa]

Seq. No.	385763
Contig ID	558_1.R1084
5'-most EST	g218180
Method	BLASTX
NCBI GI	g129231
BLAST score	2276
E value	0.0e+00
Match length	458
% identity	93
NCBI Description	ORYZAIN ALPHA CHAIN PRECURSOR >gi_67644_pir__KHRZOA oryzain (EC 3.4.22.-) alpha precursor - rice >gi_218181_dbj_BAA14402_ (D90406) oryzain alpha precursor [Oryza sativa]

Seq. No.	385764
Contig ID	558_3.R1084
5'-most EST	g3761115
Method	BLASTN
NCBI GI	g218180
BLAST score	224
E value	1.0e-123
Match length	259
% identity	96
NCBI Description	Rice mRNA for oryzain alpha (EC 3.4.22)

Seq. No.	385765
Contig ID	559_1.R1084
5'-most EST	g2800948
Method	BLASTX

NCBI GI	g129232
BLAST score	2268
E value	0.0e+00
Match length	444
% identity	95
NCBI Description	ORYZAIN BETA CHAIN PRECURSOR >gi_67645_pir__KHRZOB oryzain (EC 3.4.22.-) beta precursor - rice >gi_218183_dbj_BAA14403_ (D90407) oryzain beta precursor [Oryza sativa]

Seq. No.	385766
Contig ID	560_1.R1084
5'-most EST	LIB3431-011-P1-K1-A3
Method	BLASTX
NCBI GI	g129233
BLAST score	1763
E value	0.0e+00
Match length	362
% identity	92
NCBI Description	ORYZAIN GAMMA CHAIN PRECURSOR >gi_67646_pir__KHRZOG oryzain (EC 3.4.22.-) gamma precursor - rice >gi_218185_dbj_BAA14404_ (D90408) oryzain gamma precursor [Oryza sativa]

Seq. No.	385767
Contig ID	560_2.R1084
5'-most EST	g2431133
Method	BLASTN
NCBI GI	g218184
BLAST score	71
E value	5.0e-31
Match length	85
% identity	98
NCBI Description	Rice mRNA for oryzain gamma (EC 3.4.22)

Seq. No.	385768
Contig ID	560_3.R1084
5'-most EST	g4880173
Method	BLASTX
NCBI GI	g4210332
BLAST score	287
E value	3.0e-28
Match length	92
% identity	76
NCBI Description	(AJ223803) 2-oxoglutarate dehydrogenase E2 subunit [Arabidopsis thaliana]

Seq. No.	385769
Contig ID	561_1.R1084
5'-most EST	g1785855
Method	BLASTX
NCBI GI	g1785856
BLAST score	1515
E value	1.0e-169
Match length	269
% identity	100
NCBI Description	(D78505) w-3 fatty acid desaturase [Oryza sativa]

Seq. No.	385770
Contig ID	562_1.R1084
5'-most EST	g5038903
Method	BLASTX
NCBI GI	g1709758
BLAST score	1269
E value	1.0e-140
Match length	270
% identity	92
NCBI Description	PROTEASOME COMPONENT C2 (MACROPAIN SUBUNIT C2) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C2) >gi_1066151_dbj_BAA07128_ (D37886) proteasome C2 subunit [Oryza sativa]

Seq. No.	385771
Contig ID	563_1.R1084
5'-most EST	uC-osrocyp014d09b1
Method	BLASTX
NCBI GI	g585661
BLAST score	1521
E value	1.0e-169
Match length	304
% identity	96
NCBI Description	PEROXIDASE PRECURSOR >gi_287401_dbj_BAA03644_ (D14997) peroxidase [Oryza sativa]

Seq. No.	385772
Contig ID	565_1.R1084
5'-most EST	g568105
Method	BLASTX
NCBI GI	g453692
BLAST score	527
E value	2.0e-53
Match length	173
% identity	66
NCBI Description	(L24390) AT hook 1 from AA 98-106, AT hook 2 from AA 129-137, AT hook 3 from AA 154-162, AT hook 4 from AA 192-200. [Oryza sativa]

Seq. No.	385773
Contig ID	568_1.R1084
5'-most EST	LIB3479-005-Q6-K1-F8
Method	BLASTX
NCBI GI	g2499709
BLAST score	4334
E value	0.0e+00
Match length	812
% identity	100
NCBI Description	PHOSPHOLIPASE D 1 PRECURSOR (PLD 1) (CHOLINE PHOSPHATASE 1) (PHOSPHATIDYLCHOLINE-HYDROLYZING PHOSPHOLIPASE D 1) >gi_1020415_dbj_BAA11136_ (D73411) phospholipase D [Oryza sativa] >gi_1902903_dbj_BAA19467_ (AB001920) phospholipase D [Oryza sativa]

Seq. No.	385774
Contig ID	572_1.R1084

5'-most EST	g450299
Method	BLASTX
NCBI GI	g1076755
BLAST score	4215
E value	0.0e+00
Match length	824
% identity	97
NCBI Description	protein kinase - rice >gi_450300 (L27821) protein kinase [Oryza sativa]

Seq. No.	385775
Contig ID	576_1.R1084
5'-most EST	LIB3433-007-Q6-K1-C6
Method	BLASTX
NCBI GI	g1097875
BLAST score	1638
E value	0.0e+00
Match length	326
% identity	96
NCBI Description	peroxidase:ISOTYPE=RPA [Oryza sativa]

Seq. No.	385776
Contig ID	577_1.R1084
5'-most EST	g428324
Method	BLASTX
NCBI GI	g1853975
BLAST score	1643
E value	0.0e+00
Match length	335
% identity	96
NCBI Description	(D14482) putative peroxidase [Oryza sativa]

Seq. No.	385777
Contig ID	584_1.R1084
5'-most EST	g971279
Method	BLASTX
NCBI GI	g1710078
BLAST score	688
E value	1.0e-122
Match length	220
% identity	99
NCBI Description	RAB24 PROTEIN >gi_971280_dbj_BAA09947_ (D63917) RAB24 protein [Oryza sativa]

Seq. No.	385778
Contig ID	584_2.R1084
5'-most EST	LIB3434-035-P1-K1-G1
Method	BLASTX
NCBI GI	g1710078
BLAST score	675
E value	6.0e-71
Match length	150
% identity	81
NCBI Description	RAB24 PROTEIN >gi_971280_dbj_BAA09947_ (D63917) RAB24 protein [Oryza sativa]

Seq. No.	385779

Contig ID	586_1.R1084
5'-most EST	LIB3433-040-P1-K1-F10
Method	BLASTX
NCBI GI	g1084462
BLAST score	370
E value	4.0e-35
Match length	125
% identity	60
NCBI Description	RCg2 protein - rice >gi_786130 (L27209) RCc2 [Oryza sativa] >gi_786134 (L27210) root-specific protein [Oryza sativa]

Seq. No.	385780
Contig ID	587_1.R1084
5'-most EST	LIB3434-009-P1-K1-F10
Method	BLASTX
NCBI GI	g1084461
BLAST score	475
E value	3.0e-47
Match length	133
% identity	71
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	385781
Contig ID	587_2.R1084
5'-most EST	LIB3433-034-P1-K1-A7
Method	BLASTX
NCBI GI	g1084461
BLAST score	497
E value	6.0e-50
Match length	130
% identity	78
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	385782
Contig ID	587_3.R1084
5'-most EST	LIB3434-048-P1-K1-H12
Method	BLASTX
NCBI GI	g1084461
BLAST score	189
E value	1.0e-23
Match length	59
% identity	97
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	385783
Contig ID	588_1.R1084
5'-most EST	g2311837
Method	BLASTX
NCBI GI	g505136
BLAST score	776
E value	1.0e-82
Match length	148
% identity	100
NCBI Description	(D30794) ferredoxin [Oryza sativa]

Seq. No.	385784
Contig ID	588_2.R1084

5'-most EST	LIB3433-015-Q6-K1-C6
Method	BLASTX
NCBI GI	g2073385
BLAST score	293
E value	3.0e-26
Match length	54
% identity	100
NCBI Description	(D83660) root ferredoxin [Oryza sativa]

Seq. No.	385785
Contig ID	589_1.R1084
5'-most EST	g218227
Method	BLASTX
NCBI GI	g730512
BLAST score	1097
E value	1.0e-120
Match length	217
% identity	100
NCBI Description	RAS-RELATED PROTEIN RIC2 >gi_481506_pir__S38741 GTP-binding protein ric2 - rice >gi_218228_dbj_BAA02904_ (D13758) ras-related GTP binding protein [Oryza sativa]

Seq. No.	385786
Contig ID	589_2.R1084
5'-most EST	LIB3434-011-P1-K1-C10
Method	BLASTX
NCBI GI	g3024552
BLAST score	981
E value	1.0e-106
Match length	213
% identity	92
NCBI Description	RAS-RELATED PROTEIN RGP2 (GTP-BINDING REGULATORY PROTEIN RGP2) >gi_419797_pir__S30273 GTP-binding protein rgp2 - rice >gi_218204_dbj_BAA02437_ (D13152) GTP binding protein [Oryza sativa] >gi_446772_prf__1912297A rgp2 gene [Oryza sativa]

Seq. No.	385787
Contig ID	594_1.R1084
5'-most EST	LIB3479-008-Q6-K1-E2
Method	BLASTX
NCBI GI	g548770
BLAST score	2056
E value	0.0e+00
Match length	389
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	385788
Contig ID	594_2.R1084
5'-most EST	uC-osflcyp124b01b1
Method	BLASTX
NCBI GI	g548770
BLAST score	595
E value	1.0e-61

Match length	117
% identity	96
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	385789
Contig ID	596_1.R1084
5'-most EST	LIB3434-019-P1-K1-D2
Method	BLASTX
NCBI GI	g548774
BLAST score	846
E value	1.0e-120
Match length	254
% identity	89
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	385790
Contig ID	596_2.R1084
5'-most EST	g2443027
Method	BLASTX
NCBI GI	g548774
BLAST score	663
E value	1.0e-112
Match length	258
% identity	79
NCBI Description	60S RIBOSOMAL PROTEIN L7A >gi_542158_pir__S38360 ribosomal protein L7a - rice >gi_303855_dbj_BAA02156_ (D12631) ribosomal protein L7A [Oryza sativa]

Seq. No.	385791
Contig ID	597_1.R1084
5'-most EST	g2799213
Method	BLASTX
NCBI GI	g1350777
BLAST score	410
E value	8.0e-40
Match length	84
% identity	99
NCBI Description	60S RIBOSOMAL PROTEIN L9 >gi_971282_dbj_BAA07209_ (D38012) ribosomal protein L9 [Oryza sativa]

Seq. No.	385792
Contig ID	598_1.R1084
5'-most EST	g6012840
Method	BLASTX
NCBI GI	g1362009
BLAST score	663
E value	2.0e-69
Match length	153
% identity	59
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	385793
Contig ID	598_2.R1084

5'-most EST	g3760730
Method	BLASTX
NCBI GI	g485518
BLAST score	667
E value	6.0e-70
Match length	129
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]

Seq. No.	385794
Contig ID	598_3.R1084
5'-most EST	LIB3433-052-P1-K1-C12
Method	BLASTX
NCBI GI	g1362009
BLAST score	663
E value	2.0e-69
Match length	152
% identity	60
NCBI Description	ubiquitin-like protein 7 - Arabidopsis thaliana

Seq. No.	385795
Contig ID	598_4.R1084
5'-most EST	LIB3434-043-P1-K1-G7
Method	BLASTX
NCBI GI	g485518
BLAST score	667
E value	6.0e-70
Match length	129
% identity	100
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice >gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]

Seq. No.	385796
Contig ID	598_6.R1084
5'-most EST	LIB3599-001-P1-K6-G2
Method	BLASTN
NCBI GI	g303856
BLAST score	205
E value	1.0e-111
Match length	277
% identity	100
NCBI Description	Rice mRNA for ubiquitin protein fused to a ribosomal protein, complete cds

Seq. No.	385797
Contig ID	598_7.R1084
5'-most EST	g4880768
Method	BLASTX
NCBI GI	g485518
BLAST score	313
E value	1.0e-31
Match length	103
% identity	73
NCBI Description	ubiquitin / ribosomal protein CEP52 - rice

	>gi_303857_dbj_BAA02154_ (D12629) ubiquitin/ribosomal polyprotein [Oryza sativa]
Seq. No.	385798
Contig ID	599_1.R1084
5'-most EST	LIB3433-058-P1-K1-A6
Method	BLASTX
NCBI GI	g1350969
BLAST score	360
E value	6.0e-34
Match length	67
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_ (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.	385799
Contig ID	599_2.R1084
5'-most EST	g2800821
Method	BLASTX
NCBI GI	g1350969
BLAST score	425
E value	2.0e-41
Match length	84
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S26 (S31) >gi_971284_dbj_BAA07208_ (D38011) ribosomal protein S31 [Oryza sativa]
Seq. No.	385800
Contig ID	599_3.R1084
5'-most EST	g2800677
Method	BLASTN
NCBI GI	g971283
BLAST score	40
E value	7.0e-13
Match length	80
% identity	89
NCBI Description	Rice mRNA for ribosomal protein S31, complete cds
Seq. No.	385801
Contig ID	600_1.R1084
5'-most EST	LIB3434-025-P1-K1-G7
Method	BLASTX
NCBI GI	g4582468
BLAST score	987
E value	1.0e-107
Match length	224
% identity	87
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]
Seq. No.	385802
Contig ID	600_2.R1084
5'-most EST	LIB3475-002-P1-K2-A4
Method	BLASTX
NCBI GI	g4582468
BLAST score	1008
E value	1.0e-109

Match length	227
% identity	88
NCBI Description	(AC007071) putative 40S ribosomal protein; contains C-terminal domain [Arabidopsis thaliana]

Seq. No.	385803
Contig ID	600_3.R1084
5'-most EST	g561664
Method	BLASTX
NCBI GI	g133940
BLAST score	178
E value	7.0e-18
Match length	73
% identity	73
NCBI Description	40S RIBOSOMAL PROTEIN S3A (S1A) >gi_70851_pir__R3XL3A ribosomal protein S3a - African clawed frog >gi_65091_emb_CAA40592_ (X57322) ribosomal protein S1a [Xenopus laevis]

Seq. No.	385804
Contig ID	601_1.R1084
5'-most EST	LIB3479-009-Q6-K1-G3
Method	BLASTX
NCBI GI	g1351014
BLAST score	954
E value	1.0e-103
Match length	212
% identity	89
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	385805
Contig ID	601_2.R1084
5'-most EST	LIB3599-002-P1-N6-E9
Method	BLASTX
NCBI GI	g1351014
BLAST score	404
E value	4.0e-39
Match length	84
% identity	93
NCBI Description	40S RIBOSOMAL PROTEIN S8 >gi_968902_dbj_BAA07207_ (D38010) ribosomal protein S8 [Oryza sativa]

Seq. No.	385806
Contig ID	601_3.R1084
5'-most EST	LIB3433-012-Q6-K1-H10
Method	BLASTX
NCBI GI	g1498053
BLAST score	675
E value	9.0e-71
Match length	220
% identity	80
NCBI Description	(U64436) ribosomal protein S8 [Zea mays]

Seq. No.	385807
Contig ID	602_1.R1084
5'-most EST	uC-osroM202018h10b1

Method	BLASTX
NCBI GI	g1172818
BLAST score	697
E value	2.0e-73
Match length	139
% identity	99
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A ribosomal protein S16 [Oryza sativa]

Seq. No.	385808
Contig ID	602_4.R1084
5'-most EST	g3763366
Method	BLASTN
NCBI GI	g2352024
BLAST score	70
E value	1.0e-30
Match length	126
% identity	86
NCBI Description	Cloning vector pRS401 with MET15 marker, complete sequence

Seq. No.	385809
Contig ID	602_5.R1084
5'-most EST	LIB3431-018-P1-N1-B3
Method	BLASTX
NCBI GI	g1172818
BLAST score	179
E value	2.0e-25
Match length	67
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A ribosomal protein S16 [Oryza sativa]

Seq. No.	385810
Contig ID	602_6.R1084
5'-most EST	uC-osf1cyp101a03b1
Method	BLASTX
NCBI GI	g1172818
BLAST score	447
E value	2.0e-44
Match length	93
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S16 >gi_538428 (L36313) ribosomal protein S16 [Oryza sativa] >gi_1096552_prf__2111468A ribosomal protein S16 [Oryza sativa]

Seq. No.	385811
Contig ID	606_1.R1084
5'-most EST	LIB3474-011-P1-K1-E4

Seq. No.	385812
Contig ID	606_2.R1084
5'-most EST	g3759087

Seq. No.	385813
Contig ID	606_3.R1084

5'-most EST	g3759086
Method	BLASTX
NCBI GI	g2407281
BLAST score	349
E value	2.0e-32
Match length	65
% identity	100
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	385814
Contig ID	606_4.R1084
5'-most EST	LIB3434-028-P1-K1-G1

Seq. No.	385815
Contig ID	606_5.R1084
5'-most EST	LIB3432-042-P2-K1-E6
Method	BLASTX
NCBI GI	g132105
BLAST score	477
E value	2.0e-75
Match length	173
% identity	88
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN C PRECURSOR (RUBISCO SMALL SUBUNIT C) >gi_68094_pir__RKRZS9 ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor (clone pOSSS1139) - rice >gi_218208_dbj_BAA00538_ (D00643) small subunit of ribulose-1,5-bisphosphate carboxylase (RuBPC) [Oryza sativa] >gi_2407283 (AF017364) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa] >gi_226375_prf__1508256A ribulose bisphosphate carboxylase S [Oryza sativa]

Seq. No.	385816
Contig ID	606_6.R1084
5'-most EST	LIB3432-005-P1-K1-E6
Method	BLASTX
NCBI GI	g2407281
BLAST score	313
E value	4.0e-61
Match length	166
% identity	81
NCBI Description	(AF017363) ribulose 1,5-bisphosphate carboxylase small subunit [Oryza sativa]

Seq. No.	385817
Contig ID	606_7.R1084
5'-most EST	g702442
Method	BLASTX
NCBI GI	g309673
BLAST score	207
E value	1.0e-15
Match length	252
% identity	25
NCBI Description	(L19651) light harvesting protein [Pisum sativum]

Seq. No. 385818

Contig ID	606_8.R1084
5'-most EST	LIB3431-040-P1-N1-H9
Method	BLASTX
NCBI GI	g81885
BLAST score	133
E value	5.0e-13
Match length	164
% identity	36
NCBI Description	ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor - kidney bean >gi_21050_emb_CAA42618_ (X60000) ribulose bisphosphate carboxylase [Phaseolus vulgaris] >gi_21053_emb_CAA40339_ (X57022) small subunit of ribulose 1,5-bisphosphate carboxylase/oxygenase [Phaseolus vulgaris]

Seq. No.	385819
Contig ID	608_1.R1084
5'-most EST	uC-osrocyp009c09b1
Method	BLASTX
NCBI GI	g4895248
BLAST score	414
E value	4.0e-60
Match length	139
% identity	88
NCBI Description	(AC007659) putative mitochondrial elongation factor G [Arabidopsis thaliana]

Seq. No.	385820
Contig ID	610_1.R1084
5'-most EST	g426709
Method	BLASTX
NCBI GI	g322787
BLAST score	753
E value	1.0e-112
Match length	238
% identity	89
NCBI Description	pyruvate kinase (EC 2.7.1.40), cytosolic - potato

Seq. No.	385821
Contig ID	611_1.R1084
5'-most EST	uC-osroM202041f03b1
Method	BLASTX
NCBI GI	g129916
BLAST score	534
E value	1.0e-54
Match length	129
% identity	83
NCBI Description	PHOSPHOGLYCERATE KINASE, CYTOSOLIC >gi_66911_pir__TVWTGY phosphoglycerate kinase (EC 2.7.2.3), cytosolic - wheat >gi_21835_emb_CAA33302_ (X15232) phosphoglycerate kinase (AA 1 - 401) [Triticum aestivum]

Seq. No.	385822
Contig ID	612_1.R1084
5'-most EST	g218213
Method	BLASTX
NCBI GI	g100654
BLAST score	148

E value	6.0e-10
Match length	42
% identity	76
NCBI Description	alpha-amylase (EC 3.2.1.1) precursor (clone pOS103) - rice >gi_169753 (M24286) alpha-amylase (EC 3.2.1.1) [Oryza sativa]

Seq. No.	385823
Contig ID	613_1.R1084
5'-most EST	LIB3475-002-P1-K2-G11
Method	BLASTX
NCBI GI	g401140
BLAST score	3452
E value	0.0e+00
Match length	651
% identity	100
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza sativa]

Seq. No.	385824
Contig ID	614_1.R1084
5'-most EST	uC-osflm202110g12b1
Method	BLASTX
NCBI GI	g2129929
BLAST score	753
E value	1.0e-104
Match length	196
% identity	95
NCBI Description	DNA-directed RNA polymerase (EC 2.7.7.6) II chain RPB2 - tomato >gi_1049068 (U28403) RNA polymerase II subunit 2 [Solanum lycopersicum]

Seq. No.	385825
Contig ID	616_1.R1084
5'-most EST	g455504
Method	BLASTN
NCBI GI	g455504
BLAST score	154
E value	2.0e-81
Match length	154
% identity	100
NCBI Description	Rice mRNA for succinate dehydrogenase flavoprotein subunit, partial sequence >gi_3106505_dbj_D42221_D42221 Rice callus cDNA, S087

Seq. No.	385826
Contig ID	617_1.R1084
5'-most EST	LIB3432-057-P1-K1-G8
Method	BLASTX
NCBI GI	g543711
BLAST score	1297
E value	1.0e-143
Match length	260
% identity	99

NCBI Description	14-3-3-LIKE PROTEIN S94 >gi_419796_pir__S30927 14-3-3 protein homolog - rice >gi_303859_dbj_BAA03711_ (D16140) brain specific protein [Oryza sativa]
Seq. No.	385827
Contig ID	617_2.R1084
5'-most EST	uC-osflm202101b04b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	899
E value	1.0e-96
Match length	553
% identity	58
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	385828
Contig ID	617_4.R1084
5'-most EST	g2311165
Method	BLASTN
NCBI GI	g303858
BLAST score	265
E value	1.0e-147
Match length	321
% identity	96
NCBI Description	Rice mRNA for brain specific protein (S94 gene), complete cds
Seq. No.	385829
Contig ID	617_5.R1084
5'-most EST	g4879985
Method	BLASTN
NCBI GI	g303858
BLAST score	228
E value	1.0e-125
Match length	248
% identity	98
NCBI Description	Rice mRNA for brain specific protein (S94 gene), complete cds
Seq. No.	385830
Contig ID	618_1.R1084
5'-most EST	g2310224
Method	BLASTX
NCBI GI	g3915029
BLAST score	1965
E value	0.0e+00
Match length	390
% identity	96
NCBI Description	ACYL-[ACYL-CARRIER PROTEIN] DESATURASE PRECURSOR (STEAROYL-ACP DESATURASE) >gi_976257_dbj_BAA07631_ (D38753) stearyl-ACP desaturase [Oryza sativa]
Seq. No.	385831
Contig ID	619_1.R1084
5'-most EST	LIB3432-015-P1-K1-E9
Method	BLASTX
NCBI GI	g134595

BLAST score	808
E value	2.0e-86
Match length	152
% identity	100
NCBI Description	SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa]

Seq. No.	385832
Contig ID	619_3.R1084
5'-most EST	LIB3431-007-P1-K1-E3
Method	BLASTX
NCBI GI	g134595
BLAST score	475
E value	1.0e-47
Match length	89
% identity	99
NCBI Description	SUPEROXIDE DISMUTASE-1 [CU-ZN] >gi_280412_pir__S22508 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodA - rice >gi_218224_dbj_BAA00799_ (D00999) copper/zinc-superoxide dismutase [Oryza sativa] >gi_685242 (L19435) cytosolic copper/zinc-superoxide dismutase [Oryza sativa] >gi_1096504_prf__2111424A Cu/Zn superoxide dismutase [Oryza sativa]

Seq. No.	385833
Contig ID	621_1.R1084
5'-most EST	g571898
Method	BLASTX
NCBI GI	g134596
BLAST score	802
E value	1.0e-85
Match length	152
% identity	100
NCBI Description	SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_100713_pir__S21136 superoxide dismutase (EC 1.15.1.1) (Cu-Zn) sodB - rice >gi_218226_dbj_BAA00800.1_ (D01000) copper/zinc-superoxide dismutase [Oryza sativa] >gi_310321 (L19434) cytosolic copper/zinc-superoxide dismutase [Oryza sativa]

Seq. No.	385834
Contig ID	623_1.R1084
5'-most EST	g3762620
Method	BLASTX
NCBI GI	g1717957
BLAST score	1105
E value	1.0e-121
Match length	248
% identity	85
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (RIESKE IRON-SULFUR PROTEIN) (RISP) >gi_100923_pir__A41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - maize

>gi_168607 (M77224) Rieske Fe-S protein [Zea mays]

Seq. No.	385835
Contig ID	624_1.R1084
5'-most EST	LIB3432-042-P2-K1-B12
Method	BLASTX
NCBI GI	g3128228
BLAST score	857
E value	4.0e-92
Match length	178
% identity	89
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	385836
Contig ID	624_2.R1084
5'-most EST	g3760982
Method	BLASTX
NCBI GI	g3402817
BLAST score	171
E value	9.0e-16
Match length	51
% identity	94
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	385837
Contig ID	624_3.R1084
5'-most EST	uC-osflcyp152c10b1
Method	BLASTX
NCBI GI	g3128228
BLAST score	858
E value	3.0e-92
Match length	178
% identity	89
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	385838
Contig ID	624_4.R1084
5'-most EST	LIB3431-015-P1-K1-F11
Method	BLASTX
NCBI GI	g3128228
BLAST score	659
E value	5.0e-69
Match length	144
% identity	85
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	385839
Contig ID	624_5.R1084
5'-most EST	uC-osflcyp126e11b1
Method	BLASTX
NCBI GI	g3128228

BLAST score	774
E value	2.0e-82
Match length	183
% identity	82
NCBI Description	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] >gi_3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]

Seq. No.	385840
Contig ID	625_1.R1084
5'-most EST	g2427850
Method	BLASTX
NCBI GI	g3789948
BLAST score	839
E value	7.0e-90
Match length	160
% identity	100
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	385841
Contig ID	625_2.R1084
5'-most EST	LIB3434-023-P1-K1-G1
Method	BLASTX
NCBI GI	g3789948
BLAST score	432
E value	3.0e-42
Match length	154
% identity	75
NCBI Description	(AF094773) translation initiation factor 5A [Oryza sativa]

Seq. No.	385842
Contig ID	627_1.R1084
5'-most EST	g1944503
Method	BLASTX
NCBI GI	g1944504
BLAST score	1589
E value	1.0e-177
Match length	302
% identity	100
NCBI Description	(D64036) protein cdc2 kinase [Oryza sativa]

Seq. No.	385843
Contig ID	630_1.R1084
5'-most EST	g2442414
Method	BLASTX
NCBI GI	g629858
BLAST score	634
E value	5.0e-66
Match length	129
% identity	92
NCBI Description	protein kinase C inhibitor - maize

Seq. No.	385844
Contig ID	632_1.R1084
5'-most EST	g4879591
Method	BLASTX
NCBI GI	g3851003

BLAST score	398
E value	2.0e-38
Match length	155
% identity	59
NCBI Description	(AF069910) pyruvate dehydrogenase E1 beta subunit isoform 3 [Zea mays]

Seq. No.	385845
Contig ID	633_1.R1084
5'-most EST	g2431356
Method	BLASTX
NCBI GI	g4567273
BLAST score	1020
E value	1.0e-111
Match length	310
% identity	66
NCBI Description	(AC006841) putative vacuolar proton ATPase subunit [Arabidopsis thaliana]

Seq. No.	385846
Contig ID	634_1.R1084
5'-most EST	uC-osf1M202091a03b1
Method	BLASTX
NCBI GI	g6094430
BLAST score	621
E value	1.0e-115
Match length	238
% identity	89
NCBI Description	TUBULIN ALPHA-2 CHAIN (ALPHA-TUBULIN 2) >gi_2511533 (AF008121) alpha-tubulin 2 [Eleusine indica]

Seq. No.	385847
Contig ID	635_1.R1084
5'-most EST	uC-osf1m202100g09b1
Method	BLASTX
NCBI GI	g459009
BLAST score	764
E value	1.0e-133
Match length	425
% identity	55
NCBI Description	(U00037) similar to multifunctional aminoacyl-tRNA synthetase, especially to the prolyl-tRNA synthetase region [Caenorhabditis elegans]

Seq. No.	385848
Contig ID	636_1.R1084
5'-most EST	g429005
Method	BLASTX
NCBI GI	g4506701
BLAST score	114
E value	2.0e-10
Match length	52
% identity	79
NCBI Description	ribosomal protein S23 >gi_730647_sp_P39028_RS23_HUMAN 40S RIBOSOMAL PROTEIN S23 >gi_543449_pir__S41955 ribosomal protein S23 - rat >gi_631360_pir__S42105 ribosomal protein S23, cytosolic - human >gi_414349_dbj_BAA03400_ (D14530)

ribosomal protein [Homo sapiens] >gi_453281_emb_CAA54584_ (X77398) ribosomal protein S23 [Rattus norvegicus]

Seq. No.	385849
Contig ID	639_1.R1084
5'-most EST	LIB3433-015-Q6-K6-F4
Method	BLASTX
NCBI GI	g1742951
BLAST score	603
E value	1.0e-62
Match length	129
% identity	87
NCBI Description	(Y09817) Ca2+-ATPase [Arabidopsis thaliana]

Seq. No.	385850
Contig ID	639_2.R1084
5'-most EST	LIB3433-008-Q6-K1-B4
Method	BLASTX
NCBI GI	g1943751
BLAST score	847
E value	1.0e-104
Match length	204
% identity	87
NCBI Description	(U93845) Arabidopsis thaliana ER-type calcium pump protein, complete sequence >gi_2078292 (U96455) ER-type Ca2+-pumping ATPase; ECA1p [Arabidopsis thaliana]

Seq. No.	385851
Contig ID	641_1.R1084
5'-most EST	LIB3431-045-P1-K1-D12
Method	BLASTX
NCBI GI	g1174780
BLAST score	897
E value	7.0e-97
Match length	188
% identity	91
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR (ORANGE PERICARP 2) >gi_320135_pir__PQ0450 tryptophan synthase (EC 4.2.1.20) beta-2 chain precursor - maize (fragment) >gi_168574 (M76685) tryptophan synthase beta-subunit [Zea mays]

Seq. No.	385852
Contig ID	644_1.R1084
5'-most EST	g2394299
Method	BLASTX
NCBI GI	g118011
BLAST score	558
E value	4.0e-57
Match length	103
% identity	100
NCBI Description	CYTOCHROME C >gi_625189_pir__CCRZ cytochrome c - rice >gi_169786 (M63704) cytochrome c [Oryza sativa] >gi_218249_dbj_BAA02159_ (D12634) 'cytochrome C' [Oryza sativa]

Seq. No.	385853
Contig ID	645_1.R1084

5'-most EST	LIB3474-011-P1-K1-F8
Method	BLASTX
NCBI GI	g3915131
BLAST score	592
E value	5.0e-61
Match length	114
% identity	100
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	385854
Contig ID	645_3.R1084
5'-most EST	g4878988
Method	BLASTX
NCBI GI	g3915131
BLAST score	505
E value	2.0e-53
Match length	111
% identity	91
NCBI Description	THIOREDOXIN H-TYPE (TRX-H) (PHLOEM SAP 13 KD PROTEIN-1) >gi_426442_dbj_BAA04864_ (D21836) thioredoxin h [Oryza sativa] >gi_454882_dbj_BAA05546_ (D26547) rice thioredoxin h [Oryza sativa] >gi_1930072 (U92541) thioredoxin h [Oryza sativa]

Seq. No.	385855
Contig ID	648_1.R1084
5'-most EST	LIB3477-002-P1-K1-F1
Method	BLASTX
NCBI GI	g2499488
BLAST score	1647
E value	0.0e+00
Match length	453
% identity	71
NCBI Description	PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-PHOSPHOTRANSFERASE ALPHA SUBUNIT (PFP) (6-PHOSPHOFRUCTOKINASE (PYROPHOSPHATE)) (PYROPHOSPHATE-DEPENDENT 6-PHOSPHOFRUCTOSE-1-KINASE) (PPI-PFK) >gi_483547_emb_CAA83682_ (Z32849) pyrophosphate-dependent phosphofructokinase alpha subunit [Ricinus communis]

Seq. No.	385856
Contig ID	649_1.R1084
5'-most EST	LIB3475-007-P1-K1-D2
Method	BLASTX
NCBI GI	g2708634
BLAST score	2432
E value	0.0e+00
Match length	469
% identity	100
NCBI Description	(AF036957) gamma-tubulin [Oryza sativa]

Seq. No.	385857
Contig ID	650_1.R1084

5'-most EST	g428067
Method	BLASTX
NCBI GI	g548770
BLAST score	762
E value	3.0e-81
Match length	167
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L3 >gi_481228_pir__S38359 ribosomal protein L3 - rice >gi_303853_dbj_BAA02155_ (D12630) ribosomal protein L3 [Oryza sativa]

Seq. No.	385858
Contig ID	654_1.R1084
5'-most EST	g429019
Method	BLASTX
NCBI GI	g4887127
BLAST score	317
E value	2.0e-55
Match length	135
% identity	74
NCBI Description	(AF134730) putative mitogen-activated protein kinase MAPK [Prunus armeniaca]

Seq. No.	385859
Contig ID	657_1.R1084
5'-most EST	g572420
Method	BLASTX
NCBI GI	g1709563
BLAST score	498
E value	1.0e-77
Match length	183
% identity	85
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_2130081_pir__S66313 phenylalanine ammonia-lyase (EC 4.3.1.5) - rice >gi_871494_emb_CAA61198_ (X87946) phenylalanine ammonia-lyase [Oryza sativa]

Seq. No.	385860
Contig ID	659_1.R1084
5'-most EST	LIB3432-015-P1-K1-E8
Method	BLASTX
NCBI GI	g1076800
BLAST score	1071
E value	1.0e-117
Match length	242
% identity	82
NCBI Description	L-ascorbate peroxidase (EC 1.11.1.11), cytosolic isozyme - maize >gi_600116_emb_CAA84406_ (Z34934) cytosolic ascorbate peroxidase [Zea mays] >gi_1096503_prf__2111423A ascorbate peroxidase [Zea mays]

Seq. No.	385861
Contig ID	660_1.R1084
5'-most EST	LIB3434-027-P1-K1-A6
Method	BLASTX
NCBI GI	g1449179
BLAST score	572

E value	4.0e-59
Match length	125
% identity	90
NCBI Description	(D86506) N-ethylmaleimide sensitive fusion protein [Nicotiana tabacum]

Seq. No.	385862
Contig ID	661_1.R1084
5'-most EST	uC-osflcyp051d11b1
Method	BLASTX
NCBI GI	g266567
BLAST score	891
E value	4.0e-96
Match length	251
% identity	68
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	385863
Contig ID	663_1.R1084
5'-most EST	g5734102
Method	BLASTX
NCBI GI	g2833377
BLAST score	3033
E value	0.0e+00
Match length	614
% identity	94
NCBI Description	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SSS) >gi_542161_pir__JQ2322 ADPglucose--starch glucosyltransferase (EC 2.4.1.21) precursor - rice >gi_450485_dbj_BAA03739_ (D16202) soluble starch synthase precursor [Oryza sativa]

Seq. No.	385864
Contig ID	666_1.R1084
5'-most EST	g2801202
Method	BLASTX
NCBI GI	g994736
BLAST score	171
E value	8.0e-18
Match length	52
% identity	77
NCBI Description	(M18327) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994738 (M18328) LacOPZ-alpha peptide from pUC9; putative [cloning vectors] >gi_994740 (M18329) LacOPZ-alpha peptide from pUC9; putative [cloning vectors]

Seq. No.	385865
Contig ID	666_4.R1084
5'-most EST	g2800400
Method	BLASTX
NCBI GI	g122106
BLAST score	356

E value	1.0e-33
Match length	89
% identity	88
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385866
Contig ID	666_5.R1084
5'-most EST	g2800633
Method	BLASTX
NCBI GI	g122106
BLAST score	409
E value	2.0e-39
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385867
Contig ID	666_6.R1084
5'-most EST	LIB3477-011-P1-K1-C7
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	7.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	385868
Contig ID	666_7.R1084
5'-most EST	g3767383
Method	BLASTX
NCBI GI	g122106
BLAST score	428
E value	5.0e-42
Match length	85
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385869
Contig ID	666_8.R1084
5'-most EST	g2799828
Method	BLASTX
NCBI GI	g122106
BLAST score	284
E value	2.0e-30
Match length	75
% identity	99
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385870
Contig ID	666_9.R1084
5'-most EST	g3090536
Method	BLASTX
NCBI GI	g224293

BLAST score	418
E value	5.0e-41
Match length	85
% identity	98
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	385871
Contig ID	666_10.R1084
5'-most EST	g3763312
Method	BLASTX
NCBI GI	g224293
BLAST score	410
E value	9.0e-40
Match length	82
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	385872
Contig ID	666_11.R1084
5'-most EST	LIB3433-036-P1-K1-F10
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	8.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385873
Contig ID	666_12.R1084
5'-most EST	g3763479
Method	BLASTX
NCBI GI	g122106
BLAST score	386
E value	6.0e-37
Match length	78
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis

thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385874
Contig ID	666_14.R1084
5'-most EST	LIB3431-047-P1-K1-G9
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	6.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_ (Z79638) histone H4 homologue [Sesbania rostrata] >gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana] >gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4 [Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_ (AB018245) histone H4-like protein [Solanum melongena] >gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385875
Contig ID	666_15.R1084
5'-most EST	LIB3434-062-P1-K1-E8
Method	BLASTX
NCBI GI	g122106
BLAST score	410
E value	8.0e-40
Match length	82
% identity	100
NCBI Description	HISTONE H4 >gi_70771_pir__HSZM4 histone H4 - maize >gi_81642_pir__S06904 histone H4 - Arabidopsis thaliana >gi_2119028_pir__S60475 histone H4 - garden pea >gi_21795_emb_CAA24924_ (X00043) histone H4 [Triticum aestivum] >gi_166740 (M17132) histone H4 [Arabidopsis thaliana] >gi_166742 (M17133) histone H4 [Arabidopsis thaliana] >gi_168499 (M36659) histone H4 (H4C13) [Zea mays] >gi_168501 (M13370) histone H4 [Zea mays] >gi_168503 (M13377) histone H4 [Zea mays] >gi_498898 (U10042) histone H4 homolog [Pisum sativum] >gi_1806285_emb_CAB01914_

(Z79638) histone H4 homologue [Sesbania rostrata]
>gi_3927823 (AC005727) histone H4 [Arabidopsis thaliana]
>gi_4580385_gb_AAD24364.1_AC007184_4 (AC007184) histone H4
[Arabidopsis thaliana] >gi_6009915_dbj_BAA85120.1_
(AB018245) histone H4-like protein [Solanum melongena]
>gi_225838_prf__1314298A histone H4 [Arabidopsis thaliana]

Seq. No.	385876
Contig ID	666_17.R1084
5'-most EST	g4714377
Method	BLASTX
NCBI GI	g224293
BLAST score	392
E value	8.0e-38
Match length	79
% identity	100
NCBI Description	histone H4 [Triticum aestivum]

Seq. No.	385877
Contig ID	667_1.R1084
5'-most EST	g436782
Method	BLASTX
NCBI GI	g1350986
BLAST score	1240
E value	1.0e-137
Match length	243
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S3A (CYC07 PROTEIN) >gi_483431_dbj_BAA05059_ (D26060) cyc07 [Oryza sativa]

Seq. No.	385878
Contig ID	667_5.R1084
5'-most EST	LIB3434-053-P1-K1-H9
Method	BLASTX
NCBI GI	g3122836
BLAST score	212
E value	6.0e-23
Match length	102
% identity	63
NCBI Description	40S RIBOSOMAL PROTEIN S3A >gi_1841932_emb_CAB05955_ (Z83368) ribosomal protein S3a [Mus musculus]

Seq. No.	385879
Contig ID	669_1.R1084
5'-most EST	g3107892
Method	BLASTX
NCBI GI	g135191
BLAST score	292
E value	6.0e-39
Match length	146
% identity	59
NCBI Description	TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS) (IFP53) >gi_107990_pir__A41706 tryptophan--tRNA ligase homolog - human >gi_30821_emb_CAA42545_ (X59892) 471 aa polypeptide (gamma2) [Homo sapiens] >gi_184657 (M77804) transfer RNA-Trp synthetase [Homo sapiens]

Seq. No.	385880
Contig ID	670_1.R1084
5'-most EST	uC-osrocyp029h08a1
Method	BLASTX
NCBI GI	g122033
BLAST score	190
E value	2.0e-14
Match length	50
% identity	82
NCBI Description	HISTONE H2B.2 >gi_70732_pir__HSWT2B histone H2B.2 - wheat

Seq. No.	385881
Contig ID	671_1.R1084
5'-most EST	LIB3434-026-P1-K1-H10
Method	BLASTX
NCBI GI	g4262250
BLAST score	570
E value	1.0e-131
Match length	286
% identity	85
NCBI Description	(AC006200) putative aldolase [Arabidopsis thaliana]

Seq. No.	385882
Contig ID	676_1.R1084
5'-most EST	LIB3431-030-P1-K2-H5
Method	BLASTX
NCBI GI	g2130127
BLAST score	352
E value	5.0e-33
Match length	74
% identity	91
NCBI Description	ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_ (X83076) ferritin [Zea mays]

Seq. No.	385883
Contig ID	676_2.R1084
5'-most EST	g2798605
Method	BLASTN
NCBI GI	g455510
BLAST score	118
E value	2.0e-59
Match length	149
% identity	96
NCBI Description	Rice mRNA for ferritin, partial sequence

Seq. No.	385884
Contig ID	681_1.R1084
5'-most EST	g454878
Method	BLASTX
NCBI GI	g1076757
BLAST score	634
E value	7.0e-66
Match length	214
% identity	63
NCBI Description	WSI18 protein - rice >gi_537402_dbj_BAA05537_ (D26536) WSI18 protein induced by water stress [Oryza sativa]

Seq. No.	385885
Contig ID	683_2.R1084
5'-most EST	uC-osflM202039e11b1
Method	BLASTX
NCBI GI	g537404
BLAST score	600
E value	3.0e-62
Match length	131
% identity	85
NCBI Description	(D26537) WSI76 protein induced by water stress [Oryza sativa]

Seq. No.	385886
Contig ID	685_1.R1084
5'-most EST	uC-osroM202035a05a1
Method	BLASTX
NCBI GI	g1710590
BLAST score	145
E value	4.0e-11
Match length	50
% identity	82
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P1 (L12) >gi_1209701 (U40147) ribosomal protein L12 [Zea mays]

Seq. No.	385887
Contig ID	686_1.R1084
5'-most EST	LIB3432-024-P1-K1-B4
Method	BLASTX
NCBI GI	g4127456
BLAST score	853
E value	2.0e-91
Match length	239
% identity	69
NCBI Description	(AJ010818) Cpn21 protein [Arabidopsis thaliana]

Seq. No.	385888
Contig ID	687_1.R1084
5'-most EST	uC-osroM202017g11b1
Method	BLASTX
NCBI GI	g401140
BLAST score	620
E value	1.0e-64
Match length	124
% identity	100
NCBI Description	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi_20095_emb_CAA41774_ (X59046) sucrose-UDP glucosyltransferase (isoenzyme 2) [Oryza sativa] >gi_1587662_prf__2207194A sucrose synthase:ISOTYPE=2 [Oryza sativa]

Seq. No.	385889
Contig ID	688_1.R1084
5'-most EST	uC-osflcyp088c11a1
Method	BLASTX
NCBI GI	g226661
BLAST score	532
E value	6.0e-54

Match length	102
% identity	100
NCBI Description	trnA intron ORF 109 [Oryza sativa]

Seq. No.	385890
Contig ID	691_1.R1084
5'-most EST	g3763322
Method	BLASTX
NCBI GI	g2431771
BLAST score	268
E value	4.0e-23
Match length	113
% identity	51
NCBI Description	(U62753) acidic ribosomal protein P2b [Zea mays]

Seq. No.	385891
Contig ID	696_1.R1084
5'-most EST	LIB3431-036-P1-K1-D11
Method	BLASTX
NCBI GI	g505482
BLAST score	1339
E value	1.0e-148
Match length	333
% identity	79
NCBI Description	(X64349) 33 kDa polypeptide of water-oxidizing complex of photosystem II [Nicotiana tabacum]

Seq. No.	385892
Contig ID	696_3.R1084
5'-most EST	LIB3432-023-P1-K1-E1
Method	BLASTX
NCBI GI	g482311
BLAST score	701
E value	7.0e-74
Match length	154
% identity	95
NCBI Description	photosystem II oxygen-evolving complex protein 1 - rice (strain Nihonbare) >gi_739292_prf__2002393A oxygen-evolving complex protein 1 [Oryza sativa]

Seq. No.	385893
Contig ID	697_1.R1084
5'-most EST	LIB3479-004-Q6-K2-G4
Method	BLASTX
NCBI GI	g2267006
BLAST score	2857
E value	0.0e+00
Match length	644
% identity	89
NCBI Description	(AF006825) endosperm lumenal binding protein [Oryza sativa]

Seq. No.	385894
Contig ID	698_1.R1084
5'-most EST	g6025152
Method	BLASTX
NCBI GI	g1170029
BLAST score	613

E value	1.0e-63
Match length	129
% identity	89
NCBI Description	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) >gi_100581_pir__A35789 glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) - barley >gi_506383 (M31545) glutamate 1-semialdehyde aminotransferase [Hordeum vulgare]

Seq. No.	385895
Contig ID	701_1.R1084
5'-most EST	g231968
Method	BLASTX
NCBI GI	g300265
BLAST score	923
E value	1.0e-149
Match length	318
% identity	86
NCBI Description	HSP68=68 kda heat-stress DnaK homolog [Lycopersicon peruvianum=tomatoes, Peptide Mitochondrial Partial, 580 aa]

Seq. No.	385896
Contig ID	704_1.R1084
5'-most EST	g571727
Method	BLASTX
NCBI GI	g2196672
BLAST score	322
E value	1.0e-32
Match length	107
% identity	72
NCBI Description	(Y08807) HMGd1 [Zea mays]

Seq. No.	385897
Contig ID	705_1.R1084
5'-most EST	LIB3431-006-P1-K1-H10
Method	BLASTX
NCBI GI	g1362184
BLAST score	390
E value	2.0e-37
Match length	91
% identity	88
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	385898
Contig ID	705_2.R1084
5'-most EST	LIB3432-059-P1-K1-E2
Method	BLASTX
NCBI GI	g122022
BLAST score	447
E value	5.0e-44
Match length	91
% identity	100
NCBI Description	HISTONE H2B >gi_283025_pir__S22323 histone H2B - wheat >gi_21801_emb_CAA42530_ (X59873) histone H2B [Triticum aestivum]

Seq. No.	385899
Contig ID	705_3.R1084
5'-most EST	LIB3431-025-P1-K1-B2
Method	BLASTX
NCBI GI	g1362184
BLAST score	447
E value	4.0e-44
Match length	91
% identity	100
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	385900
Contig ID	705_4.R1084
5'-most EST	LIB3433-039-P1-K1-F8
Method	BLASTX
NCBI GI	g629864
BLAST score	435
E value	1.0e-42
Match length	90
% identity	98
NCBI Description	histone H2B - garden asparagus >gi_563329_emb_CAA57778_ (X82362) histone 2B [Asparagus officinalis]

Seq. No.	385901
Contig ID	705_5.R1084
5'-most EST	g2442195
Method	BLASTX
NCBI GI	g1362184
BLAST score	394
E value	7.0e-38
Match length	92
% identity	88
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	385902
Contig ID	705_6.R1084
5'-most EST	LIB3433-023-P1-K1-F12
Method	BLASTX
NCBI GI	g1362184
BLAST score	236
E value	2.0e-39
Match length	92
% identity	100
NCBI Description	histone H2B-8 - wheat >gi_531058_dbj_BAA07157_ (D37943) protein H2B-8 [Triticum aestivum]

Seq. No.	385903
Contig ID	705_7.R1084
5'-most EST	g425849
Method	BLASTX
NCBI GI	g1362183
BLAST score	267
E value	1.0e-39
Match length	92
% identity	100

NCBI Description	histone H2B-6 - wheat >gi_531056_dbj_BAA07156_ (D37942) protein H2B-6 [Triticum aestivum]

Seq. No.	385904
Contig ID	705_10.R1084
5'-most EST	g3766959
Method	BLASTX
NCBI GI	g1362183
BLAST score	394
E value	4.0e-38
Match length	92
% identity	88
NCBI Description	histone H2B-6 - wheat >gi_531056_dbj_BAA07156_ (D37942) protein H2B-6 [Triticum aestivum]

Seq. No.	385905
Contig ID	705_11.R1084
5'-most EST	g3763401
Method	BLASTX
NCBI GI	g3913804
BLAST score	457
E value	2.0e-45
Match length	123
% identity	77
NCBI Description	HISTONE H2B.3 >gi_577825_emb_CAA49584_ (X69960) H2B histone [Zea mays]

Seq. No.	385906
Contig ID	706_1.R1084
5'-most EST	LIB3432-018-P1-K1-D12
Method	BLASTX
NCBI GI	g417103
BLAST score	492
E value	1.0e-49
Match length	124
% identity	82
NCBI Description	HISTONE H3.2, MINOR >gi_282871_pir__S24346 histone H3.3-like protein - Arabidopsis thaliana >gi_16324_emb_CAA42957_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_404825_emb_CAA42958_ (X60429) histone H3.3 like protein [Arabidopsis thaliana] >gi_488563 (U09458) histone H3.2 [Medicago sativa] >gi_488567 (U09460) histone H3.2 [Medicago sativa] >gi_488569 (U09461) histone H3.2 [Medicago sativa] >gi_488575 (U09464) histone H3.2 [Medicago sativa] >gi_488577 (U09465) histone H3.2 [Medicago sativa] >gi_510911_emb_CAA56153_ (X79714) histone H3 [Lolium temulentum] >gi_1435157_emb_CAA58445_ (X83422) histone H3 variant H3.3 [Lycopersicon esculentum] >gi_2558944 (AF024716) histone 3 [Gossypium hirsutum] >gi_3273350_dbj_BAA31218_ (AB015760) histone H3 [Nicotiana tabacum] >gi_3885890 (AF093633) histone H3 [Oryza sativa] >gi_4038469_gb_AAC97380_ (AF109910) histone H3 [Porteresia coarctata] >gi_4490754_emb_CAB38916.1_ (AL035708) histone H3.3 [Arabidopsis thaliana] >gi_4490755_emb_CAB38917.1_ (AL035708) Histon H3 [Arabidopsis thaliana] >gi_6006364_dbj_BAA84794.1_ (AP000559) EST D15300(C0425) corresponds to a region of the predicted gene.; Similar to

histone H3 (AB015760) [Oryza sativa]

Seq. No.	385907
Contig ID	707_1.R1084
5'-most EST	LIB3433-049-P1-K1-A12
Method	BLASTN
NCBI GI	g2314803
BLAST score	262
E value	1.0e-145
Match length	282
% identity	99
NCBI Description	Oryza sativa signal recognition particle RNA sequence

Seq. No.	385908
Contig ID	708_1.R1084
5'-most EST	g568466
Method	BLASTN
NCBI GI	g433815
BLAST score	252
E value	1.0e-139
Match length	515
% identity	37
NCBI Description	O.sativa gene for hydroxyproline-rich glycoprotein

Seq. No.	385909
Contig ID	711_1.R1084
5'-most EST	LIB3432-045-P1-K1-G3
Method	BLASTX
NCBI GI	g2911358
BLAST score	521
E value	5.0e-53
Match length	142
% identity	70
NCBI Description	(AF041043) NADPH HC toxin reductase [Zea mays]

Seq. No.	385910
Contig ID	714_1.R1084
5'-most EST	LIB3433-003-Q6-K6-H12
Method	BLASTX
NCBI GI	g1174162
BLAST score	712
E value	2.0e-75
Match length	139
% identity	89
NCBI Description	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana] >gi_3746915 (AF091106) E2 ubiquitin-conjugating-like enzyme [Arabidopsis thaliana]

Seq. No.	385911
Contig ID	716_1.R1084
5'-most EST	LIB3433-011-Q6-K1-A7
Method	BLASTX
NCBI GI	g3212879
BLAST score	611
E value	2.0e-63
Match length	141
% identity	79

NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	385912
Contig ID	716_2.R1084
5'-most EST	uC-osroM202038e11b1
Method	BLASTX
NCBI GI	g3212879
BLAST score	340
E value	2.0e-31
Match length	161
% identity	55
NCBI Description	(AC004005) putative ribosomal protein L7 [Arabidopsis thaliana]

Seq. No.	385913
Contig ID	717_1.R1084
5'-most EST	LIB3434-035-P1-K1-H12
Method	BLASTX
NCBI GI	g1729971
BLAST score	1061
E value	1.0e-116
Match length	250
% identity	84
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]

Seq. No.	385914
Contig ID	717_2.R1084
5'-most EST	LIB3434-044-P1-K1-G10
Method	BLASTX
NCBI GI	g3264596
BLAST score	907
E value	9.0e-98
Match length	217
% identity	80
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	385915
Contig ID	717_3.R1084
5'-most EST	LIB3434-058-P1-K1-G2
Method	BLASTX
NCBI GI	g4099408
BLAST score	734
E value	6.0e-78
Match length	155
% identity	59
NCBI Description	(U86763) delta-type tonoplast intrinsic protein [Triticum aestivum]

Seq. No.	385916
Contig ID	717_4.R1084
5'-most EST	g3767605
Method	BLASTX
NCBI GI	g3264596

BLAST score	326
E value	1.0e-38
Match length	89
% identity	92
NCBI Description	(AF057183) putative tonoplast aquaporin [Zea mays]

Seq. No.	385917
Contig ID	717_5.R1084
5'-most EST	LIB3431-024-P1-K1-C6
Method	BLASTX
NCBI GI	g3695375
BLAST score	952
E value	1.0e-103
Match length	252
% identity	69
NCBI Description	(AF096370) contains similarity to the major intrinsic protein domain (Pfam: PF00230 MIP, E-value: 5.7e-111) [Arabidopsis thaliana]

Seq. No.	385918
Contig ID	717_12.R1084
5'-most EST	g4714426
Method	BLASTX
NCBI GI	g1729971
BLAST score	237
E value	4.0e-42
Match length	130
% identity	78
NCBI Description	TONOPLAST INTRINSIC PROTEIN, GAMMA (GAMMA TIP) (AQUAPORIN-TIP) >gi_1076745_pir__S52004 gamma-Tip protein - rice >gi_473997_dbj_BAA05017_ (D25534) gamma-Tip [Oryza sativa]

Seq. No.	385919
Contig ID	718_1.R1084
5'-most EST	g5004613
Method	BLASTX
NCBI GI	g1545805
BLAST score	415
E value	2.0e-65
Match length	267
% identity	60
NCBI Description	(D64052) cytochrome P450 like_TBP [Nicotiana tabacum]

Seq. No.	385920
Contig ID	718_2.R1084
5'-most EST	g5005260
Method	BLASTX
NCBI GI	g2995384
BLAST score	422
E value	7.0e-41
Match length	88
% identity	93
NCBI Description	(AJ004810) cytochrome P450 monooxygenase [Zea mays]

Seq. No.	385921
Contig ID	718_3.R1084

5'-most EST	LIB3431-034-P1-K1-A2
Method	BLASTX
NCBI GI	g548605
BLAST score	608
E value	6.0e-63
Match length	133
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	385922
Contig ID	718_4.R1084
5'-most EST	LIB3431-044-P1-K1-D2
Method	BLASTX
NCBI GI	g5734790
BLAST score	1666
E value	0.0e+00
Match length	362
% identity	91
NCBI Description	(AC007980) ATP-dependent metalloprotease [Arabidopsis thaliana]

Seq. No.	385923
Contig ID	718_6.R1084
5'-most EST	g4714202
Method	BLASTX
NCBI GI	g3377797
BLAST score	269
E value	5.0e-51
Match length	185
% identity	65
NCBI Description	(AF075597) Similar to 60S ribosome protein L19; coded for by A. thaliana cDNA T04719; coded for by A. thaliana cDNA H36046; coded for by A. thaliana cDNA T44067; coded for by A. thaliana cDNA T14056; coded for by A. thaliana cDNA R90691 [Ara

Seq. No.	385924
Contig ID	718_7.R1084
5'-most EST	g5005323
Method	BLASTX
NCBI GI	g548605
BLAST score	353
E value	4.0e-33
Match length	107
% identity	71
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR (LIGHT-HARVESTING COMPLEX I 7 KD PROTEIN) (PSI-K) >gi_539055_pir__A48527 photosystem I protein psaK precursor - barley >gi_304220 (L12707) photosystem I PSI-K subunit [Hordeum vulgare]

Seq. No.	385925
Contig ID	718_8.R1084

5'-most EST	g5004037
Method	BLASTN
NCBI GI	g169818
BLAST score	513
E value	0.0e+00
Match length	602
% identity	97
NCBI Description	Rice 25S ribosomal RNA gene

Seq. No.	385926
Contig ID	719_1.R1084
5'-most EST	g2431278
Method	BLASTX
NCBI GI	g1076748
BLAST score	1268
E value	1.0e-140
Match length	281
% identity	88
NCBI Description	major intrinsic protein - rice >gi_440869_dbj_BAA04257_ (D17443) major intrinsic protein [Oryza sativa]

Seq. No.	385927
Contig ID	720_1.R1084
5'-most EST	g2311764
Method	BLASTX
NCBI GI	g1173027
BLAST score	434
E value	9.0e-43
Match length	113
% identity	75
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	385928
Contig ID	721_1.R1084
5'-most EST	g5607537
Method	BLASTX
NCBI GI	g4090257
BLAST score	465
E value	2.0e-46
Match length	91
% identity	97
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	385929
Contig ID	721_2.R1084
5'-most EST	g4878654
Method	BLASTX
NCBI GI	g4090257
BLAST score	457
E value	2.0e-45
Match length	91
% identity	95
NCBI Description	(AJ131732) ribosomal protein L37A [Pseudotsuga menziesii]

Seq. No.	385930
Contig ID	722_1.R1084

5'-most EST	g2799053
Method	BLASTX
NCBI GI	g3122724
BLAST score	171
E value	2.0e-12
Match length	52
% identity	77
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	385931
Contig ID	722_2.R1084
5'-most EST	LIB3432-031-P1-K1-E3
Method	BLASTX
NCBI GI	g3122724
BLAST score	313
E value	2.0e-28
Match length	69
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	385932
Contig ID	722_3.R1084
5'-most EST	uC-osrocyp011b05a1
Method	BLASTN
NCBI GI	g1835728
BLAST score	57
E value	4.0e-23
Match length	96
% identity	91
NCBI Description	Oryza sativa ribosomal protein mRNA, complete cds

Seq. No.	385933
Contig ID	722_5.R1084
5'-most EST	LIB3434-047-P1-K1-H2
Method	BLASTX
NCBI GI	g3122724
BLAST score	313
E value	2.0e-28
Match length	69
% identity	86
NCBI Description	60S RIBOSOMAL PROTEIN L38 >gi_2289009 (AC002335) ribosomal protein L38 isolog [Arabidopsis thaliana]

Seq. No.	385934
Contig ID	723_1.R1084
5'-most EST	g3767155
Method	BLASTX
NCBI GI	g3402817
BLAST score	250
E value	7.0e-28
Match length	72
% identity	82
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	385935

Contig ID	723_2.R1084
5'-most EST	LIB3431-033-P1-K1-G6
Method	BLASTX
NCBI GI	g1710551
BLAST score	277
E value	2.0e-24
Match length	51
% identity	98
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728.1_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No.	385936
Contig ID	723_3.R1084
5'-most EST	g3763482
Method	BLASTX
NCBI GI	g567893
BLAST score	249
E value	2.0e-30
Match length	72
% identity	82
NCBI Description	(L37382) beta-galactosidase-complementation protein [Cloning vector]

Seq. No.	385937
Contig ID	723_4.R1084
5'-most EST	g4714240
Method	BLASTX
NCBI GI	g1710551
BLAST score	281
E value	7.0e-25
Match length	51
% identity	100
NCBI Description	60S RIBOSOMAL PROTEIN L39 >gi_1177369_emb_CAA64728.1_ (X95458) ribosomal protein L39 [Zea mays]

Seq. No.	385938
Contig ID	724_1.R1084
5'-most EST	LIB3433-015-Q6-K1-B8
Method	BLASTX
NCBI GI	g2431769
BLAST score	279
E value	1.0e-24
Match length	110
% identity	56
NCBI Description	(U62752) acidic ribosomal protein P1a [Zea mays]

Seq. No.	385939
Contig ID	725_1.R1084
5'-most EST	LIB3432-013-P1-K1-A10
Method	BLASTX
NCBI GI	g399213
BLAST score	1907
E value	0.0e+00
Match length	457
% identity	84
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato

>gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No.	385940
Contig ID	726_1.R1084
5'-most EST	LIB3432-045-P1-K1-G2
Method	BLASTX
NCBI GI	g3043428
BLAST score	889
E value	8.0e-96
Match length	192
% identity	89
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	385941
Contig ID	726_3.R1084
5'-most EST	g427982
Method	BLASTX
NCBI GI	g3043428
BLAST score	459
E value	3.0e-60
Match length	142
% identity	83
NCBI Description	(AJ005346) 40S ribosomal protein S5 [Cicer arietinum]

Seq. No.	385942
Contig ID	727_1.R1084
5'-most EST	LIB3434-016-P1-K1-H11
Method	BLASTX
NCBI GI	g133867
BLAST score	675
E value	9.0e-71
Match length	145
% identity	88
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	385943
Contig ID	727_2.R1084
5'-most EST	g3759934
Method	BLASTX
NCBI GI	g133867
BLAST score	478
E value	5.0e-48
Match length	112
% identity	82
NCBI Description	40S RIBOSOMAL PROTEIN S11 >gi_82722_pir__S16577 ribosomal protein S11 - maize >gi_22470_emb_CAA39438_ (X55967) ribosomal protein S11 [Zea mays]

Seq. No.	385944
Contig ID	730_1.R1084
5'-most EST	g3767824
Method	BLASTX
NCBI GI	g1170937
BLAST score	2006

E value	0.0e+00
Match length	396
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) >gi_450549_emb_CAA81481_ (Z26867) S-adenosyl methionine synthetase [Oryza sativa]

Seq. No.	385945
Contig ID	730_2.R1084
5'-most EST	LIB3434-041-P1-K1-B11
Method	BLASTX
NCBI GI	g730456
BLAST score	765
E value	4.0e-81
Match length	146
% identity	100
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	385946
Contig ID	730_3.R1084
5'-most EST	uC-osroM202007e02b1
Method	BLASTX
NCBI GI	g730456
BLAST score	377
E value	3.0e-74
Match length	146
% identity	98
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	385947
Contig ID	730_9.R1084
5'-most EST	uC-osflcyp036e09b1
Method	BLASTX
NCBI GI	g730456
BLAST score	585
E value	3.0e-67
Match length	147
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S19

Seq. No.	385948
Contig ID	731_1.R1084
5'-most EST	g3766899
Method	BLASTX
NCBI GI	g4263519
BLAST score	388
E value	3.0e-37
Match length	81
% identity	91
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	385949
Contig ID	731_2.R1084
5'-most EST	g2311582
Method	BLASTX

NCBI GI	g4263519
BLAST score	461
E value	9.0e-46
Match length	96
% identity	93
NCBI Description	(AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]

Seq. No.	385950
Contig ID	736_1.R1084
5'-most EST	g6025087
Method	BLASTX
NCBI GI	g3643611
BLAST score	673
E value	7.0e-71
Match length	142
% identity	88
NCBI Description	(AC005395) putative casein kinase [Arabidopsis thaliana]

Seq. No.	385951
Contig ID	738_1.R1084
5'-most EST	g3061039
Method	BLASTX
NCBI GI	g730580
BLAST score	1326
E value	1.0e-147
Match length	319
% identity	85
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_455401_dbj_BAA04668_ (D21130) acidic ribosomal protein P0 [Oryza sativa]

Seq. No.	385952
Contig ID	738_4.R1084
5'-most EST	g426536
Method	BLASTX
NCBI GI	g730580
BLAST score	390
E value	5.0e-52
Match length	115
% identity	94
NCBI Description	60S ACIDIC RIBOSOMAL PROTEIN P0 >gi_455401_dbj_BAA04668_ (D21130) acidic ribosomal protein P0 [Oryza sativa]

Seq. No.	385953
Contig ID	739_1.R1084
5'-most EST	g702544
Method	BLASTX
NCBI GI	g3821793
BLAST score	1615
E value	1.0e-180
Match length	333
% identity	91
NCBI Description	(Y11526) casein kinase II alpha subunit [Zea mays]

Seq. No.	385954
Contig ID	739_2.R1084
5'-most EST	g2317547

Method	BLASTX
NCBI GI	g2827314
BLAST score	222
E value	2.0e-18
Match length	52
% identity	93
NCBI Description	(AF042199) casein kinase [Oryza sativa]

Seq. No.	385955
Contig ID	746_1.R1084
5'-most EST	g2160781
Method	BLASTX
NCBI GI	g2160782
BLAST score	2639
E value	0.0e+00
Match length	533
% identity	94
NCBI Description	(AF001505) putative ammonium transporter OsAMT1p [Oryza sativa]

Seq. No.	385956
Contig ID	748_1.R1084
5'-most EST	g2246624
Method	BLASTX
NCBI GI	g2246625
BLAST score	2088
E value	0.0e+00
Match length	439
% identity	94
NCBI Description	(AF004947) protein kinase [Oryza sativa]

Seq. No.	385957
Contig ID	749_1.R1084
5'-most EST	g2253277
Method	BLASTX
NCBI GI	g2253278
BLAST score	926
E value	1.0e-100
Match length	368
% identity	55
NCBI Description	(AF005492) RF2a [Oryza sativa]

Seq. No.	385958
Contig ID	753_1.R1084
5'-most EST	g2800202
Method	BLASTX
NCBI GI	g3885896
BLAST score	605
E value	1.0e-62
Match length	145
% identity	82
NCBI Description	(AF093636) plastocyanin precursor [Oryza sativa]

Seq. No.	385959
Contig ID	753_2.R1084
5'-most EST	g3885895
Method	BLASTX

NCBI GI	g3885896
BLAST score	605
E value	1.0e-62
Match length	145
% identity	82
NCBI Description	(AF093636) plastocyanin precursor [Oryza sativa]

Seq. No.	385960
Contig ID	753_3.R1084
5'-most EST	LIB3432-002-P1-K1-G8
Method	BLASTX
NCBI GI	g130274
BLAST score	292
E value	3.0e-26
Match length	66
% identity	85
NCBI Description	PLASTOCYANIN >gi_82500_pir__S06105 plastocyanin - rice

Seq. No.	385961
Contig ID	754_1.R1084
5'-most EST	g1632220
Method	BLASTX
NCBI GI	g2267597
BLAST score	463
E value	5.0e-46
Match length	93
% identity	100
NCBI Description	(AF009413) 10 kDa chaperonin [Oryza sativa]

Seq. No.	385962
Contig ID	755_1.R1084
5'-most EST	g2800066
Method	BLASTX
NCBI GI	g2305113
BLAST score	229
E value	1.0e-18
Match length	65
% identity	68
NCBI Description	(AF009959) metallothionein-like protein [Oryza sativa]

Seq. No.	385963
Contig ID	757_1.R1084
5'-most EST	LIB3431-036-P1-K1-B4
Method	BLASTX
NCBI GI	g1076724
BLAST score	1046
E value	1.0e-114
Match length	208
% identity	89
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	385964
Contig ID	757_3.R1084
5'-most EST	LIB3431-037-P1-K1-F1
Method	BLASTX

NCBI GI	g1076724
BLAST score	280
E value	5.0e-48
Match length	97
% identity	96
NCBI Description	LHCI-680, photosystem I antenna protein - barley >gi_666054_emb_CAA59049_ (X84308) LHCI-680, photosystem I antenna protein [Hordeum vulgare]

Seq. No.	385965
Contig ID	757_6.R1084
5'-most EST	g701930
Method	BLASTX
NCBI GI	g2306981
BLAST score	351
E value	3.0e-33
Match length	89
% identity	72
NCBI Description	(AF010321) photosystem I antenna protein [Oryza sativa]

Seq. No.	385966
Contig ID	757_7.R1084
5'-most EST	LIB3431-048-P1-N1-F4
Method	BLASTN
NCBI GI	g2306980
BLAST score	73
E value	5.0e-33
Match length	89
% identity	96
NCBI Description	Oryza sativa photosystem I antenna protein (Lhca) mRNA, complete cds

Seq. No.	385967
Contig ID	760_1.R1084
5'-most EST	g2331134
Method	BLASTX
NCBI GI	g4176424
BLAST score	468
E value	2.0e-46
Match length	116
% identity	91
NCBI Description	(AB022674) ribosomal protein L12 [Oryza sativa]

Seq. No.	385968
Contig ID	762_1.R1084
5'-most EST	uC-osroM202040c05b1
Method	BLASTX
NCBI GI	g2130089
BLAST score	1368
E value	1.0e-152
Match length	290
% identity	91
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	385969
Contig ID	762_2.R1084
5'-most EST	g3767664
Method	BLASTX
NCBI GI	g2130089
BLAST score	338
E value	2.0e-31
Match length	66
% identity	89
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	385970
Contig ID	762_3.R1084
5'-most EST	g569600
Method	BLASTX
NCBI GI	g2130089
BLAST score	264
E value	6.0e-23
Match length	59
% identity	86
NCBI Description	2-oxoglutarate/malate translocator (clone OMT103), mitochondrial membrane - proso millet >gi_1100743_dbj_BAA08105_ (D45075) 2-oxoglutarate/malate translocator [Panicum miliaceum]

Seq. No.	385971
Contig ID	766_1.R1084
5'-most EST	LIB3475-007-P1-K1-B1
Method	BLASTX
NCBI GI	g2293568
BLAST score	472
E value	4.0e-47
Match length	89
% identity	100
NCBI Description	(AF012897) HvB12D homolog [Oryza sativa]

Seq. No.	385972
Contig ID	767_1.R1084
5'-most EST	uC-osflm202100h03b1
Method	BLASTX
NCBI GI	g2281705
BLAST score	2869
E value	0.0e+00
Match length	636
% identity	89
NCBI Description	(AF013979) ethylene responsive factor [Oryza sativa]

Seq. No.	385973
Contig ID	767_2.R1084
5'-most EST	uC-osroM202011h02b1
Method	BLASTX
NCBI GI	g2281705
BLAST score	735
E value	7.0e-78

Match length	157
% identity	88
NCBI Description	(AF013979) ethylene responsive factor [Oryza sativa]

Seq. No.	385974
Contig ID	767_3.R1084
5'-most EST	uC-osflm202002h03b1
Method	BLASTX
NCBI GI	g2281705
BLAST score	210
E value	2.0e-24
Match length	65
% identity	94
NCBI Description	(AF013979) ethylene responsive factor [Oryza sativa]

Seq. No.	385975
Contig ID	771_1.R1084
5'-most EST	g2311652
Method	BLASTN
NCBI GI	g3282393
BLAST score	569
E value	0.0e+00
Match length	603
% identity	99
NCBI Description	Oryza sativa aie2 mRNA, partial cds

Seq. No.	385976
Contig ID	771_2.R1084
5'-most EST	g2311795
Method	BLASTN
NCBI GI	g3282393
BLAST score	474
E value	0.0e+00
Match length	597
% identity	96
NCBI Description	Oryza sativa aie2 mRNA, partial cds

Seq. No.	385977
Contig ID	771_5.R1084
5'-most EST	g2800811
Method	BLASTN
NCBI GI	g3282393
BLAST score	136
E value	4.0e-70
Match length	266
% identity	92
NCBI Description	Oryza sativa aie2 mRNA, partial cds

Seq. No.	385978
Contig ID	771_6.R1084
5'-most EST	g2800604
Method	BLASTN
NCBI GI	g3282393
BLAST score	170
E value	2.0e-90
Match length	281
% identity	91

NCBI Description	Oryza sativa aie2 mRNA, partial cds

Seq. No.	385979
Contig ID	775_1.R1084
5'-most EST	uC-osflcyp168g01b1
Method	BLASTX
NCBI GI	g2384758
BLAST score	2258
E value	0.0e+00
Match length	444
% identity	97
NCBI Description	(AF016896) GDP dissociation inhibitor protein OsGDI1 [Oryza sativa]

Seq. No.	385980
Contig ID	775_2.R1084
5'-most EST	g2384759
Method	BLASTX
NCBI GI	g2384760
BLAST score	2252
E value	0.0e+00
Match length	428
% identity	100
NCBI Description	(AF016897) GDP dissociation inhibitor protein OsGDI2 [Oryza sativa]

Seq. No.	385981
Contig ID	775_3.R1084
5'-most EST	uC-osflM202048a12b1
Method	BLASTX
NCBI GI	g2501850
BLAST score	1203
E value	1.0e-132
Match length	265
% identity	85
NCBI Description	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]

Seq. No.	385982
Contig ID	777_1.R1084
5'-most EST	g2407266
Method	BLASTX
NCBI GI	g5042444
BLAST score	268
E value	3.0e-41
Match length	112
% identity	82
NCBI Description	(AC007789) putative low molecular early light-inducible protein [Oryza sativa]

Seq. No.	385983
Contig ID	777_3.R1084
5'-most EST	g2798608
Method	BLASTX
NCBI GI	g5042444
BLAST score	322
E value	2.0e-29
Match length	109

% identity	62
NCBI Description	(AC007789) putative low molecular early light-inducible protein [Oryza sativa]

Seq. No.	385984
Contig ID	777_4.R1084
5'-most EST	LIB3432-003-P1-K1-D10
Method	BLASTN
NCBI GI	g5042437
BLAST score	36
E value	1.0e-10
Match length	107
% identity	88
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	385985
Contig ID	777_5.R1084
5'-most EST	g2801206
Method	BLASTX
NCBI GI	g2407267
BLAST score	222
E value	6.0e-18
Match length	78
% identity	63
NCBI Description	(AF017356) low molecular early light-inducible protein [Oryza sativa]

Seq. No.	385986
Contig ID	783_1.R1084
5'-most EST	LIB3431-051-P1-K1-B1
Method	BLASTX
NCBI GI	g3913018
BLAST score	945
E value	0.0e+00
Match length	369
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	385987
Contig ID	783_2.R1084
5'-most EST	LIB3431-016-P1-K1-H6
Method	BLASTX
NCBI GI	g3913018
BLAST score	1977
E value	0.0e+00
Match length	388
% identity	99
NCBI Description	FRUCTOSE-BISPHOSPHATE ALDOLASE, CHLOROPLAST PRECURSOR (ALDP) >gi_218155_dbj_BAA02730_ (D13513) chloroplastic aldolase [Oryza sativa]

Seq. No.	385988
Contig ID	783_3.R1084
5'-most EST	g2800672
Method	BLASTN

NCBI GI	g218154
BLAST score	190
E value	1.0e-102
Match length	275
% identity	94
NCBI Description	Oryza sativa gene for cytoplasmic aldolase, complete cds, clone:Aldp

Seq. No.	385989
Contig ID	783_4.R1084
5'-most EST	LIB3432-041-P1-K1-A7
Method	BLASTX
NCBI GI	g2407279
BLAST score	580
E value	8.0e-60
Match length	115
% identity	97
NCBI Description	(AF017362) aldolase [Oryza sativa]

Seq. No.	385990
Contig ID	787_1.R1084
5'-most EST	g427621
Method	BLASTX
NCBI GI	g2829913
BLAST score	338
E value	2.0e-59
Match length	196
% identity	62
NCBI Description	(AC002291) putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	385991
Contig ID	787_2.R1084
5'-most EST	g2800271
Method	BLASTX
NCBI GI	g2829913
BLAST score	367
E value	8.0e-35
Match length	99
% identity	74
NCBI Description	(AC002291) putative carboxyphosphonoenolpyruvate mutase [Arabidopsis thaliana]

Seq. No.	385992
Contig ID	787_3.R1084
5'-most EST	LIB3433-059-P1-K1-G5
Method	BLASTX
NCBI GI	g2497883
BLAST score	226
E value	3.0e-18
Match length	56
% identity	75
NCBI Description	METALLOTHIONEIN-LIKE PROTEIN TYPE 1 >gi_1362174_pir__S57768 metallothionein-like protein - rice >gi_687638 (U18404) metallothionein-like protein [Oryza sativa] >gi_1815626 (U43529) metallothionein-like type 1 [Oryza sativa] >gi_4097154_gb_AAD10376.1_ (U46159) type 1 rice

metallothionein-like gene; Method: conceptual translation supplied by author. [Oryza sativa]

Seq. No.	385993
Contig ID	790_1.R1084
5'-most EST	LIB3431-025-P1-K1-E6
Method	BLASTX
NCBI GI	g2425101
BLAST score	1700
E value	0.0e+00
Match length	333
% identity	99
NCBI Description	(AF019743) cationic peroxidase [Oryza sativa]

Seq. No.	385994
Contig ID	791_1.R1084
5'-most EST	uC-osflcyp125f10b1
Method	BLASTX
NCBI GI	g2511541
BLAST score	1801
E value	0.0e+00
Match length	393
% identity	91
NCBI Description	(AF020787) DNA-binding protein GBP16 [Oryza sativa]

Seq. No.	385995
Contig ID	792_1.R1084
5'-most EST	g3492927
Method	BLASTX
NCBI GI	g3334280
BLAST score	605
E value	2.0e-62
Match length	148
% identity	84
NCBI Description	OLEOSIN 16 KD (OSE701) >gi_1171352 (U43930) 16 kDa oleosin [Oryza sativa]

Seq. No.	385996
Contig ID	793_1.R1084
5'-most EST	LIB3432-013-P1-K1-H10
Method	BLASTX
NCBI GI	g120657
BLAST score	1619
E value	0.0e+00
Match length	402
% identity	80
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE A PRECURSOR, CHLOROPLAST >gi_66024_pir__DEZMG3 glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) A precursor, chloroplast - maize >gi_168479 (M18976) glyceraldehyde-3-phosphate dehydrogenase [Zea mays] >gi_763035_emb_CAA33455_ (X15408) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]

Seq. No.	385997
Contig ID	794_1.R1084
5'-most EST	LIB3431-028-P1-K1-A1

Method	BLASTX
NCBI GI	g2570497
BLAST score	666
E value	1.0e-69
Match length	141
% identity	94
NCBI Description	(AF022731) H protein subunit of glycine decarboxylase [Oryza sativa]

Seq. No.	385998
Contig ID	796_1.R1084
5'-most EST	LIB3431-019-P1-K1-B12
Method	BLASTX
NCBI GI	g3885882
BLAST score	1116
E value	1.0e-122
Match length	214
% identity	100
NCBI Description	(AF093629) inorganic pyrophosphatase [Oryza sativa]

Seq. No.	385999
Contig ID	798_1.R1084
5'-most EST	LIB3431-011-P1-K1-D11
Method	BLASTX
NCBI GI	g2570505
BLAST score	1296
E value	1.0e-143
Match length	261
% identity	97
NCBI Description	(AF022735) proteasome component [Oryza sativa]

Seq. No.	386000
Contig ID	799_1.R1084
5'-most EST	LIB3433-060-P1-K1-G3
Method	BLASTX
NCBI GI	g1172816
BLAST score	793
E value	1.0e-84
Match length	178
% identity	88
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	386001
Contig ID	799_2.R1084
5'-most EST	LIB3433-047-P1-K1-A1
Method	BLASTX
NCBI GI	g1172816
BLAST score	786
E value	9.0e-84
Match length	178
% identity	87
NCBI Description	60S RIBOSOMAL PROTEIN L11A (L16A) >gi_624938_emb_CAA57395_ (X81799) ribosomal protein L16 [Arabidopsis thaliana]

Seq. No.	386002
Contig ID	799_3.R1084

5'-most EST	g3767103
Method	BLASTX
NCBI GI	g6093997
BLAST score	161
E value	2.0e-16
Match length	62
% identity	81
NCBI Description	60S RIBOSOMAL PROTEIN L11 >gi_2570507 (AF022736) ribosomal protein [Oryza sativa]

Seq. No.	386003
Contig ID	799_4.R1084
5'-most EST	LIB3434-033-P1-K1-G4
Method	BLASTX
NCBI GI	g6093997
BLAST score	249
E value	3.0e-21
Match length	70
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L11 >gi_2570507 (AF022736) ribosomal protein [Oryza sativa]

Seq. No.	386004
Contig ID	801_1.R1084
5'-most EST	LIB3432-042-P2-K1-D5
Method	BLASTX
NCBI GI	g115793
BLAST score	1227
E value	1.0e-135
Match length	264
% identity	88
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN OF LHCII TYPE III PRECURSOR (CAB) >gi_72749_pir__CDBH3 chlorophyll a/b-binding protein type III precursor - barley >gi_19023_emb_CAA44881_ (X63197) type III LHCII CAB precursor protein [Hordeum vulgare]

Seq. No.	386005
Contig ID	801_3.R1084
5'-most EST	LIB3432-020-P1-K1-F3
Method	BLASTX
NCBI GI	g479406
BLAST score	585
E value	2.0e-60
Match length	136
% identity	66
NCBI Description	chlorophyll a/b-binding protein - garden pea >gi_20671_emb_CAA49149_ (X69215) chlorophyll a/b-binding protein [Pisum sativum]

Seq. No.	386006
Contig ID	803_1.R1084
5'-most EST	uC-osf1M202123b12b1
Method	BLASTX
NCBI GI	g2570515
BLAST score	1635
E value	0.0e+00

Match length	360
% identity	90
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	386007
Contig ID	803_2.R1084
5'-most EST	g1631606
Method	BLASTX
NCBI GI	g217909
BLAST score	705
E value	1.0e-128
Match length	276
% identity	85
NCBI Description	(D14044) glycolate oxidase [Cucurbita sp.]

Seq. No.	386008
Contig ID	803_4.R1084
5'-most EST	g2801293
Method	BLASTX
NCBI GI	g2570515
BLAST score	474
E value	4.0e-47
Match length	199
% identity	46
NCBI Description	(AF022740) glycolate oxidase [Oryza sativa]

Seq. No.	386009
Contig ID	803_8.R1084
5'-most EST	LIB3432-043-P1-K1-A4
Method	BLASTX
NCBI GI	g121530
BLAST score	446
E value	3.0e-44
Match length	139
% identity	69
NCBI Description	(S)-2-HYDROXY-ACID OXIDASE, PEROXISOMAL (GLYCOLATE OXIDASE) (GOX) (SHORT CHAIN ALPHA-HYDROXY ACID OXIDASE) >gi_65974_pir__OXSPH (S)-2-hydroxy-acid oxidase (EC 1.1.3.15), peroxisomal - spinach >gi_229945_pdb_1GOX_ Glycolate Oxidase (E.C.1.1.3.1) >gi_170113 (J03492) glycolate oxidase (EC 1.1.3.15) [Spinacia oleracea]

Seq. No.	386010
Contig ID	803_10.R1084
5'-most EST	g2798302
Method	BLASTN
NCBI GI	g2570514
BLAST score	120
E value	1.0e-60
Match length	175
% identity	92
NCBI Description	Oryza sativa glycolate oxidase (GOX) mRNA, complete cds

Seq. No.	386011
Contig ID	804_1.R1084
5'-most EST	LIB3431-006-P1-K1-B7
Method	BLASTX

NCBI GI	g2570517
BLAST score	276
E value	7.0e-47
Match length	138
% identity	75
NCBI Description	(AF022741) thioredoxin F isoform [Oryza sativa]

Seq. No.	386012
Contig ID	805_1.R1084
5'-most EST	g701227
Method	BLASTX
NCBI GI	g3913239
BLAST score	3025
E value	0.0e+00
Match length	594
% identity	98
NCBI Description	PROBABLE 1-DEOXYXYLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) >gi_2612941 (AF024512) CLA1 transketolase-like protein [Oryza sativa]

Seq. No.	386013
Contig ID	806_1.R1084
5'-most EST	g2781432
Method	BLASTX
NCBI GI	g2827139
BLAST score	3149
E value	0.0e+00
Match length	813
% identity	74
NCBI Description	(AF027172) cellulose synthase catalytic subunit [Arabidopsis thaliana] >gi_4049343_emb_CAA22568.1_ (AL034567) cellulose synthase catalytic subunit (RSW1) [Arabidopsis thaliana]

Seq. No.	386014
Contig ID	807_1.R1084
5'-most EST	g2800298
Method	BLASTX
NCBI GI	g2623783
BLAST score	1687
E value	0.0e+00
Match length	334
% identity	97
NCBI Description	(AF030166) glucanase [Oryza sativa]

Seq. No.	386015
Contig ID	809_1.R1084
5'-most EST	g2642216
Method	BLASTX
NCBI GI	g2642217
BLAST score	442
E value	1.0e-43
Match length	82
% identity	100
NCBI Description	(AF030387) NOI protein [Oryza sativa]

Seq. No.	386016

Contig ID	813_1.R1084
5'-most EST	LIB3433-055-P1-K1-F12
Method	BLASTX
NCBI GI	g2655285
BLAST score	1091
E value	1.0e-119
Match length	206
% identity	100
NCBI Description	(AF032971) germin-like protein 1 [Oryza sativa]

Seq. No.	386017
Contig ID	814_1.R1084
5'-most EST	LIB3433-051-P1-K1-G6
Method	BLASTX
NCBI GI	g2655287
BLAST score	1097
E value	1.0e-120
Match length	208
% identity	100
NCBI Description	(AF032972) germin-like protein 2 [Oryza sativa]

Seq. No.	386018
Contig ID	814_2.R1084
5'-most EST	LIB3433-015-Q6-K1-G10
Method	BLASTX
NCBI GI	g2655287
BLAST score	642
E value	9.0e-70
Match length	144
% identity	87
NCBI Description	(AF032972) germin-like protein 2 [Oryza sativa]

Seq. No.	386019
Contig ID	815_1.R1084
5'-most EST	g2801802
Method	BLASTX
NCBI GI	g2801803
BLAST score	1035
E value	1.0e-113
Match length	202
% identity	99
NCBI Description	(AF042489) germin-like protein 16 [Oryza sativa]

Seq. No.	386020
Contig ID	816_1.R1084
5'-most EST	uC-osrocyp028e02b1
Method	BLASTX
NCBI GI	g2655291
BLAST score	924
E value	1.0e-100
Match length	187
% identity	95
NCBI Description	(AF032974) germin-like protein 4 [Oryza sativa]

Seq. No.	386021
Contig ID	818_1.R1084
5'-most EST	LIB3433-052-P1-K1-D12

Method	BLASTX
NCBI GI	g2655295
BLAST score	725
E value	1.0e-125
Match length	225
% identity	100
NCBI Description	(AF032976) germin-like protein 6 [Oryza sativa]

Seq. No.	386022
Contig ID	820_1.R1084
5'-most EST	g2801535
Method	BLASTX
NCBI GI	g2801536
BLAST score	1586
E value	1.0e-177
Match length	304
% identity	100
NCBI Description	(AF039531) lysophospholipase homolog [Oryza sativa]

Seq. No.	386023
Contig ID	821_1.R1084
5'-most EST	g2801537
Method	BLASTX
NCBI GI	g2801538
BLAST score	897
E value	1.0e-96
Match length	205
% identity	88
NCBI Description	(AF039532) harpin induced gene 1 homolog [Oryza sativa]

Seq. No.	386024
Contig ID	822_1.R1084
5'-most EST	LIB3434-030-P1-K1-G3
Method	BLASTN
NCBI GI	g2773153
BLAST score	809
E value	0.0e+00
Match length	813
% identity	100
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No.	386025
Contig ID	822_2.R1084
5'-most EST	LIB3432-044-P1-K1-H4
Method	BLASTX
NCBI GI	g2773154
BLAST score	271
E value	9.0e-24
Match length	78
% identity	64
NCBI Description	(AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No.	386026
Contig ID	823_1.R1084
5'-most EST	g4091007

Method	BLASTX
NCBI GI	g4091008
BLAST score	4078
E value	0.0e+00
Match length	788
% identity	98
NCBI Description	(AF040700) methionyl-tRNA synthetase [Oryza sativa]

Seq. No.	386027
Contig ID	827_1.R1084
5'-most EST	g3560530
Method	BLASTX
NCBI GI	g3560531
BLAST score	1763
E value	0.0e+00
Match length	349
% identity	96
NCBI Description	(AF042332) cycloartenol [illegible] ryza sativa subsp. japonica]

Seq. No.	386028
Contig ID	828_1.R1084
5'-most EST	g3560532
Method	BLASTX
NCBI GI	
BLAST score	
E value	0.0e+00
Match length	363
% identity	100
NCBI Description	(AF042333) 24-methylene lophenol C24(1)methyltransferase

Seq. No.	
Contig ID	830_1.R1084
5'-most EST	g2832303
Method	BLASTX
NCBI GI	g2832304
BLAST score	2126
E value	0.0e+00
Match length	413
% identity	100
NCBI Description	(AF044489) receptor-like protein kinase [Oryza sativa]

Seq. No.	386030
Contig ID	834_1.R1084
5'-most EST	g4091079
Method	BLASTX
NCBI GI	g4091117
BLAST score	1051
E value	1.0e-114
Match length	250
% identity	80
NCBI Description	(AF047428) nucleic acid binding protein [Oryza sativa]

Seq. No.	386031
Contig ID	835_1.R1084
5'-most EST	g2895865

Method	BLASTX
NCBI GI	g2895866
BLAST score	2449
E value	0.0e+00
Match length	525
% identity	92
NCBI Description	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]

Seq. No.	386032
Contig ID	837_1.R1084
5'-most EST	uC-osflcyp122d06b1
Method	BLASTX
NCBI GI	g4105561
BLAST score	1216
E value	1.0e-134
Match length	274
% identity	89
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	386033
Contig ID	838_1.R1084
5'-most EST	g700527
Method	BLASTX
NCBI GI	g2920654
BLAST score	2969
E value	0.0e+00
Match length	551
% identity	100
NCBI Description	(AF047697) putative high-pI laccase [Oryza sativa]

Seq. No.	386034
Contig ID	840_1.R1084
5'-most EST	g4105680
Method	BLASTX
NCBI GI	g4105681
BLAST score	1278
E value	1.0e-141
Match length	393
% identity	58
NCBI Description	(AF049348) unknown [Oryza sativa]

Seq. No.	386035
Contig ID	841_1.R1084
5'-most EST	g4105638
Method	BLASTX
NCBI GI	g4105639
BLAST score	2950
E value	0.0e+00
Match length	566
% identity	100
NCBI Description	(AF049356) phytoene desaturase precursor [Oryza sativa]

Seq. No.	386036
Contig ID	844_1.R1084
5'-most EST	g4105682
Method	BLASTX

NCBI GI	g4105683
BLAST score	1194
E value	1.0e-131
Match length	234
% identity	94
NCBI Description	(AF049892) unknown [Oryza sativa] >gi_4105692 (AF050155) embryo-specific protein [Oryza sativa subsp. indica]

Seq. No.	386037
Contig ID	845_1.R1084
5'-most EST	g2310238
Method	BLASTX
NCBI GI	g2944088
BLAST score	963
E value	1.0e-104
Match length	231
% identity	82
NCBI Description	(AF050102) glutathione s-transferase [Oryza sativa]

Seq. No.	386038
Contig ID	845_2.R1084
5'-most EST	g5003394
Method	BLASTX
NCBI GI	g3885334
BLAST score	1017
E value	1.0e-110
Match length	291
% identity	67
NCBI Description	(AC005623) putative argonaute protein [Arabidopsis thaliana]

Seq. No.	386039
Contig ID	848_1.R1084
5'-most EST	g2311319
Method	BLASTX
NCBI GI	g2952338
BLAST score	1088
E value	1.0e-119
Match length	199
% identity	99
NCBI Description	(AF050200) submergence induced protein 2 [Oryza sativa]

Seq. No.	386040
Contig ID	849_1.R1084
5'-most EST	LIB3432-037-P1-K1-C5
Method	BLASTX
NCBI GI	g2961176
BLAST score	773
E value	3.0e-82
Match length	195
% identity	79
NCBI Description	(AF050674) ribosomal protein L27 precursor [Oryza sativa]

Seq. No.	386041
Contig ID	849_2.R1084
5'-most EST	g701209

Seq. No.	386042
Contig ID	850_1.R1084
5'-most EST	g2961177
Method	BLASTX
NCBI GI	g2961178
BLAST score	1057
E value	1.0e-115
Match length	203
% identity	100
NCBI Description	(AF050675) GTP-binding protein [Oryza sativa]

Seq. No.	386043
Contig ID	851_1.R1084
5'-most EST	g4096172
Method	BLASTX
NCBI GI	g4096173
BLAST score	337
E value	2.0e-93
Match length	358
% identity	70
NCBI Description	(U25968) early embryogenesis protein [Oryza sativa]

Seq. No.	386044
Contig ID	852_1.R1084
5'-most EST	g1632065
Method	BLASTX
NCBI GI	g100876
BLAST score	606
E value	3.0e-86
Match length	296
% identity	59
NCBI Description	globulin-2 precursor - maize >gi_228310_prf__1802402A globulin 2 [Zea mays]

Seq. No.	386045
Contig ID	857_1.R1084
5'-most EST	LIB3477-001-P1-K1-A11
Method	BLASTX
NCBI GI	g4079800
BLAST score	1128
E value	1.0e-124
Match length	227
% identity	96
NCBI Description	(AF052503) S-phase-specific ribosomal protein [Oryza sativa]

Seq. No.	386046
Contig ID	858_1.R1084
5'-most EST	g3377508
Method	BLASTX
NCBI GI	g3377509
BLAST score	2871
E value	0.0e+00
Match length	595
% identity	94
NCBI Description	(AF056027) auxin transport protein REH1 [Oryza sativa]

Seq. No.	386047
Contig ID	859_1.R1084
5'-most EST	LIB3431-019-P1-K1-F9
Method	BLASTX
NCBI GI	g3075488
BLAST score	1348
E value	1.0e-149
Match length	275
% identity	93
NCBI Description	(AF058796) chlorophyll a/b-binding protein [Oryza sativa]

Seq. No.	386048
Contig ID	859_2.R1084
5'-most EST	g3768671
Method	BLASTN
NCBI GI	g3075487
BLAST score	304
E value	1.0e-170
Match length	319
% identity	99
NCBI Description	Oryza sativa chlorophyll a/b-binding protein (RCABP69) mRNA, complete cds

Seq. No.	386049
Contig ID	859_3.R1084
5'-most EST	LIB3431-049-P1-N1-B11
Method	BLASTX
NCBI GI	g2326947
BLAST score	153
E value	7.0e-10
Match length	56
% identity	81
NCBI Description	(Z50801) Chlorophyll a/b-binding protein CP29 precursor [Zea mays]

Seq. No.	386050
Contig ID	860_1.R1084
5'-most EST	g3075515
Method	BLASTX
NCBI GI	g3248993
BLAST score	923
E value	1.0e-100
Match length	179
% identity	99
NCBI Description	(AF067192) putative resistance protein [Oryza sativa]

Seq. No.	386051
Contig ID	865_1.R1084
5'-most EST	g5004907
Method	BLASTX
NCBI GI	g3411152
BLAST score	1105
E value	1.0e-121
Match length	212
% identity	100
NCBI Description	(AF066050) thymidine kinase [Oryza sativa]

Seq. No.	386052
Contig ID	869_1.R1084
5'-most EST	g571963
Method	BLASTX
NCBI GI	g4056615
BLAST score	1349
E value	1.0e-149
Match length	261
% identity	100
NCBI Description	(AF067401) Scl1 protein [Oryza sativa]

Seq. No.	386053
Contig ID	870_1.R1084
5'-most EST	g3201968
Method	BLASTX
NCBI GI	g3201969
BLAST score	1084
E value	1.0e-118
Match length	198
% identity	100
NCBI Description	(AF068332) submergence induced protein 2A [Oryza sativa]

Seq. No.	386054
Contig ID	871_1.R1084
5'-most EST	g287172
Method	BLASTN
NCBI GI	g3201970
BLAST score	649
E value	0.0e+00
Match length	653
% identity	100
NCBI Description	Oryza sativa hypothetical secretory protein SH27A precursor, mRNA, complete cds

Seq. No.	386055
Contig ID	873_1.R1084
5'-most EST	g3293558
Method	BLASTX
NCBI GI	g3293559
BLAST score	952
E value	1.0e-103
Match length	194
% identity	95
NCBI Description	(AF072694) germin-like protein 7 [Oryza sativa]

Seq. No.	386056
Contig ID	874_1.R1084
5'-most EST	g2276037
Method	BLASTX
NCBI GI	g3293561
BLAST score	429
E value	4.0e-42
Match length	98
% identity	87
NCBI Description	(AF072695) germin-like protein 8 [Oryza sativa]

Seq. No.	386057

Contig ID	875_1.R1084
5'-most EST	g3406754
Method	BLASTX
NCBI GI	g2982463
BLAST score	304
E value	2.0e-33
Match length	91
% identity	79
NCBI Description	(AL022223) putative protein [Arabidopsis thaliana]

Seq. No.	386058
Contig ID	876_1.R1084
5'-most EST	g3420298
Method	BLASTX
NCBI GI	g3420299
BLAST score	1753
E value	0.0e+00
Match length	360
% identity	94
NCBI Description	(AF072849) jab1 protein [Oryza sativa subsp. indica]

Seq. No.	386059
Contig ID	877_1.R1084
5'-most EST	LIB3474-006-P1-K1-E5
Method	BLASTX
NCBI GI	g4574135
BLAST score	1514
E value	1.0e-169
Match length	321
% identity	94
NCBI Description	(AF073695) cysteine synthase [Oryza sativa]

Seq. No.	386060
Contig ID	878_1.R1084
5'-most EST	g4574136
Method	BLASTX
NCBI GI	g4574137
BLAST score	1764
E value	0.0e+00
Match length	357
% identity	97
NCBI Description	(AF073696) cysteine synthase [Oryza sativa]

Seq. No.	386061
Contig ID	879_1.R1084
5'-most EST	LIB3433-003-Q6-K6-A10
Method	BLASTX
NCBI GI	g4574139
BLAST score	1487
E value	1.0e-166
Match length	325
% identity	92
NCBI Description	(AF073697) cysteine synthase [Oryza sativa]

Seq. No.	386062
Contig ID	880_1.R1084
5'-most EST	g4574140

Method	BLASTX
NCBI GI	g4574141
BLAST score	1666
E value	0.0e+00
Match length	339
% identity	96
NCBI Description	(AF073698) cysteine synthase [Oryza sativa]

Seq. No.	386063
Contig ID	884_1.R1084
5'-most EST	g3421414
Method	BLASTX
NCBI GI	g3421413
BLAST score	2579
E value	0.0e+00
Match length	531
% identity	93
NCBI Description	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] >gi_3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]

Seq. No.	386064
Contig ID	886_1.R1084
5'-most EST	g428223
Method	BLASTX
NCBI GI	g3603473
BLAST score	749
E value	2.0e-79
Match length	144
% identity	100
NCBI Description	(AF090698) elicitor-responsive gene-3 [Oryza sativa]

Seq. No.	386065
Contig ID	887_1.R1084
5'-most EST	g568127
Method	BLASTX
NCBI GI	g3643271
BLAST score	1080
E value	1.0e-126
Match length	264
% identity	85
NCBI Description	(AF090872) 33 kDa secretory protein [Oryza sativa] >gi_3851590 (AF093570) 33 kDa secretory protein [Oryza sativa] >gi_4249681 (AF097724) 33 kDa secretory protein [Oryza sativa]

Seq. No.	386066
Contig ID	887_3.R1084
5'-most EST	g3090546
Method	BLASTN
NCBI GI	g3851589
BLAST score	210
E value	1.0e-114
Match length	372
% identity	92
NCBI Description	Oryza sativa 33 kDa secretory protein mRNA, complete cds

Seq. No.	386067
Contig ID	887_4.R1084
5'-most EST	g2310572
Method	BLASTN
NCBI GI	g3851589
BLAST score	220
E value	1.0e-120
Match length	372
% identity	91
NCBI Description	Oryza sativa 33 kDa secretory protein mRNA, complete cds

Seq. No.	386068
Contig ID	888_1.R1084
5'-most EST	g6006606
Method	BLASTX
NCBI GI	g6006607
BLAST score	1212
E value	1.0e-133
Match length	249
% identity	96
NCBI Description	(AJ011675) MADS box protein, MADS28 [Oryza sativa]

Seq. No.	386069
Contig ID	890_1.R1084
5'-most EST	g431842
Method	BLASTX
NCBI GI	g3885880
BLAST score	1549
E value	1.0e-173
Match length	322
% identity	94
NCBI Description	(AF093628) protochlorophyllide reductase homolog [Oryza sativa]

Seq. No.	386070
Contig ID	892_1.R1084
5'-most EST	LIB3433-054-P1-K1-G5
Method	BLASTX
NCBI GI	g3885884
BLAST score	846
E value	7.0e-91
Match length	164
% identity	97
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	386071
Contig ID	892_2.R1084
5'-most EST	uC-osf1cyp026a07b1
Method	BLASTX
NCBI GI	g3885884
BLAST score	864
E value	6.0e-93
Match length	164
% identity	99
NCBI Description	(AF093630) 60S ribosomal protein L21 [Oryza sativa]

Seq. No.	386072

Contig ID	893_1.R1084
5'-most EST	LIB3432-056-P1-K1-G8
Method	BLASTX
NCBI GI	g3885886
BLAST score	1198
E value	1.0e-132
Match length	224
% identity	100
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	386073
Contig ID	893_4.R1084
5'-most EST	LIB3431-045-P1-N1-B1
Method	BLASTX
NCBI GI	g3885886
BLAST score	163
E value	4.0e-11
Match length	32
% identity	84
NCBI Description	(AF093631) Rieske Fe-S precursor protein [Oryza sativa]

Seq. No.	386074
Contig ID	894_1.R1084
5'-most EST	g3760566
Method	BLASTX
NCBI GI	g3885888
BLAST score	316
E value	1.0e-28
Match length	107
% identity	65
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	386075
Contig ID	894_2.R1084
5'-most EST	LIB3433-039-P1-K1-E2
Method	BLASTX
NCBI GI	g3885888
BLAST score	262
E value	2.0e-22
Match length	54
% identity	96
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	386076
Contig ID	894_3.R1084
5'-most EST	uC-osflcyp171c11b1
Method	BLASTN
NCBI GI	g3885887
BLAST score	161
E value	4.0e-85
Match length	177
% identity	98
NCBI Description	Oryza sativa high mobility group protein (HMG) mRNA, complete cds

Seq. No.	386077
Contig ID	894_4.R1084

5'-most EST	LIB3432-041-P1-K1-G5
Method	BLASTX
NCBI GI	g3885888
BLAST score	287
E value	2.0e-25
Match length	101
% identity	63
NCBI Description	(AF093632) high mobility group protein [Oryza sativa]

Seq. No.	386078
Contig ID	896_1.R1084
5'-most EST	g701200
Method	BLASTX
NCBI GI	g3885892
BLAST score	773
E value	4.0e-82
Match length	207
% identity	73
NCBI Description	(AF093634) photosystem-1 F subunit precursor [Oryza sativa]

Seq. No.	386079
Contig ID	896_2.R1084
5'-most EST	LIB3432-020-P1-K1-E6
Method	BLASTX
NCBI GI	g2582822
BLAST score	895
E value	2.0e-96
Match length	230
% identity	75
NCBI Description	(Y09987) CDSP32 protein (Chloroplast Drought-induced Stress Protein of 32kDa) [Solanum tuberosum]

Seq. No.	386080
Contig ID	896_4.R1084
5'-most EST	uC-osf1M202066d09b1

Seq. No.	386081
Contig ID	896_6.R1084
5'-most EST	LIB3432-034-P2-K1-B10
Method	BLASTN
NCBI GI	g3885891
BLAST score	258
E value	1.0e-143
Match length	278
% identity	98
NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	386082
Contig ID	896_8.R1084
5'-most EST	LIB3432-031-P1-K1-A4
Method	BLASTN
NCBI GI	g3885891
BLAST score	188
E value	1.0e-101
Match length	188
% identity	100

NCBI Description	Oryza sativa photosystem-1 F subunit precursor (PSI-F) mRNA, complete cds

Seq. No.	386083
Contig ID	897_1.R1084
5'-most EST	LIB3431-058-P1-K1-F12
Method	BLASTX
NCBI GI	g3885894
BLAST score	585
E value	4.0e-60
Match length	142
% identity	82
NCBI Description	(AF093635) photosystem-1 H subunit GOS5 [Oryza sativa]

Seq. No.	386084
Contig ID	901_1.R1084
5'-most EST	LIB3432-014-P1-K1-A2
Method	BLASTX
NCBI GI	g3789952
BLAST score	1249
E value	1.0e-138
Match length	244
% identity	97
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	386085
Contig ID	901_2.R1084
5'-most EST	LIB3431-006-P1-K1-B10
Method	BLASTX
NCBI GI	g3789952
BLAST score	484
E value	2.0e-48
Match length	121
% identity	71
NCBI Description	(AF094775) chlorophyll a/b-binding protein presursor [Oryza sativa]

Seq. No.	386086
Contig ID	902_1.R1084
5'-most EST	LIB3431-044-P1-K1-A9
Method	BLASTX
NCBI GI	g3789954
BLAST score	1290
E value	1.0e-142
Match length	239
% identity	100
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	386087
Contig ID	902_2.R1084
5'-most EST	LIB3432-037-P1-K1-D10
Method	BLASTX
NCBI GI	g548603
BLAST score	764
E value	4.0e-81

Match length	189
% identity	80
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT II PRECURSOR (PHOTOSYSTEM I 20 KD SUBUNIT) (PSI-D) >gi_478404_pir__JQ2247 photosystem I chain D precursor - barley >gi_167085 (M98254) PSI-D subunit [Hordeum vulgare]

Seq. No.	386088
Contig ID	902_3.R1084
5'-most EST	g6025111
Method	BLASTX
NCBI GI	g2459421
BLAST score	297
E value	3.0e-27
Match length	178
% identity	39
NCBI Description	(AC002332) putative calcium-binding EF-hand protein [Arabidopsis thaliana]

Seq. No.	386089
Contig ID	902_4.R1084
5'-most EST	LIB34[illegible] P1-K1-B4
Method	BLASTX
NCBI GI	g3789954
BLAST score	382
E value	3.0e-36
Match length	72
% identity	63
NCBI Description	(AF0[illegible] lorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	386090
Contig ID	902_5.R1084
5'-most EST	uC-osflcyp017b11b1

Seq. No.	386091
Contig ID	902_7.R1084
5'-most EST	LIB3431-041-P2-K1-G8
Method	BLASTX
NCBI GI	g1055130
BLAST score	420
E value	1.0e-40
Match length	249
% identity	37
NCBI Description	(U39998) coded for by C. elegans cDNA yk92b11.3; coded for by C. elegans cDNA yk92b11.5; coded for by C. elegans cDNA yk78c2.5; coded for by C. elegans cDNA cm9[illegible] coded for by C. elegans cDNA yk66h8.3; coded for by C. elegans cDNA yk78c2.3

Seq. No.	386092
Contig ID	902_10.R1084
5'-most EST	LIB3431-054-P1-K1-G3
Method	BLASTX
NCBI GI	g3789954
BLAST score	624
E value	5.0e-65

Match length	129
% identity	78
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	386093
Contig ID	902_11.R1084
5'-most EST	LIB3431-036-P1-K1-D1
Method	BLASTX
NCBI GI	g4105561
BLAST score	186
E value	1.0e-13
Match length	80
% identity	54
NCBI Description	(AF047444) ribulose-5-phosphate-3-epimerase [Oryza sativa]

Seq. No.	386094
Contig ID	902_12.R1084
5'-most EST	LIB3431-022-P1-K1-D12
Method	BLASTX
NCBI GI	g3789954
BLAST score	800
E value	2.0e-90
Match length	164
% identity	73
NCBI Description	(AF094776) chlorophyll a/b-binding protein precursor [Oryza sativa]

Seq. No.	386095
Contig ID	903_1.R1084
5'-most EST	g3777597
Method	BLASTX
NCBI GI	g3777598
BLAST score	434
E value	2.0e-42
Match length	118
% identity	76
NCBI Description	(AF095707) 30S ribosomal protein S17 [Oryza sativa]

Seq. No.	386096
Contig ID	904_1.R1084
5'-most EST	LIB3434-028-P1-K1-H7
Method	BLASTX
NCBI GI	g3777600
BLAST score	1192
E value	1.0e-131
Match length	280
% identity	85
NCBI Description	(AF095708) 50S ribosomal protein L5 [Oryza sativa]

Seq. No.	386097
Contig ID	905_1.R1084
5'-most EST	g3777601
Method	BLASTX
NCBI GI	g3777602
BLAST score	1048
E value	1.0e-114

Match length	220
% identity	95
NCBI Description	(AF095709) 50S ribosomal protein L10 [Oryza sativa]

Seq. No.	386098
Contig ID	909_1.R1084
5'-most EST	uC-osflcyp029b01b1
Method	BLASTX
NCBI GI	g3859568
BLAST score	867
E value	4.0e-93
Match length	161
% identity	100
NCBI Description	(AF098752) unknown [Oryza sativa]

Seq. No.	386099
Contig ID	910_1.R1084
5'-most EST	g3859569
Method	BLASTX
NCBI GI	g3859570
BLAST score	902
E value	2.0e-97
Match length	186
% identity	92
NCBI Description	(AF098753) unknown [Oryza sativa]

Seq. No.	386100
Contig ID	911_1.R1084
5'-most EST	g4416348
Method	BLASTX
NCBI GI	g4416349
BLAST score	1371
E value	1.0e-152
Match length	265
% identity	100
NCBI Description	(AF110268) plasma membrane proton-ATPase gene OSA3 [Oryza sativa]

Seq. No.	386101
Contig ID	912_1.R1084
5'-most EST	LIB3474-012-P1-K1-C7
Method	BLASTX
NCBI GI	g6014938
BLAST score	1526
E value	1.0e-170
Match length	387
% identity	80
NCBI Description	UROPORPHYRINOGEN DECARBOXYLASE PRECURSOR (UPD) >gi_3420233 (AF058763) uroporphyrinogen decarboxylase [Zea mays]

Seq. No.	386102
Contig ID	914_1.R1084
5'-most EST	g5001829
Method	BLASTX
NCBI GI	g5001830
BLAST score	1674
E value	0.0e+00

Match length	348
% identity	92
NCBI Description	(AF132743) 3-phosphoinositide-dependent protein kinase-1 [Oryza sativa]

Seq. No.	386103
Contig ID	915_1.R1084
5'-most EST	g2431337
Method	BLASTX
NCBI GI	g4581047
BLAST score	1675
E value	0.0e+00
Match length	330
% identity	98
NCBI Description	(AF134807) putative dihydroflavonol reductase [Oryza sativa]

Seq. No.	386104
Contig ID	918_1.R1084
5'-most EST	g4768969
Method	BLASTN
NCBI GI	g4768969
BLAST score	387
E value	0.0e+00
Match length	399
% identity	99
NCBI Description	Oryza sativa unknown mRNA

Seq. No.	386105
Contig ID	919_1.R1084
5'-most EST	LIB3433-007-Q6-K1-B12
Method	BLASTX
NCBI GI	g4768972
BLAST score	547
E value	5.0e-56
Match length	105
% identity	97
NCBI Description	(AF140486) cytochrome P450 [Oryza sativa]

Seq. No.	386106
Contig ID	920_1.R1084
5'-most EST	g4969132
Method	BLASTX
NCBI GI	g4768974
BLAST score	605
E value	2.0e-62
Match length	125
% identity	98
NCBI Description	(AF140487) origin recognition complex protein [Oryza sativa]

Seq. No.	386107
Contig ID	921_1.R1084
5'-most EST	g569139
Method	BLASTX
NCBI GI	g4768976
BLAST score	459

E value	5.0e-46
Match length	88
% identity	99
NCBI Description	(AF140488) hypothetical protein [Oryza sativa]

Seq. No.	386108
Contig ID	924_1.R1084
5'-most EST	uC-osflM202092c04b1
Method	BLASTX
NCBI GI	g4768982
BLAST score	600
E value	2.0e-61
Match length	130
% identity	88
NCBI Description	(AF140491) hypothetical protein [Oryza sativa]

Seq. No.	386109
Contig ID	927_1.R1084
5'-most EST	g2443186
Method	BLASTX
NCBI GI	g5816996
BLAST score	543
E value	2.0e-55
Match length	133
% identity	79
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	386110
Contig ID	927_2.R1084
5'-most EST	g3767072
Method	BLASTX
NCBI GI	g5816996
BLAST score	438
E value	3.0e-43
Match length	99
% identity	85
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	386111
Contig ID	927_3.R1084
5'-most EST	uC-osflcyp080f06b1
Method	BLASTX
NCBI GI	g5816996
BLAST score	546
E value	8.0e-56
Match length	133
% identity	80
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	386112
Contig ID	927_4.R1084
5'-most EST	LIB3431-058-P1-K1-C9
Method	BLASTX
NCBI GI	g5816996

BLAST score	301
E value	3.0e-27
Match length	107
% identity	67
NCBI Description	(AL110123) ribosomal protein L32-like protein [Arabidopsis thaliana]

Seq. No.	386113
Contig ID	929_1.R1084
5'-most EST	g4768991
Method	BLASTX
NCBI GI	g4768992
BLAST score	629
E value	2.0e-65
Match length	122
% identity	100
NCBI Description	(AF140496) cholinephosphate cytidylyltransfe... [Oryza sativa]

Seq. No.	386114
Contig ID	930_1.R1084
5'-most EST	g4768993
Method	BLASTX
NCBI GI	[illegible]
BLAST score	[illegible]
E value	[illegible]
Match [illegible]	137
% iden[illegible]y	100
NCBI Description	(AF140497) hypothetical protein [Oryza sativa]

Seq. No.	[illegible]
Contig [illegible]	[illegible]
5'-mos[illegible]	[illegible]
Metho[illegible]	BLASTX
NCBI GI	g4102839
BLAST score	1556
E value	1.0e-173
Match length	574
% identity	52
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]

Seq. No.	386116
Contig ID	936_1.R1084
5'-most EST	g5499729
Method	BLASTX
NCBI GI	g5499730
BLAST score	1103
E value	1.0e-121
Match length	207
% identity	100
NCBI Description	(AF141878) germin-like protein 1 precursor [Oryza sativa] >gi_5499734_gb_AAD43973.1_AF141880_1 (AF141880) germin-like protein 1 precursor [Oryza sativa]

Seq. No.	386117
Contig ID	939_1.R1084
5'-most EST	g3760340

Method	BLASTN
NCBI GI	g5051932
BLAST score	200
E value	1.0e-108
Match length	256
% identity	100
NCBI Description	Oryza sativa MADS-box protein FDRMADS8 mRNA, complete cds

Seq. No.	386118
Contig ID	939_2.R1084
5'-most EST	g5051932
Method	BLASTX
NCBI GI	g5051933
BLAST score	1144
E value	1.0e-125
Match length	228
% identity	100
NCBI Description	(AF141965) MADS-box protein FDRMADS8 [Oryza sativa]

Seq. No.	386119
Contig ID	941_1.R1084
5'-most EST	g1914837
Method	BLASTX
NCBI GI	g1914838
BLAST score	1143
E value	1.0e-125
Match length	225
% identity	100
NCBI Description	(U78890) MADS box protein [Oryza sativa] >gi_5295964_dbj_BAA81865.1_ (AB026295) EST D15657(C1032) corresponds to a region of the predicted gene.; Oryza sativa MADS box protein (OsMADS5) mRNA, complete cds.(U78890)

Seq. No.	386120
Contig ID	942_1.R1084
5'-most EST	g4880229
Method	BLASTX
NCBI GI	g4769012
BLAST score	3141
E value	0.0e+00
Match length	622
% identity	98
NCBI Description	(AF143746) CER1 [Oryza sativa]

Seq. No.	386121
Contig ID	943_1.R1084
5'-most EST	uC-osflm202112b10b1
Method	BLASTX
NCBI GI	g6006848
BLAST score	287
E value	3.0e-50
Match length	154
% identity	68
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	386122
Contig ID	944_1.R1084
5'-most EST	g2427622
Method	BLASTX
NCBI GI	g4973431
BLAST score	2450
E value	0.0e+00
Match length	486
% identity	98
NCBI Description	(AF148877) putative aldehyde dehydrogenase OS-ALDH [Oryza sativa subsp. indica]

Seq. No.	386123
Contig ID	945_1.R1084
5'-most EST	LIB3434-033-P1-K1-F8
Method	BLASTX
NCBI GI	g5107149
BLAST score	309
E value	5.0e-28
Match length	84
% identity	73
NCBI Description	(AF150080) small zinc finger-like protein [Oryza sativa]

Seq. No.	386124
Contig ID	946_1.R1084
5'-most EST	g5107213
Method	BLASTX
NCBI GI	g5107214
BLAST score	482
E value	2.0e-48
Match length	93
% identity	100
NCBI Description	(AF150113) small zinc finger-like protein [Oryza sativa]

Seq. No.	386125
Contig ID	947_1.R1084
5'-most EST	g6470125
Method	BLASTX
NCBI GI	g951172
BLAST score	839
E value	8.0e-90
Match length	269
% identity	68
NCBI Description	(U31521) MADS box protein [Zea mays] >gi_1001934_emb_CAA56504_ (X80206) ZAG2 [Zea mays]

Seq. No.	386126
Contig ID	951_1.R1084
5'-most EST	g5360177
Method	BLASTX
NCBI GI	g5360178
BLAST score	868
E value	2.0e-93
Match length	165
% identity	100
NCBI Description	(AF159882) Cen-like protein FDR2 [Oryza sativa]

Seq. No.	386127
Contig ID	951_3.R1084
5'-most EST	g569317
Method	BLASTX
NCBI GI	g5360180
BLAST score	358
E value	9.0e-34
Match length	72
% identity	99
NCBI Description	(AF159883) Cen-like protein FDR1 [Oryza sativa]

Seq. No.	386128
Contig ID	954_1.R1084
5'-most EST	g6090878
Method	BLASTX
NCBI GI	g6090879
BLAST score	4049
E value	0.0e+00
Match length	757
% identity	98
NCBI Description	(AF169966) putative cycloartenol synthase [Oryza sativa]

Seq. No.	386129
Contig ID	955_1.R1084
5'-most EST	g5701705
Method	BLASTX
NCBI GI	g5803246
BLAST score	837
E value	2.0e-89
Match length	145
% identity	100
NCBI Description	(AP000399) ESTs AU077984(C62969),D41648(S4289), AU063584(C62969) correspond to a region of the predicted gene; similar to putative Ser/Thr protein kinase (AC003105) [Oryza sativa]

Seq. No.	386130
Contig ID	956_1.R1084
5'-most EST	g6689923
Method	BLASTX
NCBI GI	g5815410
BLAST score	2480
E value	0.0e+00
Match length	506
% identity	95
NCBI Description	(AF177392) blast and wounding induced mitogen-activated protein kinase [Oryza sativa]

Seq. No.	386131
Contig ID	958_1.R1084
5'-most EST	g6007802
Method	BLASTX
NCBI GI	g6007803
BLAST score	1114
E value	1.0e-122
Match length	217
% identity	100

NCBI Description	(AF189365) D-ribulose-5-phosphate 3-epimerase [Oryza sativa]

Seq. No.	386132
Contig ID	959_1.R1084
5'-most EST	uC-osflm202104g09b1
Method	BLASTX
NCBI GI	g3264767
BLAST score	453
E value	2.0e-44
Match length	251
% identity	44
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	386133
Contig ID	960_1.R1084
5'-most EST	g6319145
Method	BLASTX
NCBI GI	g2407800
BLAST score	496
E value	1.0e-49
Match length	109
% identity	92
NCBI Description	(Y12575) histone H2A.F/Z [Arabidopsis thaliana]

Seq. No.	386134
Contig ID	963_1.R1084
5'-most EST	g2428589
Method	BLASTX
NCBI GI	g5912299
BLAST score	4805
E value	0.0e+00
Match length	976
% identity	97
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	386135
Contig ID	963_2.R1084
5'-most EST	LIB3434-035-P1-K1-H6
Method	BLASTX
NCBI GI	g5912299
BLAST score	360
E value	4.0e-34
Match length	97
% identity	90
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	386136
Contig ID	963_8.R1084
5'-most EST	uC-osflcyp051e06b1
Method	BLASTX
NCBI GI	g5912299
BLAST score	226
E value	3.0e-18
Match length	56
% identity	75
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	386137
Contig ID	963_9.R1084
5'-most EST	LIB3475-002-P1-K2-D2
Method	BLASTX
NCBI GI	g5912299
BLAST score	828
E value	7.0e-89
Match length	169
% identity	98
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	386138
Contig ID	963_10.R1084
5'-most EST	g3768140
Method	BLASTX
NCBI GI	g5912299
BLAST score	372
E value	2.0e-35
Match length	165
% identity	94
NCBI Description	(AJ133787) gigantea homologue [Oryza sativa]

Seq. No.	386139
Contig ID	964_1.R1084
5'-most EST	LIB3477-004-P1-K1-B2
Method	BLASTX
NCBI GI	g3850816
BLAST score	1004
E value	1.0e-109
Match length	185
% identity	100
NCBI Description	(Y18348) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	386140
Contig ID	965_1.R1084
5'-most EST	g287210
Method	BLASTX
NCBI GI	g3850818
BLAST score	970
E value	1.0e-105
Match length	290
% identity	67
NCBI Description	(Y18349) U2 snRNP auxiliary factor, small subunit [Oryza sativa]

Seq. No.	386141
Contig ID	966_1.R1084
5'-most EST	uC-osroM202025a09b1
Method	BLASTX
NCBI GI	g5679684
BLAST score	2977
E value	0.0e+00
Match length	587
% identity	100
NCBI Description	(AJ243828) phosphatase 2A regulatory A subunit [Oryza

sativa] >gi_5679686_emb_CAB51804.1_ (AJ243829) protein phosphatase 2A A subunit [Oryza sativa]

Seq. No.	386142
Contig ID	967_1.R1084
5'-most EST	LIB3432-008-P1-K1-A8
Method	BLASTX
NCBI GI	g6094330
BLAST score	1357
E value	1.0e-150
Match length	293
% identity	86
NCBI Description	SPERMIDINE SYNTHASE 2 (PUTRESCINE AMINOPROPYLTRANSFERASE 2) (SPDSY 2) >gi_2821957_dbj_BAA24534_ (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No.	386143
Contig ID	968_1.R1084
5'-most EST	g6469282
Method	BLASTX
NCBI GI	g6094330
BLAST score	585
E value	3.0e-60
Match length	160
% identity	64
NCBI Description	SPERMIDINE SYNTHASE 2 (PUTRESCINE AMINOPROPYLTRANSFERASE 2) (SPDSY 2) >gi_2821957_dbj_BAA24534_ (AB006691) spermidine synthase 2 [Hyoscyamus niger]

Seq. No.	386144
Contig ID	969_1.R1084
5'-most EST	uC-osroM202028d09b1
Method	BLASTX
NCBI GI	g2499614
BLAST score	1606
E value	1.0e-179
Match length	362
% identity	81
NCBI Description	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF3 (P43) >gi_481830_pir__S39559 mitogen-activated protein kinase 3 homolog ntf3 - common tobacco >gi_406751_emb_CAA49592_ (X69971) NTF3 [Nicotiana tabacum]

Seq. No.	386145
Contig ID	974_1.R1084
5'-most EST	g2109456
Method	BLASTX
NCBI GI	g2109457
BLAST score	1418
E value	1.0e-158
Match length	278
% identity	92
NCBI Description	(AF001501) chitinase [Oryza sativa]

Seq. No.	386146
Contig ID	976_1.R1084
5'-most EST	g2800903

Method	BLASTX
NCBI GI	g2072322
BLAST score	2027
E value	0.0e+00
Match length	495
% identity	83
NCBI Description	(U95816) Isolation and Characterization of a cDNA Encoding 3-Hydroxy-3-Methylglutaryl-CoA Reductase from Rice [Oryza sativa]

Seq. No.	386147
Contig ID	979_1.R1084
5'-most EST	g2292977
Method	BLASTX
NCBI GI	g2292978
BLAST score	1421
E value	1.0e-158
Match length	313
% identity	89
NCBI Description	(Y10253) pantoate--beta-alanine ligase [Oryza sativa]

Seq. No.	386148
Contig ID	980_1.R1084
5'-most EST	uC-osflcyp122h10b1
Method	BLASTX
NCBI GI	g435942
BLAST score	1581
E value	1.0e-176
Match length	390
% identity	81
NCBI Description	(U04295) DNA-binding factor of bZIP class [Oryza sativa]

Seq. No.	386149
Contig ID	984_1.R1084
5'-most EST	LIB3431-036-P1-K1-A1
Method	BLASTX
NCBI GI	g2997684
BLAST score	245
E value	2.0e-20
Match length	85
% identity	56
NCBI Description	(AF053302) putative transcriptional co-activator [Arabidopsis thaliana]

Seq. No.	386150
Contig ID	986_1.R1084
5'-most EST	g700440
Method	BLASTN
NCBI GI	g571443
BLAST score	195
E value	1.0e-105
Match length	203
% identity	99
NCBI Description	Oryza sativa clone SR3 sucrose-regulated mRNA, 3'-end sequence

Seq. No.	386151

Contig ID	987_1.R1084
5'-most EST	g624220
Method	BLASTX
NCBI GI	g1711507
BLAST score	669
E value	5.0e-70
Match length	127
% identity	100
NCBI Description	SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) >gi_624221 (U19030) signal recognition particle 19 kDa protein subunit SRP19 [Oryza sativa]

Seq. No.	386152
Contig ID	988_1.R1084
5'-most EST	g1753084
Method	BLASTX
NCBI GI	g1753085
BLAST score	898
E value	1.0e-96
Match length	217
% identity	84
NCBI Description	(U25283) leucine zipper protein [Oryza sativa]

Seq. No.	386153
Contig ID	989_1.R1084
5'-most EST	g1753086
Method	BLASTN
NCBI GI	g1753086
BLAST score	204
E value	1.0e-111
Match length	443
% identity	98
NCBI Description	Oryza sativa clone OSE3 leucine zipper protein mRNA, complete cds

Seq. No.	386154
Contig ID	993_1.R1084
5'-most EST	g701216
Method	BLASTX
NCBI GI	g1041710
BLAST score	1106
E value	1.0e-121
Match length	216
% identity	93
NCBI Description	(U30477) expansin Os-EXP2 [Oryza sativa]

Seq. No.	386155
Contig ID	993_2.R1084
5'-most EST	g1815680
Method	BLASTX
NCBI GI	g1815681
BLAST score	1196
E value	1.0e-131
Match length	235
% identity	94
NCBI Description	(U85246) expansin [Oryza sativa]

Seq. No.	386156
Contig ID	994_1.R1084
5'-most EST	uC-osrocyp015a09b1
Method	BLASTX
NCBI GI	g1041712
BLAST score	1193
E value	1.0e-131
Match length	255
% identity	87
NCBI Description	(U30479) expansin Os-EXP3 [Oryza sativa]

Seq. No.	386157
Contig ID	998_1.R1084
5'-most EST	LIB3432-059-P1-K1-E7
Method	BLASTX
NCBI GI	g1261917
BLAST score	335
E value	6.0e-31
Match length	94
% identity	63
NCBI Description	(X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No.	386158
Contig ID	998_2.R1084
5'-most EST	g2442845
Method	BLASTX
NCBI GI	g1261917
BLAST score	339
E value	2.0e-31
Match length	90
% identity	68
NCBI Description	(X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No.	386159
Contig ID	998_3.R1084
5'-most EST	uC-osflcyp020f12b1
Method	BLASTX
NCBI GI	g1261917
BLAST score	339
E value	2.0e-31
Match length	90
% identity	68
NCBI Description	(X96979) lipid transfer protein 7a2b [Hordeum vulgare]

Seq. No.	386160
Contig ID	998_5.R1084
5'-most EST	LIB3477-001-P1-K1-H6
Method	BLASTX
NCBI GI	g3913517
BLAST score	1633
E value	0.0e+00
Match length	358
% identity	91
NCBI Description	3'(2'),5'-BISPHOSPHATE NUCLEOTIDASE (3'(2'),5-BISPHOSPHONUCLEOSIDE 3'(2')-PHOSPHOHYDROLASE) (DPNPASE) >gi_1109672 (U33283) 3'(2'),5-diphosphonucleoside 3'(2') phosphohydrolase [Oryza sativa]

>gi_1586671_prf__2204308A diphosphonucleoside phosphohydrolase [Oryza sativa]

Seq. No.	386161
Contig ID	999_1.R1084
5'-most EST	g286759
Method	BLASTX
NCBI GI	g1352440
BLAST score	963
E value	1.0e-104
Match length	174
% identity	99
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-4F 25 KD SUBUNIT) (EIF-4F P26 SUBUNIT) >gi_1002915 (U34597) p26 [Oryza sativa]

Seq. No.	386162
Contig ID	1000_1.R1084
5'-most EST	g1002916
Method	BLASTX
NCBI GI	g1352442
BLAST score	647
E value	2.0e-67
Match length	178
% identity	87
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 4E (EIF-4E) (EIF4E) (MRNA CAP-BINDING PROTEIN) (EIF-(ISO)4F 25 KD SUBUNIT) (EIF-(ISO)4F P28 SUBUNIT) >gi_1002917 (U34598) p28 [Oryza sativa]

Seq. No.	386163
Contig ID	1002_1.R1084
5'-most EST	LIB3431-048-P1-K1-H3
Method	BLASTX
NCBI GI	g1235664
BLAST score	808
E value	3.0e-86
Match length	187
% identity	87
NCBI Description	(U37936) novel calmodulin-like protein [Oryza sativa] >gi_3171148 (AF064456) calmodulin-like protein [Oryza sativa subsp. indica]

Seq. No.	386164
Contig ID	1002_2.R1084
5'-most EST	uC-osf1M202053f10b1

Seq. No.	386165
Contig ID	1005_1.R1084
5'-most EST	g1147631
Method	BLASTX
NCBI GI	g1147632
BLAST score	1769
E value	0.0e+00
Match length	360
% identity	96

NCBI Description (U42208) OSBZ8 [Oryza sativa]

Seq. No. 386166
Contig ID 1007_1.R1084
5'-most EST LIB3432-030-P1-K1-H6
Method BLASTX
NCBI GI g2497903
BLAST score 220
E value 2.0e-17
Match length 59
% identity 68
NCBI Description METALLOTHIONEIN-LIKE PROTEIN TYPE 2
>gi_175283 [illegible] 1_ (D89931) metallothionein-like
protein [Oryza [illegible] 1815628 (U43530)
metallothionein-like type 2 [Oryza sativa]

Seq. No. 386167
Contig ID 1009_1.R1084
5'-most EST g3090508
Method BLASTX
NCBI GI g3334279
BLAST score 289
E value 2.0e-25
Match length 109
% identity 60
NCBI Description OLEOSIN 18 KD (OSE7[illegible] Da oleosin
[Oryza sativa] >gi [illegible]02969 [illegible]9212) 18 kDa oleosin [Oryza
sativa subsp. in[illegible]a]

Seq. No. 386168
Contig ID 1013_1.R1084
5'-most EST g4097101
Method BLASTX
NCBI GI g4097102
BLAST score 1101
E value 1.0e-120
Match length 383
% identity 82
NCBI Description (U45322) globulin-like protein [Oryza sativa]

Seq. No. 386169
Contig ID 1014_1.R1084
5'-most EST uC-osflcyp159h05b1
Method BLASTX
NCBI GI g1197587
BLAST score 1473
E value 1.0e-164
Match length 327
% identity 90
NCBI Description (U46758) potassium channel beta subunit protein [Oryza
sativa]

Seq. No. 386170
Contig ID 1015_1.R1084
5'-most EST LIB3433-060-P1-K1-C3
Method BLASTN
NCBI GI g1218053

BLAST score	164
E value	1.0e-86
Match length	180
% identity	64
NCBI Description	Oryza sativa protein phosphatase 2A mRNA, complete cds

Seq. No.	386171
Contig ID	1015_2.R1084
5'-most EST	g1218053
Method	BLASTX
NCBI GI	g1218054
BLAST score	1664
E value	0.0e+00
Match length	306
% identity	100
NCBI Description	(U49113) protein phosphatase 2A [Oryza sativa]

Seq. No.	386172
Contig ID	1016_1.R1084
5'-most EST	uC-osf1M202014f01b1
Method	BLASTX
NCBI GI	g1854637
BLAST score	1849
E value	0.0e+00
Match length	371
% identity	95
NCBI Description	(U50333) gibberellin C-20 oxidase [Oryza sativa]

Seq. No.	386173
Contig ID	1018_1.R1084
5'-most EST	g2310894
Method	BLASTX
NCBI GI	g2213643
BLAST score	2584
E value	0.0e+00
Match length	533
% identity	92
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	386174
Contig ID	1018_2.R1084
5'-most EST	g3762375
Method	BLASTX
NCBI GI	g2213643
BLAST score	585
E value	2.0e-62
Match length	167
% identity	73
NCBI Description	(U57338) glossy1 homolog [Oryza sativa]

Seq. No.	386175
Contig ID	1020_1.R1084
5'-most EST	g1631978
Method	BLASTX
NCBI GI	g4097340
BLAST score	901
E value	4.0e-97

Match length	173
% identity	100
NCBI Description	(U57639) hydrophobic LEA-like protein [Oryza sativa]

Seq. No.	386176
Contig ID	1021_1.R1084
5'-most EST	g4880900
Method	BLASTX
NCBI GI	g1800227
BLAST score	1110
E value	1.0e-121
Match length	209
% identity	58
NCBI Description	(U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No.	386177
Contig ID	1021_2.R1084
5'-most EST	LIB3433-022-P1-K1-A6
Method	BLASTX
NCBI GI	g1800227
BLAST score	825
E value	2.0e-88
Match length	137
% identity	54
NCBI Description	(U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No.	386178
Contig ID	1021_3.R1084
5'-most EST	LIB3433-015-Q6-K1-B6
Method	BLASTX
NCBI GI	g1800227
BLAST score	465
E value	2.0e-46
Match length	84
% identity	36
NCBI Description	(U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No.	386179
Contig ID	1021_5.R1084
5'-most EST	g569213
Method	BLASTX
NCBI GI	g1800227
BLAST score	225
E value	2.0e-18
Match length	70
% identity	29
NCBI Description	(U76004) Bowman-Birk proteinase inhibitor [Oryza sativa]

Seq. No.	386180
Contig ID	1023_1.R1084
5'-most EST	uC-osf1cyp011a03b1
Method	BLASTX
NCBI GI	g1698582
BLAST score	1676
E value	0.0e+00
Match length	383
% identity	88

NCBI Description	(U60767) integral membrane protein OsNramp3 [Oryza sativa]

Seq. No.	386181
Contig ID	1024_1.R1084
5'-most EST	g428188
Method	BLASTX
NCBI GI	g1488297
BLAST score	1528
E value	1.0e-170
Match length	392
% identity	79
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	386182
Contig ID	1025_1.R1084
5'-most EST	g1631746
Method	BLASTX
NCBI GI	g1565308
BLAST score	2469
E value	0.0e+00
Match length	514
% identity	92
NCBI Description	(U66041) ADP-glucose pyrophosphorylase large subunit [Oryza sativa]

Seq. No.	386183
Contig ID	1026_1.R1084
5'-most EST	g5851070
Method	BLASTX
NCBI GI	g1620753
BLAST score	389
E value	1.0e-37
Match length	81
% identity	86
NCBI Description	(U72942) proteinase inhibitor [Oryza sativa] >gi_2829212_gb_AAC00503_ (AF044059) proteinase inhibitor [Oryza sativa] >gi_6063551_dbj_BAA85411.1_ (AP000615) ESTs AU069800(E3445),AU078204(E11809) correspond to a region of the predicted gene.; similar to proteinase inhibitor. (AF044059) [Oryza sativa]

Seq. No.	386184
Contig ID	1027_1.R1084
5'-most EST	uC-osf1cyp179c05b1
Method	BLASTX
NCBI GI	g3914603
BLAST score	2240
E value	0.0e+00
Match length	433
% identity	99
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	386185
Contig ID	1027_2.R1084

5'-most EST	g4714744
Method	BLASTX
NCBI GI	g167097
BLAST score	372
E value	3.0e-39
Match length	103
% identity	73
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	386186
Contig ID	1027_3.R1084
5'-most EST	g4714671
Method	BLASTX
NCBI GI	g167097
BLAST score	244
E value	5.0e-33
Match length	85
% identity	85
NCBI Description	(M55449) ribulose 1,5-bisphosphate carboxylase activase [Hordeum vulgare]

Seq. No.	386187
Contig ID	1027_4.R1084
5'-most EST	g2800738
Method	BLASTX
NCBI GI	g132166
BLAST score	160
E value	1.0e-10
Match length	31
% identity	87
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_81660_pir__S04048 ribulose-bisphosphate carboxylase activase precursor - Arabidopsis thaliana >gi_16471_emb_CAA32429_ (X14212) rubisco activase (AA 1 - 473) [Arabidopsis thaliana]

Seq. No.	386188
Contig ID	1027_5.R1084
5'-most EST	LIB3432-015-P1-K1-H5
Method	BLASTX
NCBI GI	g3914603
BLAST score	374
E value	9.0e-36
Match length	162
% identity	52
NCBI Description	RIBULOSE BISPHOSPHATE CARBOXYLASE/OXYGENASE ACTIVASE, CHLOROPLAST PRECURSOR (RUBISCO ACTIVASE) >gi_1778414 (U74321) ribulose-1,5-bisphosphate carboxylase/oxygenase activase [Oryza sativa]

Seq. No.	386189
Contig ID	1029_1.R1084
5'-most EST	LIB3434-019-P1-K1-D10
Method	BLASTX
NCBI GI	g2058496

BLAST score	849
E value	3.0e-91
Match length	169
% identity	99
NCBI Description	(U76028) hemoglobin 2 [Oryza sativa] >gi_2058502 (U76031) hemoglobin 2 [Oryza sativa]

Seq. No.	386190
Contig ID	1029_2.R1084
5'-most EST	LIB3475-012-P1-K1-C4
Method	BLASTX
NCBI GI	g2058498
BLAST score	834
E value	2.0e-89
Match length	166
% identity	100
NCBI Description	(U76029) hemoglobin 1 [Oryza sativa] >gi_2058500 (U76030) hemoglobin 1 [Oryza sativa]

Seq. No.	386191
Contig ID	1029_3.R1084
5'-most EST	g2312849
Method	BLASTX
NCBI GI	g2058496
BLAST score	173
E value	1.0e-28
Match length	82
% identity	96
NCBI Description	(U76028) hemoglobin 2 [Oryza sativa] >gi_2058502 (U76031) hemoglobin 2 [Oryza sativa]

Seq. No.	386192
Contig ID	1031_1.R1084
5'-most EST	g2062388
Method	BLASTX
NCBI GI	g2062389
BLAST score	1212
E value	1.0e-133
Match length	238
% identity	91
NCBI Description	(U77657) pathogenesis-related thaumatin-like protein [Oryza sativa]

Seq. No.	386193
Contig ID	1031_2.R1084
5'-most EST	LIB3432-048-P2-K1-B3
Method	BLASTX
NCBI GI	g2062387
BLAST score	1025
E value	1.0e-112
Match length	181
% identity	99
NCBI Description	(U77656) pathogenesis-related thaumatin-like protein [Oryza sativa]

Seq. No.	386194
Contig ID	1033_2.R1084

5'-most EST	uC-osflcyp122e09b1
Method	BLASTX
NCBI GI	g2286109
BLAST score	1284
E value	1.0e-142
Match length	250
% identity	100
NCBI Description	(U78782) MADS box protein [Oryza sativa]

Seq. No.	386195
Contig ID	1037_1.R1084
5'-most EST	g1778820
Method	BLASTX
NCBI GI	g3024122
BLAST score	1987
E value	0.0e+00
Match length	394
% identity	97
NCBI Description	S-ADENOSYLMETHIONINE SYNTHETASE 2 (METHIONINE ADENOSYLTRANSFERASE 2) (ADOMET SYNTHETASE 2) >gi_1778821 (U82833) S-adenosyl-L-methionine synthetase [Oryza sativa]

Seq. No.	386196
Contig ID	1037_2.R1084
5'-most EST	g3767130
Method	BLASTN
NCBI GI	g1778820
BLAST score	196
E value	1.0e-106
Match length	349
% identity	96
NCBI Description	Oryza sativa S-adenosyl-L-methionine synthetase (pOS-SAMS2) mRNA, complete cds

Seq. No.	386197
Contig ID	1042_1.R1084
5'-most EST	LIB3431-027-P1-K1-F6
Method	BLASTX
NCBI GI	g1835731
BLAST score	594
E value	3.0e-61
Match length	126
% identity	91
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	386198
Contig ID	1042_2.R1084
5'-most EST	LIB3431-041-P2-K1-B10
Method	BLASTX
NCBI GI	g3402817
BLAST score	241
E value	5.0e-20
Match length	65
% identity	72
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No. 386199

Contig ID	1042_3.R1084
5'-most EST	LIB3431-021-P1-K1-E10
Method	BLASTX
NCBI GI	g1835731
BLAST score	542
E value	2.0e-55
Match length	106
% identity	98
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	386200
Contig ID	1042_4.R1084
5'-most EST	LIB3432-015-P1-K1-H4
Method	BLASTX
NCBI GI	g1835731
BLAST score	588
E value	1.0e-60
Match length	126
% identity	90
NCBI Description	(U86018) photosystem II 10 kDa polypeptide [Oryza sativa]

Seq. No.	386201
Contig ID	1043_1.R1084
5'-most EST	g568726
Method	BLASTX
NCBI GI	g2286121
BLAST score	1292
E value	1.0e-143
Match length	247
% identity	99
NCBI Description	(U88068) sec14 like protein [Oryza sativa]

Seq. No.	386202
Contig ID	1044_1.R1084
5'-most EST	g426287
Method	BLASTX
NCBI GI	g3024432
BLAST score	1154
E value	1.0e-127
Match length	228
% identity	100
NCBI Description	PROTEASOME ALPHA SUBUNIT (MULTICATALYTIC ENDOPEPTIDASE COMPLEX ALPHA SUBUNIT) >gi_1930070 (U92540) proteasome alpha subunit [Oryza sativa]

Seq. No.	386203
Contig ID	1046_1.R1084
5'-most EST	g2920836
Method	BLASTX
NCBI GI	g2920837
BLAST score	832
E value	4.0e-89
Match length	159
% identity	100
NCBI Description	(U95135) Os-FIERG1 gene product [Oryza sativa]

Seq. No.	386204

Contig ID	1048_1.R1084
5'-most EST	LIB3477-011-P1-K1-G5
Method	BLASTX
NCBI GI	g3264767
BLAST score	250
E value	3.0e-37
Match length	232
% identity	44
NCBI Description	(AF071893) AP2 domain containing protein [Prunus armeniaca]

Seq. No.	386205
Contig ID	1050_1.R1084
5'-most EST	g2224914
Method	BLASTX
NCBI GI	g2224915
BLAST score	1415
E value	1.0e-157
Match length	261
% identity	100
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	386206
Contig ID	1050_2.R1084
5'-most EST	uC-osflcyp168b10b1
Method	BLASTX
NCBI GI	g2224915
BLAST score	624
E value	1.0e-96
Match length	236
% identity	69
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	386207
Contig ID	1050_3.R1084
5'-most EST	g2798242
Method	BLASTX
NCBI GI	g2224915
BLAST score	578
E value	3.0e-60
Match length	173
% identity	68
NCBI Description	(U95968) beta-expansin [Oryza sativa]

Seq. No.	386208
Contig ID	1050_6.R1084
5'-most EST	g569116
Method	BLASTN
NCBI GI	g2224914
BLAST score	73
E value	1.0e-32
Match length	116
% identity	92
NCBI Description	Oryza sativa beta-expansin mRNA, complete cds

Seq. No.	386209
Contig ID	1052_1.R1084
5'-most EST	g2231131

Method	BLASTX
NCBI GI	g2130080
BLAST score	2443
E value	0.0e+00
Match length	517
% identity	94
NCBI Description	Nramp1 protein - rice >gi_1470320_bbs_177441 (S81897) OsNramp1=Nramp1 homolog/Bcg product homolog [Oryza sativa, indica, cv. IR 36, etiolated shoots, Peptide, 517 aa] [Oryza sativa] >gi_2231132 (L41217) integral membrane protein [Oryza sativa]

Seq. No.	386210
Contig ID	1053_1.R1084
5'-most EST	g426341
Method	BLASTX
NCBI GI	g886401
BLAST score	1055
E value	1.0e-115
Match length	205
% identity	100
NCBI Description	(L37526) MADS box protein [Oryza sativa]

Seq. No.	386211
Contig ID	1054_1.R1084
5'-most EST	g2961436
Method	BLASTX
NCBI GI	g2961437
BLAST score	1090
E value	1.0e-119
Match length	210
% identity	100
NCBI Description	(L37527) MADS box protein [Oryza sativa]

Seq. No.	386212
Contig ID	1059_1.R1084
5'-most EST	g6525064
Method	BLASTX
NCBI GI	g2494261
BLAST score	1726
E value	0.0e+00
Match length	411
% identity	80
NCBI Description	ELONGATION FACTOR TU, CHLOROPLAST PRECURSOR (EF-TU) >gi_99903_pir__S21567 translation elongation factor Tu precursor - soybean chloroplast >gi_18776_emb_CAA46864_ (X66062) EF-Tu [Glycine max] >gi_448921_prf__1918220A elongation factor Tu [Glycine max]

Seq. No.	386213
Contig ID	1061_1.R1084
5'-most EST	g5006850
Method	BLASTX
NCBI GI	g5006851
BLAST score	891
E value	6.0e-96
Match length	197

% identity	90
NCBI Description	(AF145727) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	386214
Contig ID	1062_1.R1084
5'-most EST	g700117
Method	BLASTX
NCBI GI	g5006853
BLAST score	966
E value	1.0e-104
Match length	277
% identity	69
NCBI Description	(AF145728) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	386215
Contig ID	1063_1.R1084
5'-most EST	uC-osrocyp029b09b1
Method	BLASTX
NCBI GI	g5006855
BLAST score	1121
E value	1.0e-122
Match length	350
% identity	65
NCBI Description	(AF145729) homeodomain leucine zipper protein [Oryza sativa]

Seq. No.	386216
Contig ID	1066_1.R1084
5'-most EST	g700154
Method	BLASTX
NCBI GI	g3168840
BLAST score	290
E value	9.0e-26
Match length	66
% identity	83
NCBI Description	(U88711) copper homeostasis factor [Arabidopsis thaliana]

Seq. No.	386217
Contig ID	1068_1.R1084
5'-most EST	LIB3432-026-P1-K1-E1
Method	BLASTX
NCBI GI	g5596472
BLAST score	1036
E value	1.0e-113
Match length	360
% identity	59
NCBI Description	(AL096882) putative protein [Arabidopsis thaliana]

Seq. No.	386218
Contig ID	1069_1.R1084
5'-most EST	g6682926
Method	BLASTX
NCBI GI	g3342556
BLAST score	2099
E value	0.0e+00

Match length	533
% identity	77
NCBI Description	(AF077528) importin alpha [Arabidopsis thaliana]

Seq. No.	386219
Contig ID	1070_1.R1084
5'-most EST	LIB3431-012-P1-K1-A1
Method	BLASTX
NCBI GI	g2497486
BLAST score	803
E value	1.0e-85
Match length	189
% identity	84
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]

Seq. No.	386220
Contig ID	1072_1.R1084
5'-most EST	g6689915
Method	BLASTX
NCBI GI	g4322940
BLAST score	774
E value	5.0e-82
Match length	337
% identity	35
NCBI Description	(AF096299) DNA-binding protein 2 [Nicotiana tabacum]

Seq. No.	386221
Contig ID	1074_1.R1084
5'-most EST	LIB3474-007-P1-K1-B3
Method	BLASTX
NCBI GI	g1076791
BLAST score	1679
E value	0.0e+00
Match length	333
% identity	91
NCBI Description	calcium-binding protein - maize >gi_2119370_pir__S58170 Calreticulin precursor - maize >gi_577612_emb_CAA86728_ (Z46772) calcium-binding protein [Zea mays] >gi_927572_emb_CAA61939_ (X89813) Calreticulin precursor [Zea mays] >gi_1587033_prf__2205314A calreticulin [Zea mays]

Seq. No.	386222
Contig ID	1074_2.R1084
5'-most EST	LIB3432-019-P1-K1-A2
Method	BLASTX
NCBI GI	g6014707
BLAST score	151
E value	1.0e-09
Match length	26
% identity	100
NCBI Description	(AF190454) calreticulin [Zea mays]

Seq. No.	386223
Contig ID	1076_1.R1084

5'-most EST	g3760486
Method	BLASTX
NCBI GI	g4455800
BLAST score	400
E value	2.0e-38
Match length	145
% identity	54
NCBI Description	(Z97343) TEGT protein homolog [Arabidopsis thaliana]

Seq. No.	386224
Contig ID	1076_3.R1084
5'-most EST	g5701681

Seq. No.	386225
Contig ID	1077_1.R1084
5'-most EST	uC-osflcyp029g06b1
Method	BLASTX
NCBI GI	g2708745
BLAST score	2003
E value	0.0e+00
Match length	466
% identity	82
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	386226
Contig ID	1078_1.R1084
5'-most EST	g6689921
Method	BLASTX
NCBI GI	g2708745
BLAST score	2021
E value	0.0e+00
Match length	466
% identity	82
NCBI Description	(AC003952) putative calcium-dependent ser/thr protein kinase [Arabidopsis thaliana]

Seq. No.	386227
Contig ID	1081_1.R1084
5'-most EST	LIB3479-008-Q6-K1-H9
Method	BLASTX
NCBI GI	g3929545
BLAST score	1616
E value	1.0e-180
Match length	386
% identity	82
NCBI Description	(AF067194) S-adenosylmethionine decarboxylase [Oryza sativa]

Seq. No.	386228
Contig ID	1082_1.R1084
5'-most EST	LIB3434-049-P1-K1-B1
Method	BLASTX
NCBI GI	g4959465
BLAST score	912
E value	1.0e-98
Match length	196

% identity	91
NCBI Description	(AF126055) RACD small GTP binding protein [Zea mays]

Seq. No.	386229
Contig ID	1084_1.R1084
5'-most EST	g6606069
Method	BLASTX
NCBI GI	g4204232
BLAST score	781
E value	6.0e-83
Match length	240
% identity	68
NCBI Description	(AF035378) MADS-box protein 1 [Lolium temulentum]

Seq. No.	386230
Contig ID	1086_1.R1084
5'-most EST	g3762809
Method	BLASTX
NCBI GI	g2245101
BLAST score	325
E value	2.0e-40
Match length	204
% identity	52
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386231
Contig ID	1088_1.R1084
5'-most EST	LIB3431-021-P1-K1-A11
Method	BLASTX
NCBI GI	g730463
BLAST score	301
E value	5.0e-27
Match length	102
% identity	56
NCBI Description	60S RIBOSOMAL PROTEIN L33-B (L37B) (YL37) (RP47) >gi_630323_pir__S44069 ribosomal protein L35a.e.c15 - yeast (Saccharomyces cerevisiae) >gi_484241 (L23923) ribosomal protein L37 [Saccharomyces cerevisiae] >gi_1420537_emb_CAA99454_ (Z75142) ORF YOR234c [Saccharomyces cerevisiae]

Seq. No.	386232
Contig ID	1088_2.R1084
5'-most EST	uC-osrocyp010c09a1
Method	BLASTX
NCBI GI	g1350742
BLAST score	310
E value	5.0e-28
Match length	102
% identity	58
NCBI Description	PROBABLE 60S RIBOSOMAL PROTEIN L35A >gi_1086831 (U41264) coded for by C. elegans cDNA yk64g10.5; coded for by C. elegans cDNA yk51f3.5; coded for by C. elegans cDNA yk115e7.3; coded for by C. elegans cDNA yk99d1.3; coded for by C. elegans cDNA yk99d1.5; coded for by C. elegans cDNA yk64g1

Seq. No.	386233
Contig ID	1090_1.R1084
5'-most EST	LIB3431-021-P1-N1-A9
Method	BLASTX
NCBI GI	g6016678
BLAST score	186
E value	1.0e-13
Match length	47
% identity	66
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	386234
Contig ID	1093_1.R1084
5'-most EST	LIB3431-043-P1-N1-D6

Seq. No.	386235
Contig ID	1094_1.R1084
5'-most EST	LIB3432-039-P1-K1-C12
Method	BLASTX
NCBI GI	g4455169
BLAST score	936
E value	1.0e-101
Match length	360
% identity	51
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	386236
Contig ID	1094_2.R1084
5'-most EST	LIB3431-021-P1-K1-A7
Method	BLASTX
NCBI GI	g4455169
BLAST score	193
E value	1.0e-14
Match length	71
% identity	48
NCBI Description	(AL035521) putative aldehyde dehydrogenase [Arabidopsis thaliana]

Seq. No.	386237
Contig ID	1095_1.R1084
5'-most EST	uC-osroM202011b01a1
Method	BLASTX
NCBI GI	g1632831
BLAST score	610
E value	4.0e-63
Match length	142
% identity	82
NCBI Description	(Z49698) orf [Ricinus communis]

Seq. No.	386238
Contig ID	1101_1.R1084
5'-most EST	LIB3431-021-P1-N1-B2
Method	BLASTX
NCBI GI	g464986
BLAST score	765
E value	2.0e-81

Match length	147
% identity	95
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 9 (UBIQUITIN-PROTEIN LIGASE 9) (UBIQUITIN CARRIER PROTEIN 9) (UBCAT4B) >gi_421857_pir__S32674 ubiquitin--protein ligase (EC 6.3.2.19) UBC9 - Arabidopsis thaliana >gi_297884_emb_CAA78714_ (Z14990) ubiquitin conjugating enzyme homolog [Arabidopsis thaliana] >gi_349211 (L00639) ubiquitin conjugating enzyme [Arabidopsis thaliana] >gi_600391_emb_CAA51201_ (X72626) ubiquitin conjugating enzyme E2 [Arabidopsis thaliana] >gi_4455355_emb_CAB36765.1_ (AL035524) ubiquitin-protein ligase UBC9 [Arabidopsis thaliana]

Seq. No.	386239
Contig ID	1103_1.R1084
5'-most EST	LIB3431-041-P1-N1-C1
Method	BLASTX
NCBI GI	g131225
BLAST score	881
E value	7.0e-95
Match length	208
% identity	83
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	386240
Contig ID	1103_4.R1084
5'-most EST	LIB3431-013-P1-K1-C5
Method	BLASTX
NCBI GI	g131225
BLAST score	509
E value	1.0e-51
Match length	110
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT XI PRECURSOR (SUBUNIT V) (PSI-L) >gi_100605_pir__A39759 photosystem I 18K protein precursor - barley >gi_167087 (M61146) photosystem I hydrophobic protein [Hordeum vulgare]

Seq. No.	386241
Contig ID	1109_1.R1084
5'-most EST	g3767989
Method	BLASTX
NCBI GI	g1077413
BLAST score	321
E value	2.0e-34
Match length	158
% identity	48
NCBI Description	hypothetical protein YLR186w - yeast (Saccharomyces cerevisiae) >gi_577197 (U17246) Ylr186wp [Saccharomyces cerevisiae]

Seq. No.	386242
Contig ID	1116_1.R1084

5'-most EST	LIB3431-060-P1-N1-C3
Seq. No.	386243
Contig ID	1116_2.R1084
5'-most EST	LIB3431-021-P1-K1-C7
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	9.0e-12
Match length	39
% identity	61
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	386244
Contig ID	1118_1.R1084
5'-most EST	LIB3431-021-P1-N1-C9
Method	BLASTX
NCBI GI	g2239089
BLAST score	469
E value	2.0e-46
Match length	258
% identity	41
NCBI Description	(Z84386) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus] >gi_3288180_emb_CAB11466_ (Z98758) anthranilate N-hydroxycinnamoyl/benzoyltransferase [Dianthus caryophyllus]
Seq. No.	386245
Contig ID	1123_1.R1084
5'-most EST	g2800147
Method	BLASTX
NCBI GI	g125580
BLAST score	1944
E value	0.0e+00
Match length	403
% identity	93
NCBI Description	PHOSPHORIBULOKINASE PRECURSOR (PHOSPHOPENTOKINASE) (PRKASE) (PRK) >gi_100839_pir__S15743 phosphoribulokinase (EC 2.7.1.19) - wheat >gi_5924030_emb_CAB56544.1_ (X51608) phosphoribulokinase [Triticum aestivum]
Seq. No.	386246
Contig ID	1124_1.R1084
5'-most EST	g5667204
Method	BLASTX
NCBI GI	g4160402
BLAST score	963
E value	1.0e-104
Match length	363
% identity	58
NCBI Description	(AJ132240) eukaryotic translation initiation factor 5 [Zea mays]
Seq. No.	386247
Contig ID	1124_2.R1084
5'-most EST	uC-osflcyp003f09b1
Method	BLASTX

NCBI GI	g2494320
BLAST score	282
E value	9.0e-25
Match length	66
% identity	79
NCBI Description	EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) >gi_1806575_emb_CAA67868_ (X99517) Eukaryotic initiation factor-5 [Zea mays]

Seq. No.	386248
Contig ID	1128_1.R1084
5'-most EST	g4716857
Method	BLASTX
NCBI GI	g1707998
BLAST score	2206
E value	0.0e+00
Match length	488
% identity	88
NCBI Description	SERINE HYDROXYMETHYLTRANSFERASE, MITOCHONDRIAL PRECURSOR (SERINE METHYLASE) (GLYCINE HYDROXYMETHYLTRANSFERASE) (SHMT) >gi_481944_pir__S40218 glycine hydroxymethyltransferase (EC 2.1.2.1) - potato >gi_438247_emb_CAA81082_ (Z25863) glycine hydroxymethyltransferase [Solanum tuberosum]

Seq. No.	386249
Contig ID	1131_1.R1084
5'-most EST	uC-osflcyp058a01b1
Method	BLASTX
NCBI GI	g129915
BLAST score	1623
E value	0.0e+00
Match length	348
% identity	93
NCBI Description	PHOSPHOGLYCERATE KINASE, CHLOROPLAST PRECURSOR >gi_66912_pir__TVWTGC phosphoglycerate kinase (EC 2.7.2.3) precursor, chloroplast - wheat >gi_21833_emb_CAA33303_ (X15233) phosphoglycerate kinase (AA 1 - 480) [Triticum aestivum] >gi_3293043_emb_CAA51931_ (X73528) phosphoglycerate kinase [Triticum aestivum]

Seq. No.	386250
Contig ID	1131_2.R1084
5'-most EST	uC-osflcyp058b01b1
Method	BLASTX
NCBI GI	g2275202
BLAST score	427
E value	2.0e-43
Match length	135
% identity	59
NCBI Description	(AC002337) acyl-CoA synthetase isolog [Arabidopsis thaliana]

Seq. No.	386251
Contig ID	1134_1.R1084
5'-most EST	LIB3431-046-P1-N1-F12

Seq. No.	386252
Contig ID	1135_1.R1084
5'-most EST	LIB3431-021-P1-N1-E6

Seq. No.	386253
Contig ID	1140_1.R1084
5'-most EST	LIB3431-021-P1-N1-F12
Method	BLASTX
NCBI GI	g1495768
BLAST score	382
E value	2.0e-36
Match length	137
% identity	60
NCBI Description	(Z68506) chloroplast inner envelope protein, 110 kD (IEP110) [Pisum sativum]

Seq. No.	386254
Contig ID	1142_1.R1084
5'-most EST	LIB3431-058-P1-N1-C8
Method	BLASTX
NCBI GI	g2688822
BLAST score	284
E value	4.0e-25
Match length	98
% identity	63
NCBI Description	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]

Seq. No.	386255
Contig ID	1143_1.R1084
5'-most EST	LIB3431-021-P1-N1-F5

Seq. No.	386256
Contig ID	1147_1.R1084
5'-most EST	LIB3431-062-P1-N1-H1
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	5.0e-11
Match length	48
% identity	66
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386257
Contig ID	1147_2.R1084
5'-most EST	LIB3431-058-P1-N1-H7

Seq. No.	386258
Contig ID	1156_1.R1084
5'-most EST	LIB3432-022-P1-K1-E6
Method	BLASTX
NCBI GI	g4581114
BLAST score	416
E value	1.0e-43
Match length	109
% identity	79
NCBI Description	(AC005825) putative HesB-like protein;required for

efficient nitrogen fixation in Cyanobacteria [Arabidopsis thaliana]

Seq. No.	386259
Contig ID	1156_2.R1084
5'-most EST	LIB3431-021-P1-N1-G6
Method	BLASTX
NCBI GI	g1698548
BLAST score	590
E value	1.0e-60
Match length	283
% identity	46
NCBI Description	(U58971) calmodulin-binding protein [Nicotiana tabacum]

Seq. No.	386260
Contig ID	1158_1.R1084
5'-most EST	g568628

Seq. No.	386261
Contig ID	1162_1.R1084
5'-most EST	uC-osflcyp078d03a1
Method	BLASTX
NCBI GI	g2501190
BLAST score	658
E value	9.0e-69
Match length	151
% identity	86
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-2 PRECURSOR >gi_2130147_pir__S61420 thiamine biosynthetic enzyme thi1-2 - maize >gi_596080 (U17351) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	386262
Contig ID	1162_2.R1084
5'-most EST	LIB3431-037-P1-N1-G2
Method	BLASTX
NCBI GI	g2501189
BLAST score	1189
E value	1.0e-131
Match length	308
% identity	80
NCBI Description	THIAMINE BIOSYNTHETIC ENZYME 1-1 PRECURSOR >gi_2130146_pir__S61419 thiamine biosynthetic enzyme thi1-1 - maize >gi_596078 (U17350) thiamine biosynthetic enzyme [Zea mays]

Seq. No.	386263
Contig ID	1164_1.R1084
5'-most EST	LIB3431-030-P1-N1-C11
Method	BLASTX
NCBI GI	g131176
BLAST score	304
E value	2.0e-27
Match length	59
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E)

	>gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	386264
Contig ID	1164_2.R1084
5'-most EST	LIB3432-040-P1-K1-B7
Method	BLASTX
NCBI GI	g131176
BLAST score	304
E value	2.0e-27
Match length	59
% identity	98
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	386265
Contig ID	1164_3.R1084
5'-most EST	LIB3432-025-P1-K1-H1
Method	BLASTX
NCBI GI	g131176
BLAST score	285
E value	2.0e-25
Match length	77
% identity	75
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]
Seq. No.	386266
Contig ID	1164_4.R1084
5'-most EST	LIB3432-048-P2-K1-B10
Method	BLASTX
NCBI GI	g131176
BLAST score	367
E value	5.0e-35
Match length	77
% identity	91
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	386267
Contig ID	1164_5.R1084
5'-most EST	LIB3431-007-P1-N1-B2
Method	BLASTX
NCBI GI	g131176
BLAST score	240
E value	9.0e-21
Match length	62
% identity	89
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV PRECURSOR (PHOTOSYSTEM I 10.8 KD POLYPEPTIDE) (PSI-E) >gi_72683_pir__F1BH4 photosystem I chain IV precursor - barley >gi_19087_emb_CAA68782_ (Y00966) psa2 preprotein (AA -46 to 101) [Hordeum vulgare] >gi_226163_prf__1413233A 10.8kD photosystem I protein [Hordeum vulgare var. distichum]

Seq. No.	386268
Contig ID	1170_1.R1084
5'-most EST	g2800768
Method	BLASTX
NCBI GI	g439879
BLAST score	295
E value	3.0e-26
Match length	124
% identity	52
NCBI Description	(L15194) [Golden delicious apple fruit expressed mRNA, complete cds.], gene product [Malus domestica]

Seq. No.	386269
Contig ID	1170_2.R1084
5'-most EST	uC-osflcyp112h05b1

Seq. No.	386270
Contig ID	1170_3.R1084
5'-most EST	LIB3434-058-P1-K1-F8
Method	BLASTX
NCBI GI	g2244792
BLAST score	176
E value	1.0e-12
Match length	57
% identity	54
NCBI Description	(Z97336) ankyrin like protein [Arabidopsis thaliana]

Seq. No.	386271
Contig ID	1170_4.R1084
5'-most EST	uC-osflcyp037c10b1
Method	BLASTX
NCBI GI	g4337175
BLAST score	277
E value	3.0e-24
Match length	150
% identity	43
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	386272
Contig ID	1170_6.R1084
5'-most EST	uC-osflcyp122h06b1
Method	BLASTX
NCBI GI	g2995990
BLAST score	293
E value	3.0e-26
Match length	125
% identity	49
NCBI Description	(AF053746) dormancy-associated protein [Arabidopsis thaliana] >gi_2995992 (AF053747) dormancy-associated protein [Arabidopsis thaliana]

Seq. No.	386273
Contig ID	1171_1.R1084
5'-most EST	uC-osrocyp014f07a1
Method	BLASTX
NCBI GI	g3212865
BLAST score	1304
E value	1.0e-146
Match length	377
% identity	70
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	386274
Contig ID	1173_1.R1084
5'-most EST	LIB3431-022-P1-N1-A3
Method	BLASTX
NCBI GI	g5640111
BLAST score	477
E value	2.0e-47
Match length	127
% identity	76
NCBI Description	(AJ243875) RAD23 protein [Lycopersicon esculentum]

Seq. No.	386275
Contig ID	1173_2.R1084
5'-most EST	g2431315
Method	BLASTX
NCBI GI	g5640111
BLAST score	258
E value	7.0e-37
Match length	145
% identity	68
NCBI Description	(AJ243875) RAD23 protein [Lycopersicon esculentum]

Seq. No.	386276
Contig ID	1176_1.R1084
5'-most EST	LIB3432-045-P1-K1-F8
Method	BLASTX
NCBI GI	g1173347
BLAST score	1878
E value	0.0e+00
Match length	382
% identity	94
NCBI Description	SEDOHEPTULOSE-1,7-BISPHOSPHATASE, CHLOROPLAST PRECURSOR

	(SEDOHEPTULOSE-BISPHOSPHATASE) (SBPASE) (SED(1,7)P2ASE) >gi_100803_pir__S23452 sedoheptulose-bisphosphatase (EC 3.1.3.37) precursor - wheat >gi_14265_emb_CAA46507_ (X65540) sedoheptulose-1,7-bisphosphatase [Triticum aestivum]
Seq. No.	386277
Contig ID	1176_2.R1084
5'-most EST	LIB3431-010-P1-N1-F9
Method	BLASTX
NCBI GI	g687677
BLAST score	312
E value	4.0e-28
Match length	111
% identity	57
NCBI Description	(U19925) unknown [Arabidopsis thaliana]
Seq. No.	386278
Contig ID	1176_3.R1084
5'-most EST	LIB3431-003-P1-N1-C12
Method	BLASTX
NCBI GI	g2982453
BLAST score	1439
E value	1.0e-163
Match length	352
% identity	84
NCBI Description	(AL022223) fructose-bisphosphate aldolase-like protein [Arabidopsis thaliana]
Seq. No.	386279
Contig ID	1179_1.R1084
5'-most EST	LIB3599-002-P1-N6-D8
Method	BLASTX
NCBI GI	g2245086
BLAST score	1100
E value	1.0e-120
Match length	294
% identity	71
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]
Seq. No.	386280
Contig ID	1182_1.R1084
5'-most EST	uC-osflcyp083h03a1
Seq. No.	386281
Contig ID	1186_1.R1084
5'-most EST	uC-osrocyp002h09a1
Seq. No.	386282
Contig ID	1190_1.R1084
5'-most EST	uC-osrocyp003a03a1
Method	BLASTX
NCBI GI	g2984709
BLAST score	1852
E value	0.0e+00
Match length	417
% identity	86

NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.	386283
Contig ID	1190_2.R1084
5'-most EST	LIB3431-022-P1-N1-B9
Method	BLASTX
NCBI GI	g1125691
BLAST score	1283
E value	0.0e+00
Match length	407
% identity	77
NCBI Description	(X94301) DnaJ protein [Solanum tuberosum]

Seq. No.	386284
Contig ID	1190_3.R1084
5'-most EST	uC-osroM202038f08b1
Method	BLASTX
NCBI GI	g2984709
BLAST score	437
E value	4.0e-43
Match length	93
% identity	89
NCBI Description	(AF053468) DnaJ-related protein ZMDJ1 [Zea mays]

Seq. No.	386285
Contig ID	1191_1.R1084
5'-most EST	LIB3431-022-P1-N1-C1
Method	BLASTX
NCBI GI	g4929312
BLAST score	682
E value	1.0e-71
Match length	192
% identity	73
NCBI Description	(AF145045) TATC [Arabidopsis thaliana]

Seq. No.	386286
Contig ID	1193_1.R1084
5'-most EST	LIB3431-026-P1-N1-F9
Method	BLASTX
NCBI GI	g6093830
BLAST score	210
E value	3.0e-16
Match length	98
% identity	32
NCBI Description	PHOTOSYSTEM II CORE COMPLEX PROTEINS PSBY PRECURSOR (L-AME) [CONTAINS: PHOTOSYSTEM II PROTEIN PSBY-1; KD PHOTOSYSTEM II PROTEIN PSBY-2] >gi_3337435 (AF060198) PsbY precursor; putative photosytem II peptide [Spinacia oleracea]

Seq. No.	386287
Contig ID	1197_1.R1084
5'-most EST	g5003354

Seq. No.	386288
Contig ID	1201_1.R1084
5'-most EST	LIB3431-022-P1-N1-C8
Method	BLASTX

NCBI GI	g4512613
BLAST score	391
E value	1.0e-37
Match length	86
% identity	81
NCBI Description	(AC004793) F28K20.12 [Arabidopsis thaliana]

Seq. No.	386289
Contig ID	1203_1.R1084
5'-most EST	LIB3431-022-P1-N1-D1
Method	BLASTX
NCBI GI	g4371296
BLAST score	788
E value	1.0e-117
Match length	355
% identity	64
NCBI Description	(AC006260) putative receptor protein kinase [Arabidopsis thaliana]

Seq. No.	386290
Contig ID	1204_1.R1084
5'-most EST	LIB3431-008-P1-N1-B9
Method	BLASTX
NCBI GI	g461595
BLAST score	372
E value	4.0e-35
Match length	145
% identity	53
NCBI Description	ATP SYNTHASE B' CHAIN PRECURSOR (SUBUNIT II) >gi_479533_pir__S34473 H+-transporting ATP synthase (EC 3.6.1.34) chain 9 - spinach >gi_394755_emb_CAA50520_ (X71397) CF(o)II ATP synthase subunit 9 [Spinacia oleracea]

Seq. No.	386291
Contig ID	1206_1.R1084
5'-most EST	g4715945

Seq. No.	386292
Contig ID	1206_2.R1084
5'-most EST	g2798986
Method	BLASTX
NCBI GI	g517500
BLAST score	592
E value	6.0e-61
Match length	217
% identity	59
NCBI Description	(M87435) precursor of the oxygen evolving complex 17 kDa protein [Zea mays] >gi_444338_prf__1906386A photosystem II OE17 protein [Pisum sativum]

Seq. No.	386293
Contig ID	1206_5.R1084
5'-most EST	g4969335

Seq. No.	386294
Contig ID	1206_8.R1084
5'-most EST	LIB3431-055-P1-N1-C7

Method	BLASTN
NCBI GI	g5714761
BLAST score	54
E value	3.0e-21
Match length	78
% identity	92
NCBI Description	Oryza sativa subsp. indica serine/threonine protein phosphatase PP2A-4 catalytic subunit (PP2A) gene, complete cds

Seq. No.	386295
Contig ID	1207_1.R1084
5'-most EST	LIB3431-050-P1-N1-E3

Seq. No.	386296
Contig ID	1209_1.R1084
5'-most EST	g2800198
Method	BLASTX
NCBI GI	g4099148
BLAST score	785
E value	1.0e-83
Match length	197
% identity	81
NCBI Description	(U84268) YLP [Hordeum vulgare]

Seq. No.	386297
Contig ID	1209_2.R1084
5'-most EST	g3767729
Method	BLASTX
NCBI GI	g4099148
BLAST score	575
E value	5.0e-59
Match length	130
% identity	85
NCBI Description	(U84268) YLP [Hordeum vulgare]

Seq. No.	386298
Contig ID	1210_1.R1084
5'-most EST	uC-osflcyp085e03a1

Seq. No.	386299
Contig ID	1211_1.R1084
5'-most EST	g426186
Method	BLASTX
NCBI GI	g5106775
BLAST score	619
E value	3.0e-64
Match length	123
% identity	96
NCBI Description	(AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No.	386300
Contig ID	1211_2.R1084
5'-most EST	g425821
Method	BLASTX
NCBI GI	g5106775
BLAST score	646

E value	2.0e-67
Match length	137
% identity	93
NCBI Description	(AF067732) ribosomal protein S12 [Hordeum vulgare]

Seq. No.	386301
Contig ID	1214_1.R1084
5'-most EST	LIB3431-003-P1-N1-A2
Method	BLASTX
NCBI GI	g4469021
BLAST score	654
E value	3.0e-68
Match length	182
% identity	70
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386302
Contig ID	1214_2.R1084
5'-most EST	LIB3431-013-P1-K1-G9
Method	BLASTX
NCBI GI	g4469021
BLAST score	245
E value	1.0e-20
Match length	72
% identity	69
NCBI Description	(AL035602) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386303
Contig ID	1217_1.R1084
5'-most EST	jC-osleLIB3474037a05a1
Method	BLASTX
NCBI GI	g81601
BLAST score	183
E value	4.0e-13
Match length	66
% identity	55
NCBI Description	chaperonin 60 beta - Arabidopsis thaliana

Seq. No.	386304
Contig ID	1224_1.R1084
5'-most EST	g4715073
Method	BLASTX
NCBI GI	g2493494
BLAST score	547
E value	7.0e-56
Match length	112
% identity	89
NCBI Description	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) >gi_619351_bbs_153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa] >gi_6102957_emb_CAB59202.1_ (X78878) serine carboxylase II-2 [Hordeum vulgare]

Seq. No.	386305
Contig ID	1231_1.R1084
5'-most EST	LIB3431-022-P1-N1-G1

Seq. No.	386306
Contig ID	1232_1.R1084
5'-most EST	g2427695
Method	BLASTX
NCBI GI	g3928150
BLAST score	766
E value	1.0e-124
Match length	283
% identity	81
NCBI Description	(AJ131049) hypothetical protein [Cicer arietinum]

Seq. No.	386307
Contig ID	1233_1.R1084
5'-most EST	LIB3433-055-P1-K1-D3
Method	BLASTX
NCBI GI	g3879145
BLAST score	194
E value	5.0e-14
Match length	267
% identity	33
NCBI Description	(Z93386) predicted using Genefinder; Similarity to Human placenta (DIFF33) protein (TR:Q13530); cDNA EST yk198a11.5 comes from this gene [Caenorhabditis elegans]

Seq. No.	386308
Contig ID	1235_1.R1084
5'-most EST	g4715618

Seq. No.	386309
Contig ID	1237_1.R1084
5'-most EST	g3767484
Method	BLASTX
NCBI GI	g629774
BLAST score	547
E value	1.0e-55
Match length	140
% identity	74
NCBI Description	beta-ketoacyl-ACP synthase - barley >gi_498742_emb_CAA84023_ (Z34269) beta-ketoacyl-ACP synthase [Hordeum vulgare]

Seq. No.	386310
Contig ID	1239_1.R1084
5'-most EST	LIB3431-022-P1-N1-G7

Seq. No.	386311
Contig ID	1240_1.R1084
5'-most EST	g2431354

Seq. No.	386312
Contig ID	1242_1.R1084
5'-most EST	LIB3431-022-P1-N1-H10

Seq. No.	386313
Contig ID	1243_1.R1084
5'-most EST	uC-osf1cyp017h09b2
Method	BLASTX

NCBI GI	g1737492
BLAST score	1084
E value	1.0e-118
Match length	389
% identity	34
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	386314
Contig ID	1248_1.R1084
5'-most EST	g5005271
Method	BLASTX
NCBI GI	g3510256
BLAST score	151
E value	5.0e-19
Match length	101
% identity	55
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	386315
Contig ID	1248_2.R1084
5'-most EST	LIB3431-001-P1-N1-C11
Method	BLASTX
NCBI GI	g3510256
BLAST score	249
E value	6.0e-21
Match length	84
% identity	56
NCBI Description	(AC005310) unknown protein [Arabidopsis thaliana]

Seq. No.	386316
Contig ID	1251_1.R1084
5'-most EST	LIB3431-022-P1-N1-H9

Seq. No.	386317
Contig ID	1252_1.R1084
5'-most EST	LIB3431-023-P1-N1-A10
Method	BLASTX
NCBI GI	g4584358
BLAST score	702
E value	8.0e-74
Match length	213
% identity	71
NCBI Description	(AC006420) unknown protein [Arabidopsis thaliana]

Seq. No.	386318
Contig ID	1253_1.R1084
5'-most EST	LIB3431-023-P1-N1-A11
Method	BLASTX
NCBI GI	g1657621
BLAST score	437
E value	5.0e-69
Match length	158
% identity	84
NCBI Description	(U72505) G6p [Arabidopsis thaliana] >gi_3068711 (AF049236) putative acyl-coA dehydrogenase [Arabidopsis thaliana] >gi_5478795_dbj_BAA82478.1_ (AB017643) Short-chain acyl CoA oxidase [Arabidopsis thaliana]

Seq. No.	386319
Contig ID	1254_1.R1084
5'-most EST	LIB3431-023-P1-N1-A12
Method	BLASTX
NCBI GI	g4190952
BLAST score	496
E value	1.0e-49
Match length	205
% identity	52
NCBI Description	(AB022689) similar to hsr203J [Lycopersicon esculentum]

Seq. No.	386320
Contig ID	1255_1.R1084
5'-most EST	uC-osf1cyp153h03a1
Method	BLASTN
NCBI GI	g5803242
BLAST score	232
E value	1.0e-127
Match length	365
% identity	99
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	386321
Contig ID	1256_1.R1084
5'-most EST	uC-osf1M202058h07a1
Method	BLASTX
NCBI GI	g5734618
BLAST score	513
E value	1.0e-51
Match length	255
% identity	42
NCBI Description	(AP000391) Similar to Arabidopsis thaliana chromosome II BAC F5H14 genomic sequence; unknown protein (AC006234) [Oryza sativa]

Seq. No.	386322
Contig ID	1257_1.R1084
5'-most EST	g2431304
Method	BLASTX
NCBI GI	g1173327
BLAST score	235
E value	3.0e-19
Match length	117
% identity	48
NCBI Description	U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A') >gi_322619_pir__S30580 U2 snRNP ...idopsis thaliana >gi_17669_emb_CA... (X69137) ... ll nuclear ribonucleoprotein A' [Ar...psis thaliana]

Seq. No.	386323
Contig ID	1259_1.R1084
5'-most EST	LIB3431-044-P1-N1-G6
Method	BLASTX
NCBI GI	g1052960
BLAST score	1676
E value	0.0e+00

Match length	352
% identity	90
NCBI Description	(U37437) PNIL34 [Ipomoea nil]

Seq. No.	386324
Contig ID	1259_2.R1084
5'-most EST	LIB3432-044-P1-K1-B1
Method	BLASTX
NCBI GI	g1052960
BLAST score	500
E value	1.0e-50
Match length	110
% identity	88
NCBI Description	(U37437) PNIL34 [Ipomoea nil]

Seq. No.	386325
Contig ID	1261_1.R1084
5'-most EST	g3767781

Seq. No.	386326
Contig ID	1262_1.R1084
5'-most EST	LIB3431-049-P1-N1-B9

Seq. No.	386327
Contig ID	1265_1.R1084
5'-most EST	LIB3431-023-P1-K1-B4
Method	BLASTX
NCBI GI	g4530126
BLAST score	240
E value	7.0e-20
Match length	113
% identity	46
NCBI Description	(AF078082) receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris]

Seq. No.	386328
Contig ID	1267_1.R1084
5'-most EST	g4716208

Seq. No.	386329
Contig ID	1268_1.R1084
5'-most EST	LIB3431-023-P1-N1-B7

Seq. No.	386330
Contig ID	1269_1.R1084
5'-most EST	LIB3431-023-P1-N1-B8

Seq. No.	386331
Contig ID	1270_1.R1084
5'-most EST	uC-osf1M202031b05a1
Method	BLASTX
NCBI GI	g1362147
BLAST score	217
E value	2.0e-17
Match length	49
% identity	84
NCBI Description	hypothetical protein (clone AFD1) - wild oat (fragment)

>gi_726471 (U19996) putative ORF1 [Avena fatua]

Seq. No.	386332
Contig ID	1271_1.R1084
5'-most EST	LIB3431-023-P1-N1-C1

Seq. No.	386333
Contig ID	1272_1.R1084
5'-most EST	LIB3431-023-P1-N1-C10

Seq. No.	386334
Contig ID	1272_2.R1084
5'-most EST	uC-osroM202018c04b1

Seq. No.	386335
Contig ID	1275_1.R1084
5'-most EST	LIB3431-010-P1-N1-H12
Method	BLASTX
NCBI GI	g231610
BLAST score	1226
E value	1.0e-135
Match length	324
% identity	73
NCBI Description	ATP SYNTHASE GAMMA CHAIN, CHLOROPLAST PRECURSOR >gi_67880_pir__PWNTG H+-transporting ATP synthase (EC 3.6.1.34) gamma chain precursor, chloroplast - common tobacco >gi_19785_emb_CAA45152_ (X63606) ATP synthase (gamma subunit) [Nicotiana tabacum]

Seq. No.	386336
Contig ID	1278_1.R1084
5'-most EST	g2799452
Method	BLASTX
NCBI GI	g3183079
BLAST score	1496
E value	1.0e-167
Match length	350
% identity	83
NCBI Description	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR >gi_1375075_dbj_BAA12870.1_ (D85763) glyoxysomal malate dehydrogenase [Oryza sativa]

Seq. No.	386337
Contig ID	1279_1.R1084
5'-most EST	g3769123

Seq. No.	386338
Contig ID	1281_1.R1084
5'-most EST	LIB3431-023-P1-N1-C8
Method	BLASTX
NCBI GI	g4803952
BLAST score	715
E value	3.0e-75
Match length	177
% identity	77
NCBI Description	(AC006202) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386339
Contig ID	1282_1.R1084
5'-most EST	LIB3431-023-P1-N1-C9
Method	BLASTX
NCBI GI	g4455350
BLAST score	321
E value	1.0e-29
Match length	91
% identity	80
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	386340
Contig ID	1290_1.R1084
5'-most EST	LIB3431-023-P1-N1-D8
Method	BLASTX
NCBI GI	g4914457
BLAST score	326
E value	6.0e-30
Match length	142
% identity	44
NCBI Description	(AL050400) putative protein [Arabidopsis thaliana]

Seq. No.	386341
Contig ID	1294_1.R1084
5'-most EST	g3768900

Seq. No.	386342
Contig ID	1294_2.R1084
5'-most EST	uC-osflcyp144h01b1
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	49
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386343
Contig ID	1294_3.R1084
5'-most EST	g2800143

Seq. No.	386344
Contig ID	1294_4.R1084
5'-most EST	uC-osflcyp031h01a1

Seq. No.	386345
Contig ID	1294_6.R1084
5'-most EST	g701377

Seq. No.	386346
Contig ID	1295_1.R1084
5'-most EST	g4715350
Method	BLASTX
NCBI GI	g563249
BLAST score	296
E value	2.0e-43
Match length	126

% identity	63
NCBI Description	(U16280) acetolactate synthase precursor [Xanthium sp.]

Seq. No.	386347
Contig ID	1296_1.R1084
5'-most EST	g5607415
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386348
Contig ID	1298_1.R1084
5'-most EST	LIB3431-023-P1-N1-E6

Seq. No.	386349
Contig ID	1299_1.R1084
5'-most EST	LIB3431-023-P1-N1-E7

Seq. No.	386350
Contig ID	1302_1.R1084
5'-most EST	g3760026

Seq. No.	386351
Contig ID	1302_2.R1084
5'-most EST	uC-osf1M202092c12b1

Seq. No.	386352
Contig ID	1311_1.R1084
5'-most EST	g1036981

Seq. No.	386353
Contig ID	1312_1.R1084
5'-most EST	g4715447
Method	BLASTX
NCBI GI	g170131
BLAST score	629
E value	3.0e-65
Match length	225
% identity	57
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No.	386354
Contig ID	1312_2.R1084
5'-most EST	g4715446
Method	BLASTX
NCBI GI	g170131
BLAST score	330
E value	2.0e-30
Match length	81
% identity	72
NCBI Description	(M55322) ribosomal protein 30S subunit [Spinacia oleracea]

Seq. No. 386355

Contig ID	1314_1.R1084
5'-most EST	uC-osflcyp002a12b1

Seq. No.	386356
Contig ID	1319_1.R1084
5'-most EST	LIB3431-023-P1-N1-G7
Method	BLASTX
NCBI GI	g4972093
BLAST score	534
E value	4.0e-54
Match length	183
% identity	57
NCBI Description	(AL078468) putative protein [Arabidopsis thaliana]

Seq. No.	386357
Contig ID	1328_1.R1084
5'-most EST	g5056134

Seq. No.	386358
Contig ID	1330_1.R1084
5'-most EST	g3762645
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	1.0e-09
Match length	35
% identity	58
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386359
Contig ID	1330_2.R1084
5'-most EST	LIB3434-013-P1-K1-B6

Seq. No.	386360
Contig ID	1332_1.R1084
5'-most EST	g3762860
Method	BLASTX
NCBI GI	g3914425
BLAST score	1042
E value	1.0e-113
Match length	276
% identity	73
NCBI Description	PROTEASOME EPSILON CHAIN PRECURSOR (MACROPAIN EPSILON CHAIN) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX EPSILON CHAIN) >gi_2511596_emb_CAA74029.1_ (Y13695) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421117 (AF043536) 20S proteasome beta subunit PBE1 [Arabidopsis thaliana] >gi_4850389_gb_AAD31059.1_AC007357_8 (AC007357) Identical to gb_Y13695 multicatalytic endopeptidase complex, proteasome precursor, beta subunit (prce) from Arabidopsis thaliana. ESTs gb_Y09360, gb_F13852, gb_T20555, gb_T44620, gb_AI099779 and gb_AA5861

Seq. No.	386361
Contig ID	1333_1.R1084
5'-most EST	LIB3431-024-P1-N1-A1

Seq. No.	386362
Contig ID	1335_1.R1084
5'-most EST	LIB3431-024-P1-N1-A12
Method	BLASTX
NCBI GI	g4581162
BLAST score	526
E value	3.0e-53
Match length	117
% identity	85
NCBI Description	(AC006220) putative symbiosis-related protein [Arabidopsis thaliana]

Seq. No.	386363
Contig ID	1339_1.R1084
5'-most EST	LIB3431-024-P1-N1-A5
Method	BLASTN
NCBI GI	g5295936
BLAST score	36
E value	2.0e-10
Match length	200
% identity	59
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	386364
Contig ID	1340_1.R1084
5'-most EST	LIB3431-024-P1-N1-A7

Seq. No.	386365
Contig ID	1341_1.R1084
5'-most EST	uC-osroM202010f11a1

Seq. No.	386366
Contig ID	1344_1.R1084
5'-most EST	g3768768
Method	BLASTX
NCBI GI	g729478
BLAST score	1434
E value	1.0e-159
Match length	365
% identity	75
NCBI Description	FERREDOXIN--NADP REDUCTASE, LEAF ISOZYME PRECURSOR (FNR) >gi_442481_dbj_BAA04616_ (D17790) ferredoxin-NADP+ reductase [Oryza sativa] >gi_6069649_dbj_BAA85425.1_ (AP000616) ESTs AU078647(E1557),C72400(E1557) correspond to a region of the predicted gene.; similar to ferredoxin-NADP+ reductase (D17790) [Oryza sativa]

Seq. No.	386367
Contig ID	1353_1.R1084
5'-most EST	LIB3431-024-P1-N1-C1
Method	BLASTX
NCBI GI	g4512616
BLAST score	497
E value	3.0e-50
Match length	120

% identity	79
NCBI Description	(AC004793) Contains similarity to gi_1653332 extragenic suppressor (SuhB) from Synechocystis sp. gb_D90912 and is a member of the Inositol monophophatase family PF_00459. EST gb_AA597395 comes from this gene. [Arabidopsis tha

Seq. No.	386368
Contig ID	1360_1.R1084
5'-most EST	g4714130

Seq. No.	386369
Contig ID	1362_1.R1084
5'-most EST	LIB3431-024-P1-N1-C7
Method	BLASTX
NCBI GI	g3402713
BLAST score	732
E value	3.0e-77
Match length	211
% identity	65
NCBI Description	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386370
Contig ID	1371_1.R1084
5'-most EST	LIB3431-024-P1-N1-D4

Seq. No.	386371
Contig ID	1372_1.R1084
5'-most EST	LIB3431-024-P1-N1-D5

Seq. No.	386372
Contig ID	1373_1.R1084
5'-most EST	g5455597
Method	BLASTX
NCBI GI	g2342719
BLAST score	251
E value	2.0e-41
Match length	215
% identity	48
NCBI Description	(AC002341) SF16 protein isolog [Arabidopsis thaliana]

Seq. No.	386373
Contig ID	1377_1.R1084
5'-most EST	LIB3432-013-P1-K1-A1

Seq. No.	386374
Contig ID	1377_3.R1084
5'-most EST	LIB3432-058-P1-K1-E6

Seq. No.	386375
Contig ID	1382_1.R1084
5'-most EST	LIB3431-024-P1-N1-E5

Seq. No.	386376
Contig ID	1383_1.R1084
5'-most EST	LIB3431-024-P1-N1-E7
Method	BLASTN
NCBI GI	g3821780

BLAST score	35
E value	1.0e-09
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	386377
Contig ID	1388_1.R1084
5'-most EST	LIB3431-024-P1-N1-F11

Seq. No.	386378
Contig ID	1392_1.R1084
5'-most EST	uC-osf1cyp157h04b1
Method	BLASTX
NCBI GI	g4582436
BLAST score	162
E value	1.0e-10
Match length	77
% identity	47
NCBI Description	(AC007196) unknown protein [Arabidopsis thaliana]

Seq. No.	386379
Contig ID	1397_1.R1084
5'-most EST	LIB3431-054-P1-K1-H12
Method	BLASTX
NCBI GI	g2245062
BLAST score	465
E value	6.0e-46
Match length	109
% identity	79
NCBI Description	(Z97342) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386380
Contig ID	1398_1.R1084
5'-most EST	g3768797

Seq. No.	386381
Contig ID	1403_1.R1084
5'-most EST	LIB3431-024-P1-N1-G3

Seq. No.	386382
Contig ID	1407_1.R1084
5'-most EST	LIB3431-024-P1-N1-G7
Method	BLASTX
NCBI GI	g3386621
BLAST score	162
E value	6.0e-11
Match length	36
% identity	83
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	386383
Contig ID	1408_1.R1084
5'-most EST	LIB3431-031-P1-N1-A2
Method	BLASTX
NCBI GI	g4538947
BLAST score	176

E value	2.0e-12
Match length	49
% identity	65
NCBI Description	(AL049483) putative mitochondrial carrier protein [Arabidopsis thaliana]

Seq. No.	386384
Contig ID	1411_1.R1084
5'-most EST	LIB3431-024-P1-N1-H10

Seq. No.	386385
Contig ID	1415_1.R1084
5'-most EST	LIB3431-034-P1-N1-B4
Method	BLASTX
NCBI GI	g1498315
BLAST score	713
E value	2.0e-84
Match length	333
% identity	52
NCBI Description	(U56419) IAP100 [Pisum sativum]

Seq. No.	386386
Contig ID	1417_1.R1084
5'-most EST	LIB3431-024-P1-N1-H6
Method	BLASTX
NCBI GI	g4454458
BLAST score	155
E value	1.0e-12
Match length	56
% identity	73
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	386387
Contig ID	1421_1.R1084
5'-most EST	LIB3431-025-P1-N1-A10
Method	BLASTX
NCBI GI	g2911085
BLAST score	150
E value	3.0e-09
Match length	119
% identity	31
NCBI Description	(AL021960) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana] >gi_3402748_emb_CAA20194.1_ (AL031187) photosystem II oxygen-evolving complex protein 3-like [Arabidopsis thaliana]

Seq. No.	386388
Contig ID	1422_1.R1084
5'-most EST	g4716585
Method	BLASTX
NCBI GI	g3808101
BLAST score	796
E value	6.0e-85
Match length	176
% identity	89
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	386389
Contig ID	1422_3.R1084
5'-most EST	g2798706
Method	BLASTX
NCBI GI	g4325041
BLAST score	744
E value	6.0e-79
Match length	182
% identity	80
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	386390
Contig ID	1422_4.R1084
5'-most EST	LIB3432-003-P1-K1-H11
Method	BLASTX
NCBI GI	g3808101
BLAST score	1673
E value	0.0e+00
Match length	413
% identity	82
NCBI Description	(AJ012165) chloroplast protease [Capsicum annuum]

Seq. No.	386391
Contig ID	1422_5.R1084
5'-most EST	uC-osflcyp022d08b1
Method	BLASTX
NCBI GI	g4325041
BLAST score	540
E value	3.0e-55
Match length	157
% identity	75
NCBI Description	(AF117339) FtsH-like protein Pftf precursor [Nicotiana tabacum]

Seq. No.	386392
Contig ID	1424_1.R1084
5'-most EST	LIB3431-025-P1-N1-A2

Seq. No.	386393
Contig ID	1425_1.R1084
5'-most EST	LIB3431-025-P1-N1-A3

Seq. No.	386394
Contig ID	1426_1.R1084
5'-most EST	g5607339
Method	BLASTX
NCBI GI	g5702231
BLAST score	175
E value	6.0e-24
Match length	114
% identity	43
NCBI Description	(AF145386) hypersensitive reaction associated Ca2+-binding protein [Phaseolus vulgaris]

Seq. No.	386395
Contig ID	1427_1.R1084

5'-most EST	g4715547
Method	BLASTX
NCBI GI	g4504379
BLAST score	189
E value	2.0e-13
Match length	390
% identity	27
NCBI Description	G protein-coupled receptor 49 >gi_3366802 (AF062006) orphan G protein-coupled receptor HG38 [Homo sapiens]

Seq. No.	386396
Contig ID	1427_2.R1084
5'-most EST	uC-osrocyp028f09a1

Seq. No.	386397
Contig ID	1428_1.R1084
5'-most EST	LIB3431-025-P1-K1-A6
Method	BLASTX
NCBI GI	g2623310
BLAST score	272
E value	2.0e-23
Match length	168
% identity	44
NCBI Description	(AC002409) unknown protein [Arabidopsis thaliana] >gi_3402721 (AC004261) unknown protein [Arabidopsis thaliana]

Seq. No.	386398
Contig ID	1430_1.R1084
5'-most EST	g5803368

Seq. No.	386399
Contig ID	1431_1.R1084
5'-most EST	LIB3431-025-P1-N1-A9
Method	BLASTX
NCBI GI	g4877984
BLAST score	356
E value	2.0e-33
Match length	77
% identity	90
NCBI Description	(AF145755) THA4 [Zea mays]

Seq. No.	386400
Contig ID	1438_1.R1084
5'-most EST	LIB3431-001-P1-N1-A12
Method	BLASTX
NCBI GI	g3551954
BLAST score	773
E value	4.0e-82
Match length	271
% identity	54
NCBI Description	(AF082030) senescence-associated protein 5 [Hemerocallis hybrid cultivar]

Seq. No.	386401
Contig ID	1439_1.R1084
5'-most EST	LIB3431-025-P1-N1-B7

Method	BLASTX
NCBI GI	g4753659
BLAST score	923
E value	1.0e-99
Match length	209
% identity	82
NCBI Description	(AL049751) putative protein [Arabidopsis thaliana]

Seq. No.	386402
Contig ID	1441_1.R1084
5'-most EST	g5038655
Method	BLASTX
NCBI GI	g729135
BLAST score	1381
E value	1.0e-153
Match length	368
% identity	74
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No.	386403
Contig ID	1441_2.R1084
5'-most EST	g3767800
Method	BLASTX
NCBI GI	g729135
BLAST score	219
E value	3.0e-17
Match length	100
% identity	67
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No.	386404
Contig ID	1441_5.R1084
5'-most EST	g700264
Method	BLASTX
NCBI GI	g729135
BLAST score	239
E value	6.0e-42
Match length	155
% identity	87
NCBI Description	CAFFEIC ACID 3-O-METHYLTRANSFERASE (S-ADENOSYSL-L-METHIONINE:CAFFEIC ACID 3-O-METHYLTRANSFERASE) (COMT) >gi_283034_pir__S28612 catechol O-methyltransferase (EC 2.1.1.6) - maize >gi_168532 (M73235) O-methyltransferase [Zea mays]

Seq. No.	386405
Contig ID	1443_1.R1084
5'-most EST	LIB3431-025-P1-N1-C10

Seq. No.	386406
Contig ID	1444_1.R1084
5'-most EST	g3764137
Method	BLASTX
NCBI GI	g629829
BLAST score	1266
E value	1.0e-146
Match length	380
% identity	74
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) - wheat >gi_510677_emb_CAA54042_ (X76532) protochlorophyilide reductase [Triticum aestivum]

Seq. No.	386407
Contig ID	1444_2.R1084
5'-most EST	LIB3431-020-P1-N1-H11
Method	BLASTX
NCBI GI	g419742
BLAST score	596
E value	8.0e-87
Match length	173
% identity	93
NCBI Description	protochlorophyllide reductase (EC 1.3.1.33) precursor - loblolly pine

Seq. No.	386408
Contig ID	1444_4.R1084
5'-most EST	g3768594
Method	BLASTN
NCBI GI	g19060
BLAST score	43
E value	7.0e-15
Match length	127
% identity	89
NCBI Description	Barley mRNA for NADPH-protochlorophyllide oxidoreductase (PCR)

Seq. No.	386409
Contig ID	1445_1.R1084
5'-most EST	uC-osroM202004e05a2

Seq. No.	386410
Contig ID	1446_1.R1084
5'-most EST	g4714353

Seq. No.	386411
Contig ID	1450_1.R1084
5'-most EST	g4714621
Method	BLASTX
NCBI GI	g4337177
BLAST score	1335
E value	1.0e-163
Match length	352
% identity	80
NCBI Description	(AC006416) Identical to gb_Y10557 g5bf gene from Arabidopsis thaliana. ESTs gb_R30578, gb_R90475, gb_T22384, gb_T22425, gb_N64934 and gb_T46767 come from

this gene. [Arabidopsis thaliana]

Seq. No.	386412
Contig ID	1450_2.R1084
5'-most EST	LIB3431-038-P1-N1-B7
Method	BLASTX
NCBI GI	g400879
BLAST score	456
E value	4.0e-45
Match length	149
% identity	62
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_479690_pir__S35159 photosystem I chain psaN - barley >gi_19095_emb_CAA47056_ (X66428) photosystem I subunit N [Hordeum vulgare]

Seq. No.	386413
Contig ID	1450_5.R1084
5'-most EST	LIB3431-014-P1-N1-B3
Method	BLASTX
NCBI GI	g3914466
BLAST score	251
E value	4.0e-38
Match length	87
% identity	84
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT PSAN PRECURSOR (PSI-N) >gi_2981214 (AF052429) photosystem I complex PsaN subunit precursor [Zea mays]

Seq. No.	386414
Contig ID	1450_6.R1084
5'-most EST	LIB3431-036-P1-K1-B2
Method	BLASTN
NCBI GI	g19094
BLAST score	52
E value	4.0e-20
Match length	64
% identity	95
NCBI Description	H.vulgare mRNA PsaN for photosystem I subunit N

Seq. No.	386415
Contig ID	1451_1.R1084
5'-most EST	LIB3431-025-P1-K1-C8
Method	BLASTX
NCBI GI	g2673904
BLAST score	143
E value	3.0e-13
Match length	78
% identity	50
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386416
Contig ID	1453_1.R1084
5'-most EST	g4715578
Method	BLASTX
NCBI GI	g1353352
BLAST score	656

E value	1.0e-111
Match length	327
% identity	60
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	386417
Contig ID	1453_2.R1084
5'-most EST	LIB3432-024-P1-K1-H5
Method	BLASTX
NCBI GI	g1353352
BLAST score	581
E value	8.0e-60
Match length	158
% identity	72
NCBI Description	(U31975) alanine aminotransferase [Chlamydomonas reinhardtii]

Seq. No.	386418
Contig ID	1455_1.R1084
5'-most EST	g3768580
Method	BLASTX
NCBI GI	g5091556
BLAST score	206
E value	2.0e-18
Match length	95
% identity	52
NCBI Description	(AC007067) T10O24.25 [Arabidopsis thaliana]

Seq. No.	386419
Contig ID	1457_1.R1084
5'-most EST	g3760497

Seq. No.	386420
Contig ID	1462_1.R1084
5'-most EST	g2797050
Method	BLASTX
NCBI GI	g2055273
BLAST score	1645
E value	0.0e+00
Match length	386
% identity	81
NCBI Description	(D85339) hydroxypyruvate reductase [Arabidopsis thaliana]

Seq. No.	386421
Contig ID	1468_1.R1084
5'-most EST	LIB3431-025-P1-N1-E3
Method	BLASTX
NCBI GI	g4567263
BLAST score	282
E value	5.0e-25
Match length	70
% identity	74
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	386422

Contig ID	1469_1.R1084
5'-most EST	LIB3431-025-P1-N1-E4

Seq. No.	386423
Contig ID	1474_2.R1084
5'-most EST	g2800286
Method	BLASTX
NCBI GI	g799369
BLAST score	273
E value	2.0e-31
Match length	112
% identity	68
NCBI Description	(U25111) metalloendopeptidase [Pisum sativum]

Seq. No.	386424
Contig ID	1476_1.R1084
5'-most EST	LIB3431-019-P1-N1-F2
Method	BLASTX
NCBI GI	g1777961
BLAST score	640
E value	1.0e-66
Match length	201
% identity	64
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	386425
Contig ID	1479_1.R1084
5'-most EST	LIB3431-025-P1-N1-F3
Method	BLASTX
NCBI GI	g4467098
BLAST score	324
E value	1.0e-29
Match length	136
% identity	44
NCBI Description	(AL035538) putative protein [Arabidopsis thaliana]

Seq. No.	386426
Contig ID	1480_1.R1084
5'-most EST	LIB3431-025-P1-K1-F4
Method	BLASTX
NCBI GI	g4960154
BLAST score	340
E value	1.0e-31
Match length	91
% identity	73
NCBI Description	(AF153283) putative progesterone-binding protein homolog [Arabidopsis thaliana]

Seq. No.	386427
Contig ID	1486_1.R1084
5'-most EST	uC-osflcyp078c04a1

Seq. No.	386428
Contig ID	1492_1.R1084
5'-most EST	LIB3431-036-P1-N1-A3

Seq. No.	386429
Contig ID	1495_1.R1084
5'-most EST	LIB3431-025-P1-N1-G8

Seq. No.	386430
Contig ID	1497_1.R1084
5'-most EST	LIB3431-025-P1-N1-H1
Method	BLASTX
NCBI GI	g4322346
BLAST score	310
E value	6.0e-28
Match length	163
% identity	38
NCBI Description	(AF081825) sodium-dependent high-affinity dicarboxylate transporter [Rattus norvegicus] >gi_4837725_gb_AAD30657.1_AF080451_1 (AF080451) sodium-dependent dicarboxylate transporter SDCT2 [Rattus norvegicus]

Seq. No.	386431
Contig ID	1498_1.R1084
5'-most EST	uC-osf1cyp083f08a1
Method	BLASTX
NCBI GI	g1737492
BLAST score	339
E value	3.0e-59
Match length	198
% identity	64
NCBI Description	(U81318) poly(A)-binding protein [Triticum aestivum]

Seq. No.	386432
Contig ID	1499_1.R1084
5'-most EST	g4715880
Method	BLASTX
NCBI GI	g3790581
BLAST score	269
E value	6.0e-23
Match length	143
% identity	49
NCBI Description	(AF079179) RING-H2 finger protein RHB1a [Arabidopsis thaliana]

Seq. No.	386433
Contig ID	1501_1.R1084
5'-most EST	LIB3432-041-P1-K1-G11
Method	BLASTX
NCBI GI	g1651922
BLAST score	181
E value	4.0e-13
Match length	60
% identity	57
NCBI Description	(D90901) hypothetical protein [Synechocystis sp.]

Seq. No.	386434
Contig ID	1503_1.R1084
5'-most EST	uC-osroM202020d10a1
Method	BLASTX

NCBI GI	g4678280
BLAST score	257
E value	3.0e-21
Match length	146
% identity	36
NCBI Description	(AL049660) zinc finger-like protein [Arabidopsis thaliana]

Seq. No.	386435
Contig ID	1505_1.R1084
5'-most EST	LIB3431-025-P1-N1-H6
Method	BLASTN
NCBI GI	g6015437
BLAST score	37
E value	6.0e-11
Match length	59
% identity	54
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386436
Contig ID	1514_1.R1084
5'-most EST	g4715553
Method	BLASTX
NCBI GI	g2462763
BLAST score	471
E value	1.0e-132
Match length	321
% identity	78
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	386437
Contig ID	1514_2.R1084
5'-most EST	g3768551
Method	BLASTX
NCBI GI	g2462763
BLAST score	517
E value	1.0e-121
Match length	310
% identity	75
NCBI Description	(AC002292) Highly similar to auxin-induced protein (aldo/keto reductase family) [Arabidopsis thaliana]

Seq. No.	386438
Contig ID	1517_1.R1084
5'-most EST	LIB3431-026-P1-N1-A6
Method	BLASTX
NCBI GI	g4538920
BLAST score	629
E value	3.0e-65
Match length	179
% identity	73
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	386439
Contig ID	1518_1.R1084
5'-most EST	g3760155

Method	BLASTX
NCBI GI	g3913437
BLAST score	180
E value	3.0e-13
Match length	38
% identity	84
NCBI Description	PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE >gi_1402875_emb_CAA66825_ (X98130) RNA helicase [Arabidopsis thaliana] >gi_1495271_emb_CAA66613_ (X97970) RNA helicase [Arabidopsis thaliana]

Seq. No.	386440
Contig ID	1523_1.R1084
5'-most EST	LIB3431-045-P1-N1-G5
Method	BLASTX
NCBI GI	g4006881
BLAST score	594
E value	4.0e-61
Match length	167
% identity	69
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	386441
Contig ID	1524_1.R1084
5'-most EST	g426094
Method	BLASTX
NCBI GI	g4588906
BLAST score	651
E value	7.0e-68
Match length	166
% identity	78
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	386442
Contig ID	1524_2.R1084
5'-most EST	LIB3474-008-P1-K1-B3
Method	BLASTX
NCBI GI	g4588906
BLAST score	517
E value	3.0e-67
Match length	146
% identity	80
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	386443
Contig ID	1533_1.R1084
5'-most EST	g3768475
Method	BLASTX
NCBI GI	g2262105
BLAST score	983
E value	1.0e-107
Match length	290
% identity	59
NCBI Description	(AC002343) unknown protein [Arabidopsis thaliana]

Seq. No.	386444
Contig ID	1535_1.R1084

5'-most EST	LIB3431-026-P1-N1-C12
Method	BLASTX
NCBI GI	g4455296
BLAST score	575
E value	5.0e-59
Match length	183
% identity	64
NCBI Description	(AL035528) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386445
Contig ID	1536_1.R1084
5'-most EST	LIB3431-045-P1-N1-D2

Seq. No.	386446
Contig ID	1543_1.R1084
5'-most EST	g5004950
Method	BLASTX
NCBI GI	g5669640
BLAST score	792
E value	3.0e-84
Match length	182
% identity	88
NCBI Description	(AF096249) ethylene-responsive small GTP-binding protein [Lycopersicon esculentum]

Seq. No.	386447
Contig ID	1546_1.R1084
5'-most EST	g2799228
Method	BLASTN
NCBI GI	g5764544
BLAST score	40
E value	8.0e-13
Match length	40
% identity	100
NCBI Description	Shuttle vector pSLIRES11, complete sequence

Seq. No.	386448
Contig ID	1548_1.R1084
5'-most EST	uC-osroM202001e09b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	1089
E value	1.0e-119
Match length	298
% identity	33
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	386449
Contig ID	1550_1.R1084
5'-most EST	uC-osf1M202065f04a1
Method	BLASTX
NCBI GI	g543939
BLAST score	197
E value	8.0e-15
Match length	45
% identity	87
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 PRECURSOR

	>gi_541819_pir__S40210 chlorophyll a/b-binding protein CP24 precursor - spinach >gi_437991_emb_CAA81105.1_ (Z25886) 20 kDa protein of CP24 precursor protein [Spinacia oleracea]
Seq. No.	386450
Contig ID	1550_2.R1084
5'-most EST	uC-osflcyp037g07a1
Method	BLASTX
NCBI GI	g733458
BLAST score	693
E value	1.0e-107
Match length	223
% identity	87
NCBI Description	(U23190) chlorophyll a/b-binding apoprotein CP24 precursor [Zea mays]
Seq. No.	386451
Contig ID	1550_3.R1084
5'-most EST	g5005273
Method	BLASTX
NCBI GI	g115834
BLAST score	114
E value	3.0e-10
Match length	56
% identity	60
NCBI Description	CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR (CAB-10B) (LHCP) >gi_100202_pir__S11878 chlorophyll a/b-binding protein Cab10B - tomato >gi_170400 (M32606) chlorophyll b-binding protein [Lycopersicon esculentum]
Seq. No.	386452
Contig ID	1555_1.R1084
5'-most EST	uC-osflm202002g11b1
Method	BLASTX
NCBI GI	g2673913
BLAST score	394
E value	6.0e-38
Match length	110
% identity	69
NCBI Description	(AC002561) hypothetical protein [Arabidopsis thaliana]
Seq. No.	386453
Contig ID	1558_2.R1084
5'-most EST	g4715254
Seq. No.	386454
Contig ID	1559_1.R1084
5'-most EST	g569092
Method	BLASTN
NCBI GI	g2293479
BLAST score	35
E value	1.0e-09
Match length	40
% identity	43
NCBI Description	Oryza sativa glycine-rich protein mRNA, complete cds
Seq. No.	386455

Contig ID	1559_2.R1084
5'-most EST	LIB3431-054-P1-N1-A7
Seq. No.	386456
Contig ID	1559_3.R1084
5'-most EST	LIB3431-026-P1-K1-E3
Seq. No.	386457
Contig ID	1560_1.R1084
5'-most EST	g5455424
Method	BLASTN
NCBI GI	g5777612
BLAST score	34
E value	2.0e-09
Match length	62
% identity	90
NCBI Description	Oryza sativa chromosome 4 BAC q3037-207F1 complete genome
Seq. No.	386458
Contig ID	1561_1.R1084
5'-most EST	g2312766
Method	BLASTX
NCBI GI	g4455208
BLAST score	1207
E value	1.0e-136
Match length	399
% identity	67
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	386459
Contig ID	1561_3.R1084
5'-most EST	LIB3434-029-P1-K1-B7
Method	BLASTX
NCBI GI	g4455208
BLAST score	518
E value	1.0e-52
Match length	151
% identity	65
NCBI Description	(AL035440) putative protein [Arabidopsis thaliana]
Seq. No.	386460
Contig ID	1565_1.R1084
5'-most EST	g4715923
Seq. No.	386461
Contig ID	1565_2.R1084
5'-most EST	LIB3431-063-P1-K1-H9
Method	BLASTX
NCBI GI	g2688824
BLAST score	194
E value	2.0e-14
Match length	133
% identity	42
NCBI Description	(U93273) putative auxin-repressed protein [Prunus armeniaca]
Seq. No.	386462

Contig ID	1571_1.R1084
5'-most EST	g4715964
Seq. No.	386463
Contig ID	1572_1.R1084
5'-most EST	g4878853
Seq. No.	386464
Contig ID	1574_1.R1084
5'-most EST	LIB3431-054-P1-K1-F5
Seq. No.	386465
Contig ID	1576_1.R1084
5'-most EST	g3758991
Seq. No.	386466
Contig ID	1580_1.R1084
5'-most EST	g4715305
Seq. No.	386467
Contig ID	1588_1.R1084
5'-most EST	g3763529
Method	BLASTX
NCBI GI	g3292814
BLAST score	427
E value	7.0e-42
Match length	105
% identity	71
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]
Seq. No.	386468
Contig ID	1589_1.R1084
5'-most EST	LIB3431-026-P1-N1-H12
Seq. No.	386469
Contig ID	1590_1.R1084
5'-most EST	g5455610
Seq. No.	386470
Contig ID	1590_2.R1084
5'-most EST	g5455598
Seq. No.	386471
Contig ID	1595_1.R1084
5'-most EST	LIB3431-026-P1-N1-H7
Method	BLASTX
NCBI GI	g4539305
BLAST score	296
E value	2.0e-26
Match length	102
% identity	53
NCBI Description	(AL049480) putative protein [Arabidopsis thaliana]
Seq. No.	386472
Contig ID	1599_1.R1084
5'-most EST	LIB3431-005-P1-N1-C8
Method	BLASTX

NCBI GI	g1168587
BLAST score	665
E value	2.0e-69
Match length	241
% identity	62
NCBI Description	ATP SYNTHASE DELTA CHAIN, CHLOROPLAST PRECURSOR >gi_1084467_pir__S43728 H+-transporting ATP synthase (EC 3.6.1.34) - sorghum >gi_311231_emb_CAA46803_ (X66004) H(+)-transporting ATP synthase [Sorghum bicolor]

Seq. No.	386473
Contig ID	1599_2.R1084
5'-most EST	LIB3433-049-P1-K1-A6
Method	BLASTN
NCBI GI	g311230
BLAST score	59
E value	3.0e-24
Match length	115
% identity	90
NCBI Description	S.bicolor mRNA for ATPase (delta subunit)

Seq. No.	386474
Contig ID	1600_1.R1084
5'-most EST	g5003231
Method	BLASTX
NCBI GI	g3413423
BLAST score	169
E value	8.0e-12
Match length	64
% identity	48
NCBI Description	(AJ006309) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386475
Contig ID	1601_1.R1084
5'-most EST	g2798844
Method	BLASTX
NCBI GI	g2493650
BLAST score	1966
E value	0.0e+00
Match length	454
% identity	89
NCBI Description	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) >gi_1167858_emb_CAA93139_ (Z68903) chaperonin [Secale cereale]

Seq. No.	386476
Contig ID	1602_1.R1084
5'-most EST	g4878901

Seq. No.	386477
Contig ID	1605_1.R1084
5'-most EST	g3766758
Method	BLASTX
NCBI GI	g4093157
BLAST score	288
E value	1.0e-40

Match length	254
% identity	49
NCBI Description	(AF087936) phytochrome-associated protein 2 [Arabidopsis thaliana] >gi_4972054_emb_CAB43922.1_ (AL078470) phytochrome-associated protein PAP2 [Arabidopsis thaliana]

Seq. No.	386478
Contig ID	1605_2.R1084
5'-most EST	g4714401
Method	BLASTX
NCBI GI	g4093169
BLAST score	481
E value	3.0e-56
Match length	160
% identity	71
NCBI Description	(AF095933) p20-Arc [Dictyostelium discoideum]

Seq. No.	386479
Contig ID	1605_5.R1084
5'-most EST	g2428469

Seq. No.	386480
Contig ID	1612_1.R1084
5'-most EST	LIB3433-032-P1-K1-H4

Seq. No.	386481
Contig ID	1620_1.R1084
5'-most EST	LIB3431-027-P1-N1-B9

Seq. No.	386482
Contig ID	1622_1.R1084
5'-most EST	uC-osflcyp082g01a1

Seq. No.	386483
Contig ID	1626_1.R1084
5'-most EST	LIB3431-027-P1-N1-C4
Method	BLASTX
NCBI GI	g1669341
BLAST score	281
E value	2.0e-24
Match length	182
% identity	40
NCBI Description	(D45066) AOBP (ascorbate oxidase promoter-binding protein) [Cucurbita maxima]

Seq. No.	386484
Contig ID	1628_1.R1084
5'-most EST	g426813

Seq. No.	386485
Contig ID	1629_1.R1084
5'-most EST	LIB3431-035-P1-N1-H12
Method	BLASTX
NCBI GI	g6063542
BLAST score	517
E value	2.0e-52
Match length	96

% identity	100
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	386486
Contig ID	1629_2.R1084
5'-most EST	LIB3479-003-Q6-K2-A12
Method	BLASTN
NCBI GI	g1245217
BLAST score	303
E value	1.0e-170
Match length	324
% identity	98
NCBI Description	Oryza sativa subsp. indica large ribosomal RNA gene, chloroplast gene encoding chloroplast rRNA, partial sequence

Seq. No.	386487
Contig ID	1631_1.R1084
5'-most EST	LIB3431-027-P1-N1-D1
Method	BLASTX
NCBI GI	g2244926
BLAST score	318
E value	5.0e-29
Match length	103
% identity	59
NCBI Description	(Z97339) glutaredoxin homolog [Arabidopsis thaliana]

Seq. No.	386488
Contig ID	1633_1.R1084
5'-most EST	g6062511

Seq. No.	386489
Contig ID	1643_1.R1084
5'-most EST	LIB3433-027-P1-K1-G9
Method	BLASTX
NCBI GI	g4678948
BLAST score	181
E value	6.0e-13
Match length	73
% identity	47
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	386490
Contig ID	1646_1.R1084
5'-most EST	LIB3431-049-P1-N1-E4

Seq. No.	386491
Contig ID	1648_1.R1084
5'-most EST	uC-osf1M202064d12a1
Method	BLASTX
NCBI GI	g451193
BLAST score	1069
E value	1.0e-117
Match length	254
% identity	84

NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.	386492
Contig ID	1648_2.R1084
5'-most EST	g3761990
Method	BLASTX
NCBI GI	g451193
BLAST score	484
E value	1.0e-52
Match length	266
% identity	34
NCBI Description	(L28008) wali7 [Triticum aestivum] >gi_1090845_prf__2019486B wali7 gene [Triticum aestivum]
Seq. No.	386493
Contig ID	1649_1.R1084
5'-most EST	LIB3431-027-P1-N1-E6
Method	BLASTX
NCBI GI	g5354158
BLAST score	440
E value	5.0e-83
Match length	226
% identity	66
NCBI Description	(AF149841) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_5354160_gb_AAD42379.1_AF149842_1 (AF149842) digalactosyldiacylglycerol synthase [Arabidopsis thaliana] >gi_6041825_gb_AAF02140.1_AC009918_12 (AC009918) digalactosyldiacylglycerol synthase [Arabidopsis thaliana]
Seq. No.	386494
Contig ID	1650_1.R1084
5'-most EST	LIB3431-031-P1-N1-G12
Method	BLASTX
NCBI GI	g729668
BLAST score	245
E value	3.0e-20
Match length	69
% identity	64
NCBI Description	HISTONE H1 >gi_2147479_pir__S65059 histone H1, drought-inducible - Lycopersicon pennellii >gi_436823 (U01890) Solanum pennellii histone H1 [Solanum pennellii]
Seq. No.	386495
Contig ID	1650_2.R1084
5'-most EST	LIB3431-060-P1-K1-A1
Seq. No.	386496
Contig ID	1653_1.R1084
5'-most EST	g4716778
Method	BLASTX
NCBI GI	g3328221
BLAST score	992
E value	1.0e-108
Match length	205
% identity	92
NCBI Description	(AF076920) thioredoxin peroxidase [Secale cereale]

Seq. No.	386497
Contig ID	1654_1.R1084
5'-most EST	LIB3431-017-P1-N1-C3
Method	BLASTX
NCBI GI	g2826842
BLAST score	143
E value	2.0e-17
Match length	75
% identity	60
NCBI Description	(AJ002236) loxc homologue [Lycopersicon pimpinellifolium]

Seq. No.	386498
Contig ID	1656_1.R1084
5'-most EST	g3768522

Seq. No.	386499
Contig ID	1657_1.R1084
5'-most EST	LIB3431-027-P1-N1-F2
Method	BLASTX
NCBI GI	g3204108
BLAST score	721
E value	3.0e-76
Match length	173
% identity	78
NCBI Description	(AJ006764) putative deoxycytidylate deaminase [Cicer arietinum]

Seq. No.	386500
Contig ID	1662_1.R1084
5'-most EST	LIB3431-027-P1-N1-F7

Seq. No.	386501
Contig ID	1664_1.R1084
5'-most EST	g6025096
Method	BLASTX
NCBI GI	g3913240
BLAST score	401
E value	7.0e-39
Match length	94
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D) >gi_2239151_emb_CAA71128_ (Y10022) CHLD magnesium chelatase subunit [Nicotiana tabacum]

Seq. No.	386502
Contig ID	1666_1.R1084
5'-most EST	LIB3431-027-P1-N1-G10

Seq. No.	386503
Contig ID	1669_1.R1084
5'-most EST	uC-osrocyp016c04b1

Seq. No.	386504
Contig ID	1670_1.R1084
5'-most EST	g3763721

Method	BLASTX
NCBI GI	g4753882
BLAST score	346
E value	1.0e-67
Match length	300
% identity	53
NCBI Description	(AL049754) putative aspartate aminotransferase [Streptomyces coelicolor]

Seq. No.	386505
Contig ID	1671_1.R1084
5'-most EST	g5007289
Method	BLASTX
NCBI GI	g2832672
BLAST score	575
E value	4.0e-59
Match length	129
% identity	84
NCBI Description	(AL021712) nifU-like protein [Arabidopsis thaliana]

Seq. No.	386506
Contig ID	1672_1.R1084
5'-most EST	g4715622

Seq. No.	386507
Contig ID	1674_1.R1084
5'-most EST	LIB3431-027-P1-N1-G7
Method	BLASTX
NCBI GI	g5453474
BLAST score	183
E value	2.0e-13
Match length	99
% identity	37
NCBI Description	(AF163054) meiotic DNA [illegible]ase/topoisomerase homolog variant B [M[illegible]_5453483_gb_AAD43592.1_ (AF163052) m[illegible] transesterase/topoisomerase homolog variant B [Mus musculus]

Seq. No.	386508
Contig ID	1675_1.R1084
5'-most EST	g2800643
Method	BLASTN
NCBI GI	g762924
BLAST score	49
E value	4.0e-18
Match length	67
% identity	93
NCBI Description	D.melanogaster mRNA for elastin-like protein

Seq. No.	386509
Contig ID	1675_2.R1084
5'-most EST	LIB3431-027-P1-N1-G8
Method	BLASTX
NCBI GI	g3763918
BLAST score	579
E value	2.0e-59
Match length	182

% identity	65
NCBI Description	(AC004450) putative isopropylmalate dehydratase [Arabidopsis thaliana]

Seq. No.	386510
Contig ID	1677_1.R1084
5'-most EST	g3762348

Seq. No.	386511
Contig ID	1680_1.R1084
5'-most EST	g4716618
Method	BLASTX
NCBI GI	g5777683
BLAST score	148
E value	7.0e-09
Match length	110
% identity	26
NCBI Description	(AL109989) hypothetical protein SCJ12.22 [Streptomyces coelicolor A3(2)]

Seq. No.	386512
Contig ID	1680_3.R1084
5'-most EST	g569295

Seq. No.	386513
Contig ID	1681_1.R1084
5'-most EST	g3763221
Method	BLASTX
NCBI GI	g4587571
BLAST score	419
E value	7.0e-41
Match length	104
% identity	74
NCBI Description	(AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No.	386514
Contig ID	1681_2.R1084
5'-most EST	uC-osroM202028c12b1
Method	BLASTX
NCBI GI	g4587571
BLAST score	267
E value	4.0e-44
Match length	154
% identity	55
NCBI Description	(AC006550) Belongs to the PF_01027 Uncharacterized protein family UPF0005 with 7 transmembrane domains. [Arabidopsis thaliana]

Seq. No.	386515
Contig ID	1685_1.R1084
5'-most EST	LIB3431-018-P1-N1-H2
Method	BLASTX
NCBI GI	g3881189
BLAST score	606
E value	1.0e-62

Match length	180
% identity	59
NCBI Description	(Z99281) similar to ADP-ribosylation factor; cDNA EST EMBL:C08179 comes from this gene; cDNA EST EMBL:C08337 comes from this gene; cDNA EST EMBL:C09829 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST y

Seq. No.	386516
Contig ID	1691_1.R1084
5'-most E.	LIB3431-011-P1-N1-G6
Method	BLASTX
NCBI GI	g3643602
BLAST score	495
E value	1.0e-49
Match length	172
% identity	56
NCBI Description	(AC005395) putative tonoplast intrinsic protein [Arabidopsis thaliana]

Seq. No.	386517
Contig ID	1692_1.R1084
5'-most EST	LIB3431-028-P1-N1-A3
Method	BLASTN
NCBI GI	g6015437
BLAST score	38
E value	1.0e-11
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386518
Contig ID	1697_1.R1084
5'-most EST	g3760289
Method	BLASTX
NCBI GI	g483410
BLAST score	421
E value	6.0e-41
Match length	128
% identity	70
NCBI Description	(L01496) calmodulin-binding protein [Zea mays]

Seq. No.	386519
Contig ID	1699_1.R1084
5'-most EST	LIB3431-028-P1-N1-B10
Method	BLASTX
NCBI GI	g5921187
BLAST score	209
E value	2.0e-16
Match length	65
% identity	57
NCBI Description	CYTOCHROME P450 71C2 >gi_550438_emb_CAA57423_ (X81829) cytochrome P450 [Zea mays] >gi_1870201_emb_CAA72208_ (Y11404) cytochrome p450 [Zea mays]

Seq. No.	386520
Contig ID	1702_1.R1084
5'-most EST	LIB3431-028-P1-N1-B2

Method	BLASTX
NCBI GI	g6002102
BLAST score	322
E value	1.0e-29
Match length	91
% identity	69
NCBI Description	(AJ249833) Acyl-CoA binding protein (ACBP) [Digitalis lanata]

Seq. No.	386521
Contig ID	1705_1.R1084
5'-most EST	g2311498

Seq. No.	386522
Contig ID	1705_3.R1084
5'-most EST	g5005149

Seq. No.	386523
Contig ID	1709_1.R1084
5'-most EST	g5667393
Method	BLASTX
NCBI GI	g5802955
BLAST score	236
E value	2.0e-19
Match length	102
% identity	45
NCBI Description	(AF178990) stress related protein [Vitis riparia]

Seq. No.	386524
Contig ID	1714_1.R1084
5'-most EST	g2800037

Seq. No.	386525
Contig ID	1719_1.R1084
5'-most EST	LIB3432-023-P1-K1-E6

Seq. No.	386526
Contig ID	1725_1.R1084
5'-most EST	LIB3431-028-P1-N1-D3

Seq. No.	386527
Contig ID	1729_1.R1084
5'-most EST	uC-osflcyp080d04a1

Seq. No.	386528
Contig ID	1733_1.R1084
5'-most EST	LIB3433-021-P1-K1-B10

Seq. No.	386529
Contig ID	1734_1.R1084
5'-most EST	LIB3433-061-P1-K1-E9

Seq. No.	386530
Contig ID	1735_1.R1084
5'-most EST	g3767719
Method	BLASTX
NCBI GI	g2633727

BLAST score	274
E value	1.0e-23
Match length	176
% identity	35
NCBI Description	(Z99111) ykrT [Bacillus subtilis]

Seq. No.	386531
Contig ID	1738_1.R1084
5'-most EST	LIB3431-028-P1-N1-E5
Method	BLASTX
NCBI GI	g836954
BLAST score	516
E value	3.0e-52
Match length	196
% identity	55
NCBI Description	(U20948) receptor protein kinase [Ipomoea trifida]

Seq. No.	386532
Contig ID	1742_1.R1084
5'-most EST	LIB3431-028-P1-N1-E9
Method	BLASTX
NCBI GI	g2144098
BLAST score	416
E value	4.0e-40
Match length	230
% identity	40
NCBI Description	SC2 - rat >gi_256994_bbs_115268 (S45663) SC2=synaptic glycoprotein [rats, brain, Peptide, 308 aa] [Rattus sp.]

Seq. No.	386533
Contig ID	1743_1.R1084
5'-most EST	uC-osflcyp135a07a1

Seq. No.	386534
Contig ID	1748_1.R1084
5'-most EST	g2800021
Method	BLASTX
NCBI GI	g1019946
BLAST score	1064
E value	1.0e-116
Match length	291
% identity	70
NCBI Description	(U37060) ascorbate peroxidase [Gossypium hirsutum]

Seq. No.	386535
Contig ID	1752_1.R1084
5'-most EST	g4715902
Method	BLASTX
NCBI GI	g3858935
BLAST score	602
E value	6.0e-62
Match length	224
% identity	51
NCBI Description	(AL021636) synaptobrevin-like protein [Arabidopsis thaliana] >gi_4103357 (AF025332) vesicle-associated membrane protein 7C; synaptobrevin 7C [Arabidopsis thaliana]

Seq. No.	386536
Contig ID	1753_1.R1084
5'-most EST	LIB3431-002-P1-N1-G12
Method	BLASTX
NCBI GI	g3033382
BLAST score	479
E value	8.0e-48
Match length	146
% identity	60
NCBI Description	(AC004238) unknown protein [Arabidopsis thaliana]

Seq. No.	386537
Contig ID	1764_1.R1084
5'-most EST	LIB3431-028-P1-N1-G7
Method	BLASTX
NCBI GI	g1350522
BLAST score	223
E value	8.0e-18
Match length	86
% identity	52
NCBI Description	(L47115) late embryogenesis abundant protein [Picea glauca]

Seq. No.	386538
Contig ID	1765_1.R1084
5'-most EST	LIB3432-013-P1-K1-G5
Method	BLASTX
NCBI GI	g2565305
BLAST score	2235
E value	0.0e+00
Match length	644
% identity	84
NCBI Description	(AF024589) glycine decarboxylase P subunit [Hordeum sp. x Triticum sp.]

Seq. No.	386539
Contig ID	1765_2.R1084
5'-most EST	uC-osflcyp132d05a1
Method	BLASTX
NCBI GI	g4760545
BLAST score	191
E value	5.0e-14
Match length	46
% identity	85
NCBI Description	(AB019492) IDN4-GGTR14 [Homo sapiens]

Seq. No.	386540
Contig ID	1765_3.R1084
5'-most EST	g4714154
Method	BLASTX
NCBI GI	g4512675
BLAST score	1385
E value	1.0e-154
Match length	303
% identity	86
NCBI Description	(AC006931) putative citrate synthase [Arabidopsis thaliana]

Seq. No.	386541
Contig ID	1765_4.R1084
5'-most EST	g2798577
Method	BLASTX
NCBI GI	g710308
BLAST score	183
E value	4.0e-13
Match length	35
% identity	94
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	386542
Contig ID	1765_5.R1084
5'-most EST	LIB3431-018-P1-N1-H12

Seq. No.	386543
Contig ID	1765_7.R1084
5'-most EST	LIB3432-060-P1-K1-F12
Method	BLASTX
NCBI GI	g710308
BLAST score	793
E value	7.0e-85
Match length	169
% identity	92
NCBI Description	(U11693) victorin binding protein [Avena sativa]

Seq. No.	386544
Contig ID	1767_1.R1084
5'-most EST	LIB3431-028-P1-N1-H1
Method	BLASTX
NCBI GI	g586038
BLAST score	355
E value	6.0e-55
Match length	192
% identity	63
NCBI Description	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN, CHLOROPLAST PRECURSOR (SRP54) (54 CHLOROPLAST PROTEIN) (54CP) (FFC) >gi_480296_pir__S36637 signal recognition particle 54CP protein precursor - Arabidopsis thaliana >gi_396701_emb_CAA79981.1_ (Z21970) 54CP [Arabidopsis thaliana]

Seq. No.	386545
Contig ID	1777_1.R1084
5'-most EST	LIB3431-028-P1-N1-H8
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	47
% identity	65
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	386546
Contig ID	1780_1.R1084
5'-most EST	g2431252
Method	BLASTX

NCBI GI	g2982362
BLAST score	811
E value	1.0e-86
Match length	170
% identity	88
NCBI Description	(AF053311) glutathione peroxidase [Zantedeschia aethiopica]

Seq. No.	386547
Contig ID	1782_1.R1084
5'-most EST	g5038702

Seq. No.	386548
Contig ID	1785_1.R1084
5'-most EST	LIB3431-029-P1-N1-A4
Method	BLASTX
NCBI GI	g3522941
BLAST score	231
E value	5.0e-19
Match length	50
% identity	86
NCBI Description	(AC004411) putative peptide chain release factor [Arabidopsis thaliana]

Seq. No.	386549
Contig ID	1791_1.R1084
5'-most EST	g3763560
Method	BLASTX
NCBI GI	g3292814
BLAST score	683
E value	1.0e-71
Match length	182
% identity	73
NCBI Description	(AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	386550
Contig ID	1791_2.R1084
5'-most EST	LIB3432-041-P1-K1-B8
Method	BLASTX
NCBI GI	g4586101
BLAST score	408
E value	1.0e-39
Match length	129
% identity	65
NCBI Description	(AL049638) putative protein [Arabidopsis thaliana]

Seq. No.	386551
Contig ID	1794_1.R1084
5'-most EST	g4715132
Method	BLASTX
NCBI GI	g2129636
BLAST score	633
E value	1.0e-65
Match length	336
% identity	39
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	386552
Contig ID	1799_1.R1084
5'-most EST	LIB3431-029-P1-N1-B6
Method	BLASTX
NCBI GI	g3608147
BLAST score	225
E value	3.0e-18
Match length	160
% identity	36
NCBI Description	(AC005314) putative chloroplast 31 kDa ribonucleoprotein precursor [Arabidopsis thaliana]

Seq. No.	386553
Contig ID	1800_1.R1084
5'-most EST	g3758928

Seq. No.	386554
Contig ID	1802_1.R1084
5'-most EST	LIB3431-062-P1-N1-D6
Method	BLASTX
NCBI GI	g2498397
BLAST score	250
E value	3.0e-21
Match length	56
% identity	82
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, VARIABLE CHAIN (FTR-V) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT A) (FTR-A)

Seq. No.	386555
Contig ID	1808_1.R1084
5'-most EST	g3760839
Method	BLASTX
NCBI GI	g2244797
BLAST score	266
E value	1.0e-22
Match length	163
% identity	38
NCBI Description	(Z97336) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386556
Contig ID	1809_1.R1084
5'-most EST	LIB3432-010-P1-K1-G12
Method	BLASTX
NCBI GI	g1001253
BLAST score	222
E value	9.0e-18
Match length	130
% identity	39
NCBI Description	(D64003) hypothetical protein [Synechocystis sp.]

Seq. No.	386557
Contig ID	1813_1.R1084
5'-most EST	LIB3431-029-P1-N1-D10
Method	BLASTX
NCBI GI	g5923674
BLAST score	416
E value	5.0e-65

Match length	173
% identity	75
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]

Seq. No.	386558
Contig ID	1821_1.R1084
5'-most EST	LIB3431-029-P1-N1-D7
Method	BLASTX
NCBI GI	g2760327
BLAST score	273
E value	1.0e-23
Match length	[illegible]
% identity	
NCBI Description	[illegible] F1N21.12 [Arabidopsis thaliana]

Seq. No.	386559
Contig ID	1823_1.R1084
5'-most EST	LIB3431-029-P1-N[illegible]
Method	BLASTX
NCBI GI	g4038034
BLAST score	222
E value	5.0e-19
Match length	76
% identity	
NCBI Descr[illegible]	[illegible]aliana]

Seq [illegible]	386560
Cont[illegible]	1827_1.R1084
5'-mo[illegible] EST	LIB3431-029-P1-N1-E3

Seq. No.	
Contig ID	
5'-mo[illegible]	
Met[illegible]	BLAS[illegible]
NCBI	g4539330
BLAST [illegible]core	413
E value	5.0e-40
Match length	140
% identity	59
NCBI Description	(AL035679) putative receptor-like protein kinase (fragment) [Arabidopsis thaliana]

Seq. No.	386562
Contig ID	1848_1.R1084
5'-most EST	g5038666
Method	BLASTX
NCBI GI	g4406764
BLAST score	149
E value	2.0e-09
Match length	71
% identity	52
NCBI Description	(AC006836) putative uridylyl transferase [Arabidopsis thaliana]

Seq. No.	386563
Contig ID	1852_1.R1084
5'-most EST	g2801187

Seq. No.	386564
Contig ID	1854_1.R1084
5'-most EST	g4714360
Method	BLASTX
NCBI GI	g2982243
BLAST score	448
E value	3.0e-44
Match length	142
% identity	61
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	386565
Contig ID	1854_2.R1084
5'-most EST	LIB3477-009-P1-K1-H8
Method	BLASTX
NCBI GI	g2982243
BLAST score	257
E value	7.0e-22
Match length	89
% identity	56
NCBI Description	(AF051204) hypothetical protein [Picea mariana]

Seq. No.	386566
Contig ID	1858_1.R1084
5'-most EST	LIB3431-029-P1-N1-H1
Method	BLASTX
NCBI GI	g3980400
BLAST score	783
E value	3.0e-83
Match length	263
% identity	59
NCBI Description	(AC004561) putative tropinone reductase [Arabidopsis thaliana]

Seq. No.	386567
Contig ID	1860_1.R1084
5'-most EST	uC-osf1cyp050e10b1

Seq. No.	386568
Contig ID	1861_1.R1084
5'-most EST	g4716535
Method	BLASTX
NCBI GI	g2191138
BLAST score	394
E value	8.0e-38
Match length	91
% identity	79
NCBI Description	(AF007269) A_IG002N01.18 gene product [Arabidopsis thaliana]

Seq. No.	386569
Contig ID	1871_1.R1084
5'-most EST	LIB3431-050-P1-N1-G9

Seq. No.	386570
Contig ID	1874_1.R1084

5'-most EST	g5003744
Method	BLASTX
NCBI GI	g3334323
BLAST score	435
E value	1.0e-77
Match length	190
% identity	79
NCBI Description	GTP-BINDING PROTEIN SAR1A >gi_1314860 (U56929) Sar1 homolog [Arabidopsis thaliana] >gi_2104532_gb_AAC78700.1_ (AF001308) SAR1/GTP-binding secretory factor [Arabidopsis thaliana] >gi_2104550 (AF001535) AGAA.4 [Arabidopsis thaliana]

Seq. No.	386571
Contig ID	1874_2.R1084
5'-most EST	g5816528
Method	BLASTN
NCBI GI	g5922603
BLAST score	84
E value	5.0e-39
Match length	255
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	386572
Contig ID	1874_3.R1084
5'-most EST	LIB3434-034-P1-K1-D2
Method	BLASTX
NCBI GI	g5922611
BLAST score	722
E value	3.0e-76
Match length	194
% identity	76
NCBI Description	(AP000492) ESTs AU078117(E1380),C72293(E1380) correspond to a region of the predicted gene.; similar to SAR1/GTP-binding secretory factor. (AF001308) [Oryza sativa]

Seq. No.	386573
Contig ID	1880_1.R1084
5'-most EST	uC-osf1cyp152a07a1
Method	BLASTX
NCBI GI	g2344897
BLAST score	269
E value	2.0e-23
Match length	92
% identity	57
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	386574
Contig ID	1881_1.R1084
5'-most EST	g3767707
Method	BLASTX
NCBI GI	g2832681
BLAST score	493
E value	2.0e-49
Match length	104

% identity	84
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	386575
Contig ID	1881_2.R1084
5'-most EST	g4714176
Method	BLASTX
NCBI GI	g2832681
BLAST score	491
E value	3.0e-49
Match length	104
% identity	84
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	386576
Contig ID	1881_3.R1084
5'-most EST	LIB3433-012-Q6-K1-D5
Method	BLASTX
NCBI GI	g2832681
BLAST score	399
E value	1.0e-38
Match length	90
% identity	78
NCBI Description	(AL021712) putative protein [Arabidopsis thaliana]

Seq. No.	386577
Contig ID	1883_1.R1084
5'-most EST	LIB3431-038-P1-N1-G11
Method	BLASTN
NCBI GI	g5734616
BLAST score	401
E value	0.0e+00
Match length	499
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	386578
Contig ID	1894_1.R1084
5'-most EST	LIB3431-014-P1-N1-H12

Seq. No.	386579
Contig ID	1897_1.R1084
5'-most EST	LIB3431-030-P1-N1-C8
Method	BLASTX
NCBI GI	g3776581
BLAST score	350
E value	5.0e-33
Match length	118
% identity	58
NCBI Description	(AC005388) Similar to Beta integral membrane protein homolog gb_U43629 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	386580
Contig ID	1901_1.R1084
5'-most EST	g2431296
Method	BLASTX
NCBI GI	g1488297

BLAST score	789
E value	1.0e-110
Match length	397
% identity	55
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	386581
Contig ID	1901_2.R1084
5'-most EST	LIB3431-061-P1-K1-D1

Seq. No.	386582
Contig ID	1901_4.R1084
5'-most EST	g428978
Method	BLASTX
NCBI GI	g1488297
BLAST score	319
E value	2.0e-29
Match length	93
% identity	66
NCBI Description	(U63530) osRAD23 [Oryza sativa]

Seq. No.	386583
Contig ID	1907_1.R1084
5'-most EST	uC-osflcyp099c08a1
Method	BLASTX
NCBI GI	g1362066
BLAST score	841
E value	4.0e-90
Match length	201
% identity	84
NCBI Description	small GTP-binding protein - garden pea >gi_871510_emb_CAA90080_ (Z49900) small GTP-binding protein [Pisum sativum]

Seq. No.	386584
Contig ID	1907_2.R1084
5'-most EST	uC-osrocyp036a09a1
Method	BLASTX
NCBI GI	g5669640
BLAST score	778
E value	1.0e-82
Match length	181
% identity	86
NCBI Description	(AF096249) ethylene-responsive small GTP-binding protein [Lycopersicon esculentum]

Seq. No.	386585
Contig ID	1909_1.R1084
5'-most EST	g2311063
Method	BLASTX
NCBI GI	g4586021
BLAST score	324
E value	7.0e-30
Match length	73
% identity	78
NCBI Description	(AC007170) putative cytoplasmic aconitate hydratase [Arabidopsis thaliana]

Seq. No.	386586
Contig ID	1913_1.R1084
5'-most EST	uC-osflcyp055h09a1
Method	BLASTX
NCBI GI	g1709619
BLAST score	1242
E value	1.0e-174
Match length	450
% identity	47
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_2146814_pir__S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No.	386587
Contig ID	1913_2.R1084
5'-most EST	g4715735
Method	BLASTX
NCBI GI	g3334320
BLAST score	620
E value	4.0e-64
Match length	148
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	386588
Contig ID	1913_3.R1084
5'-most EST	g3763815
Method	BLASTX
NCBI GI	g3551245
BLAST score	1054
E value	1.0e-115
Match length	293
% identity	72
NCBI Description	(AB012702) P40-like protein [Daucus carota]

Seq. No.	386589
Contig ID	1913_4.R1084
5'-most EST	uC-osrocyp011h07a1

Seq. No.	386590
Contig ID	1913_5.R1084
5'-most EST	g2800047

Seq. No.	386591
Contig ID	1913_6.R1084
5'-most EST	uC-osflcyp174f06b1
Method	BLASTX
NCBI GI	g3334320
BLAST score	667
E value	1.0e-106
Match length	247
% identity	78
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	386592
Contig ID	1913_8.R1084
5'-most EST	LIB3475-007-P1-K1-E12
Method	BLASTX
NCBI GI	g3334320
BLAST score	686
E value	2.0e-72
Match length	137
% identity	96
NCBI Description	40S RIBOSOMAL PROTEIN SA (P40) >gi_2444420 (AF020553) ribosome-associated protein p40 [Glycine max]

Seq. No.	386593
Contig ID	1913_12.R1084
5'-most EST	LIB3434-051-P1-K1-E3
Method	BLASTX
NCBI GI	g1709619
BLAST score	498
E value	4.0e-50
Match length	145
% identity	44
NCBI Description	PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) >gi_2146814_pir__S69181 protein disulfide isomerase (EC 5.3.4.1) precursor - maize >gi_625148 (L39014) protein disulfide isomerase [Zea mays]

Seq. No.	386594
Contig ID	1915_1.R1084
5'-most EST	LIB3431-030-P1-N1-E3

Seq. No.	386595
Contig ID	1918_1.R1084
5'-most EST	uC-osrocyp025d05a1

Seq. No.	386596
Contig ID	1919_1.R1084
5'-most EST	uC-osflcyp160b12a1
Method	BLASTX
NCBI GI	g5802606
BLAST score	2278
E value	0.0e+00
Match length	586
% identity	91
NCBI Description	(AF174486) methylenetetrahydrofolate reductase [Zea mays]

Seq. No.	386597
Contig ID	1924_1.R1084
5'-most EST	g3759818
Method	BLASTX
NCBI GI	g1587206
BLAST score	827
E value	1.0e-177
Match length	390
% identity	86
NCBI Description	T complex protein [Cucumis sativus]

Seq. No.	386598
Contig ID	1925_1.R1084
5'-most EST	g5038781
Method	BLASTX
NCBI GI	g5053118
BLAST score	741
E value	1.0e-78
Match length	199
% identity	72
NCBI Description	(AF156695) inorganic phosphate transporter [Solanum tuberosum]

Seq. No.	386599
Contig ID	1926_1.R1084
5'-most EST	LIB3431-030-P1-N1-F5
Method	BLASTX
NCBI GI	g4929208
BLAST score	574
E value	7.0e-59
Match length	140
% identity	79
NCBI Description	(AF143501) delta-9-stearoyl desaturase [Elaeis guineensis var. tenera]

Seq. No.	386600
Contig ID	1932_1.R1084
5'-most EST	LIB3431-030-P1-N1-G10

Seq. No.	386601
Contig ID	1933_1.R1084
5'-most EST	LIB3431-030-P1-N1-G11
Method	BLASTX
NCBI GI	g4185499
BLAST score	157
E value	4.0e-23
Match length	204
% identity	34
NCBI Description	(AF096095) fertilization-independent seed 2 protein [Arabidopsis thaliana] >gi_4185501 (AF096096) fertilization-independent seed 2 protein [Arabidopsis thaliana]

Seq. No.	386602
Contig ID	1935_1.R1084
5'-most EST	LIB3431-030-P1-N1-G2

Seq. No.	386603
Contig ID	1936_1.R1084
5'-most EST	g4716829

Seq. No.	386604
Contig ID	1939_1.R1084
5'-most EST	g2797386
Method	BLASTX
NCBI GI	g2316016
BLAST score	198
E value	3.0e-18

Match length	86
% identity	60
NCBI Description	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq. No.	386605
Contig ID	1940_1.R1084
5'-most EST	uC-osroM202006e07b1

Seq. No.	386606
Contig ID	1948_1.R1084
5'-most EST	LIB3431-030-P1-N1-H4
Method	BLASTX
NCBI GI	g1911774
BLAST score	177
E value	2.0e-12
Match length	81
% identity	37
NCBI Description	(S83364) putative Rab5-interacting protein {clone L1-57} [human, HeLa cells, Peptide Partial, 122 aa] [Homo sapiens]

Seq. No.	386607
Contig ID	1948_2.R1084
5'-most EST	g428775

Seq. No.	386608
Contig ID	1954_1.R1084
5'-most EST	g2797766

Seq. No.	386609
Contig ID	1962_1.R1084
5'-most EST	LIB3475-007-P1-K1-B8
Method	BLASTX
NCBI GI	g4914452
BLAST score	853
E value	2.0e-91
Match length	265
% identity	62
NCBI Description	(AL050398) putative protein [Arabidopsis thaliana]

Seq. No.	386610
Contig ID	1962_2.R1084
5'-most EST	LIB3431-006-P1-K1-A9
Method	BLASTX
NCBI GI	g4914452
BLAST score	444
E value	4.0e-44
Match length	132
% identity	51
NCBI Description	(AL050398) putative protein [Arabidopsis thaliana]

Seq. No.	386611
Contig ID	1968_1.R1084
5'-most EST	LIB3431-031-P1-N1-B12

Seq. No.	386612
Contig ID	1969_1.R1084
5'-most EST	LIB3431-031-P1-N1-B5

Method	BLASTX
NCBI GI	g4753651
BLAST score	625
E value	1.0e-87
Match length	206
% identity	79
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	386613
Contig ID	1969_2.R1084
5'-most EST	g4716117
Method	BLASTX
NCBI GI	g4753651
BLAST score	829
E value	1.0e-88
Match length	206
% identity	75
NCBI Description	(AL049751) ribosomal protein L13a like protein [Arabidopsis thaliana]

Seq. No.	386614
Contig ID	1983_1.R1084
5'-most EST	g3761230

Seq. No.	386615
Contig ID	1987_1.R1084
5'-most EST	uC-osflcyp070a02a1
Method	BLASTX
NCBI GI	g4567247
BLAST score	230
E value	6.0e-37
Match length	186
% identity	46
NCBI Description	(AC007070) unknown protein [Arabidopsis thaliana]

Seq. No.	386616
Contig ID	1988_1.R1084
5'-most EST	g3762142

Seq. No.	386617
Contig ID	1990_1.R1084
5'-most EST	g3761030
Method	BLASTX
NCBI GI	g5669656
BLAST score	246
E value	1.0e-23
Match length	103
% identity	59
NCBI Description	(AF096263) ER33 protein [Lycopersicon esculentum]

Seq. No.	386618
Contig ID	1998_1.R1084
5'-most EST	uC-osrocyp034f07a1
Method	BLASTX
NCBI GI	g1076422
BLAST score	229

E value	2.0e-18
Match length	85
% identity	60
NCBI Description	transcription factor OBF4 - Arabidopsis thaliana >gi_414613_emb_CAA49524_ (X69899) ocs-element binding factor 4 [Arabidopsis thaliana]

Seq. No.	386619
Contig ID	1999_1.R1084
5'-most EST	g3767229
Method	BLASTX
NCBI GI	g133019
BLAST score	268
E value	1.0e-33
Match length	130
% identity	54
NCBI Description	60S RIBOSOMAL PROTEIN L7 >gi_71122_pir__R5DO7 ribosomal protein L7 - slime mold (Dictyostelium discoideum) >gi_7357_emb_CAA33035_ (X14909) ribosomal protein L7 (AA 1 - 246) [Dictyostelium discoideum]

Seq. No.	386620
Contig ID	2000_1.R1084
5'-most EST	g2427463
Method	BLASTX
NCBI GI	g4502881
BLAST score	220
E value	2.0e-17
Match length	177
% identity	33
NCBI Description	chloride intracellular channel 1 >gi_3121852_sp_O00299_CLI1_HUMAN CHLORIDE INTRACELLULAR CHANNEL PROTEIN 1 (NUCLEAR CHLORIDE ION CHANNEL 27) (P64 CLCP) >gi_2073569 (U93205) nuclear chloride ion channel protein [Homo sapiens] >gi_4588526_gb_AAD26137.1_AF109197_1 (AF109197) nuclear chloride channel [Homo sapiens]

Seq. No.	386621
Contig ID	2000_2.R1084
5'-most EST	g5003532
Method	BLASTX
NCBI GI	g895845
BLAST score	153
E value	1.0e-09
Match length	94
% identity	38
NCBI Description	(X87689) putative start codon [Homo sapiens]

Seq. No.	386622
Contig ID	2013_1.R1084
5'-most EST	LIB3431-031-P1-N1-F4

Seq. No.	386623
Contig ID	2016_1.R1084
5'-most EST	LIB3431-031-P1-N1-F7

Seq. No.	386624

Contig ID	2017_1.R1084
5'-most EST	g1944315
Method	BLASTX
NCBI GI	g4507223
BLAST score	942
E value	1.0e-102
Match length	307
% identity	61
NCBI Description	signal recognition particle receptor ('docking protein') >gi_134892_sp_P08240_SRPR_HUMAN SIGNAL RECOGNITION PARTICLE RECEPTOR ALPHA SUBUNIT (SR-ALPHA) (DOCKING PROTEIN ALPHA) (DP-ALPHA) >gi_88607_pir__A29440 signal recognition particle receptor - human >gi_30866_emb_CAA29608_ (X06272) docking protein [Homo sapiens]

Seq. No.	386625
Contig ID	2017_2.R1084
5'-most EST	g2799012
Method	BLASTX
NCBI GI	g2911886
BLAST score	262
E value	2.0e-22
Match length	89
% identity	62
NCBI Description	(AF047663) Contains similarity to Pfam domain: PF00448 (SRP54), Score=14.7, E-value=2.7e-12, N=1 [Caenorhabditis elegans]

Seq. No.	386626
Contig ID	2019_1.R1084
5'-most EST	g4714760
Method	BLASTX
NCBI GI	g3024871
BLAST score	417
E value	6.0e-52
Match length	387
% identity	37
NCBI Description	HYPOTHETICAL 77.3 KD PROTEIN SLL0005 >gi_1001579_dbj_BAA10206_ (D64000) ABC1-like [Synechocystis sp.]

Seq. No.	386627
Contig ID	2031_1.R1084
5'-most EST	LIB3474-008-P1-K1-G10

Seq. No.	386628
Contig ID	2037_1.R1084
5'-most EST	g3761256
Method	BLASTX
NCBI GI	g4587556
BLAST score	231
E value	6.0e-19
Match length	60
% identity	72
NCBI Description	(AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene.

[Arabidopsis thaliana]

Seq. No.	386629
Contig ID	2047_1.R1084
5'-most EST	LIB3431-045-P1-N1-F11
Method	BLASTX
NCBI GI	g5733866
BLAST score	1084
E value	1.0e-118
Match length	302
% identity	68
NCBI Description	(AC007932) Contains similarity to gb_M73488 1-aminocyclopropane-1-carboxylate deaminase from Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from this gene. [Arabidopsis thaliana]

Seq. No.	386630
Contig ID	2047_3.R1084
5'-most EST	LIB3477-009-P1-K1-E3
Method	BLASTX
NCBI GI	g5733866
BLAST score	250
E value	3.0e-21
Match length	69
% identity	70
NCBI Description	(AC007932) Contains similarity to gb_M73488 1-aminocyclopropane-1-carboxylate deaminase from Pseudomonas sp. ESTs gb_Z18033 and gb_Z34214 come from this gene. [Arabidopsis thaliana]

Seq. No.	386631
Contig ID	2050_1.R1084
5'-most EST	g4714703

Seq. No.	386632
Contig ID	2051_1.R1084
5'-most EST	g5005315

Seq. No.	386633
Contig ID	2053_1.R1084
5'-most EST	LIB3431-033-P1-N1-B2

Seq. No.	386634
Contig ID	2054_1.R1084
5'-most EST	LIB3431-033-P1-K1-B3

Seq. No.	386635
Contig ID	2056_1.R1084
5'-most EST	g3761219
Method	BLASTX
NCBI GI	g1421730
BLAST score	326
E value	4.0e-30
Match length	65
% identity	94
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	386636
Contig ID	2057_1.R1084
5'-most EST	LIB3431-033-P1-N1-B6
Method	BLASTX
NCBI GI	g3212854
BLAST score	598
E value	2.0e-61
Match length	294
% identity	54
NCBI Description	(AC004005) unknown protein [Arabidopsis thaliana]

Seq. No.	386637
Contig ID	2058_1.R1084
5'-most EST	g3761558
Method	BLASTX
NCBI GI	g1345977
BLAST score	647
E value	2.0e-67
Match length	141
% identity	84
NCBI Description	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 >gi_904154 (L43921) microsomal omega-6 desaturase [Glycine max]

Seq. No.	386638
Contig ID	2059_1.R1084
5'-most EST	LIB3431-033-P1-K1-B8

Seq. No.	386639
Contig ID	2061_1.R1084
5'-most EST	g3768516

Seq. No.	386640
Contig ID	2062_1.R1084
5'-most EST	LIB3431-033-P1-K1-C11
Method	BLASTX
NCBI GI	g3281853
BLAST score	231
E value	4.0e-19
Match length	90
% identity	51
NCBI Description	(AL031004) putative protein [Arabidopsis thaliana]

Seq. No.	386641
Contig ID	2065_1.R1084
5'-most EST	g2799023
Method	BLASTX
NCBI GI	g2529342
BLAST score	196
E value	1.0e-14
Match length	67
% identity	64
NCBI Description	(L76554) transketolase [Spinacia oleracea]

Seq. No.	386642
Contig ID	2065_2.R1084
5'-most EST	uC-osf1M202073e08a1

Method	BLASTX
NCBI GI	g2501353
BLAST score	1531
E value	1.0e-171
Match length	487
% identity	81
NCBI Description	TRANSKETOLASE, CHLOROPLAST (TK) >gi_1084440_pir__S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) >gi_664901_emb_CAA86607_ (Z46646) transketolase [Craterostigma plantagineum]

Seq. No.	386643
Contig ID	2071_1.R1084
5'-most EST	g3768725
Method	BLASTX
NCBI GI	g5921663
BLAST score	1118
E value	1.0e-122
Match length	256
% identity	81
NCBI Description	(AF162279) 10-formyltetrahydrofolate synthetase [Arabidopsis thaliana]

Seq. No.	386644
Contig ID	2073_1.R1084
5'-most EST	uC-osflM202064h07a1
Method	BLASTX
NCBI GI	g120900
BLAST score	174
E value	2.0e-26
Match length	338
% identity	30
NCBI Description	GALACTOKINASE >gi_421585_pir__A47032 galactokinase galK - Lactobacillus helveticus >gi_44000_emb_CAA40525_ (X57248) galactokinase [Lactobacillus helveticus]

Seq. No.	386645
Contig ID	2073_3.R1084
5'-most EST	g3761407

Seq. No.	386646
Contig ID	2077_1.R1084
5'-most EST	LIB3431-033-P1-N1-D3

Seq. No.	386647
Contig ID	2078_1.R1084
5'-most EST	g3768489
Method	BLASTX
NCBI GI	g5729802
BLAST score	676
E value	6.0e-71
Match length	142
% identity	84
NCBI Description	similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p homolog [Homo sapiens]

Seq. No. 386648

Contig ID	2078_2.R1084
5'-most EST	g3767057
Method	BLASTX
NCBI GI	g5729802
BLAST score	516
E value	4.0e-52
Match length	143
% identity	67
NCBI Description	similar to S. pombe dim1+ >gi_2565275 (AF023611) Dim1p homolog [Homo sapiens]

Seq. No.	386649
Contig ID	2081_1.R1084
5'-most EST	LIB3431-033-P1-N1-D7
Method	BLASTX
NCBI GI	g5923670
BLAST score	179
E value	4.0e-13
Match length	72
% identity	50
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]

Seq. No.	386650
Contig ID	2082_1.R1084
5'-most EST	g5005229
Method	BLASTX
NCBI GI	g3885513
BLAST score	274
E value	8.0e-24
Match length	70
% identity	64
NCBI Description	(AF084201) similar to chloroplast 50S ribosomal protein L31 [Medicago sativa]

Seq. No.	386651
Contig ID	2084_1.R1084
5'-most EST	LIB3431-033-P1-N1-E1

Seq. No.	386652
Contig ID	2096_1.R1084
5'-most EST	LIB3431-033-P1-N1-F1
Method	BLASTX
NCBI GI	g3249064
BLAST score	456
E value	7.0e-51
Match length	168
% identity	59
NCBI Description	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb_2245136 from A. thaliana chromosome 4 contig gb_Z97344. [Arabidopsis thaliana]

Seq. No.	386653
Contig ID	2099_1.R1084
5'-most EST	g3758984

Seq. No.	386654
Contig ID	2100_1.R1084

5'-most EST	g3762372
Seq. No.	386655
Contig ID	2101_1.R1084
5'-most EST	LIB3431-033-P1-K1-F3
Seq. No.	386656
Contig ID	2103_1.R1084
5'-most EST	g2800527
Seq. No.	386657
Contig ID	2103_2.R1084
5'-most EST	g3761138
Method	BLASTX
NCBI GI	g5669924
BLAST score	913
E value	2.0e-98
Match length	199
% identity	85
NCBI Description	(AF149116) soluble inorganic pyrophosphatase [Populus tremula x Populus tremuloides]
Seq. No.	386658
Contig ID	2103_3.R1084
5'-most EST	g2798571
Method	BLASTN
NCBI GI	g619119
BLAST score	97
E value	7.0e-47
Match length	135
% identity	92
NCBI Description	Calothrix D253 genomic DNA (clone AG5R)
Seq. No.	386659
Contig ID	2104_1.R1084
5'-most EST	g2317535
Method	BLASTX
NCBI GI	g4914373
BLAST score	285
E value	2.0e-25
Match length	87
% identity	56
NCBI Description	(AC007584) putative protein kinase [Arabidopsis thaliana]
Seq. No.	386660
Contig ID	2104_2.R1084
5'-most EST	LIB3431-033-P1-K1-F6
Seq. No.	386661
Contig ID	2111_1.R1084
5'-most EST	g5002999
Method	BLASTX
NCBI GI	g3928869
BLAST score	236
E value	5.0e-19
Match length	304
% identity	26

NCBI Description	(AF093420) Hsp70 binding protein HspBP1 [Homo sapiens]

Seq. No.	386662
Contig ID	2114_1.R1084
5'-most EST	LIB3431-056-P1-N1-F9
Method	BLASTX
NCBI GI	g4836892
BLAST score	1070
E value	1.0e-117
Match length	305
% identity	35
NCBI Description	(AC007369) Putative RNA helicase [Arabidopsis thaliana]

Seq. No.	386663
Contig ID	2115_1.R1084
5'-most EST	LIB3431-033-P1-N1-G5

Seq. No.	386664
Contig ID	2119_1.R1084
5'-most EST	g5002746
Method	BLASTX
NCBI GI	g3184098
BLAST score	667
E value	1.0e-81
Match length	303
% identity	52
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	386665
Contig ID	2119_2.R1084
5'-most EST	g4715941
Method	BLASTX
NCBI GI	g3184098
BLAST score	270
E value	8.0e-26
Match length	193
% identity	45
NCBI Description	(AL023777) coenzyme a synthetase [Schizosaccharomyces pombe]

Seq. No.	386666
Contig ID	2121_1.R1084
5'-most EST	LIB3431-033-P1-N1-H11

Seq. No.	386667
Contig ID	2122_1.R1084
5'-most EST	LIB3431-033-P1-N1-H12
Method	BLASTX
NCBI GI	g1170745
BLAST score	528
E value	1.0e-53
Match length	151
% identity	62
NCBI Description	LATE EMBRYOGENESIS ABUNDANT PROTEIN LEA14-A >gi_167326 (M88321) Group 4 late embryogenesis-abundant protein [Gossypium hirsutum] >gi_167328 (M88322) Group 4 late

embryogenesis-abundant protein [Gossypium hirsutum]

Seq. No.	386668
Contig ID	2131_1.R1084
5'-most EST	g3767618
Method	BLASTX
NCBI GI	g417745
BLAST score	2348
E value	0.0e+00
Match length	483
% identity	93
NCBI Description	ADENOSYLHOMOCYSTEINASE (S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE) (ADOHCYASE) >gi_170773 (L11872) S-adenosyl-L-homocysteine hydrolase [Triticum aestivum]

Seq. No.	386669
Contig ID	2131_2.R1084
5'-most EST	g3761653
Method	BLASTX
NCBI GI	g2160322
BLAST score	621
E value	9.0e-68
Match length	150
% identity	88
NCBI Description	(D16139) cytokinin binding protein CBP57 [Nicotiana sylvestris]

Seq. No.	386670
Contig ID	2134_1.R1084
5'-most EST	g5803474
Method	BLASTX
NCBI GI	g1707008
BLAST score	389
E value	2.0e-37
Match length	92
% identity	79
NCBI Description	(U78721) 30S ribosomal protein S5 isolog [Arabidopsis thaliana]

Seq. No.	386671
Contig ID	2135_1.R1084
5'-most EST	g5455592
Method	BLASTN
NCBI GI	g11957
BLAST score	286
E value	1.0e-159
Match length	494
% identity	97
NCBI Description	Rice complete chloroplast genome

Seq. No.	386672
Contig ID	2138_1.R1084
5'-most EST	jC-osleLIB3474037b06a1
Method	BLASTX
NCBI GI	g2827533
BLAST score	152
E value	1.0e-09

Match length	70
% identity	49
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386673
Contig ID	2138_2.R1084
5'-most EST	LIB3431-039-P1-N1-B4
Method	BLASTX
NCBI GI	g2369690
BLAST score	166
E value	4.0e-11
Match length	72
% identity	51
NCBI Description	(Y11988) FPF1 protein [Arabidopsis thaliana]

Seq. No.	386674
Contig ID	2139_1.R1084
5'-most EST	LIB3431-039-P1-N1-B5
Method	BLASTX
NCBI GI	g1838961
BLAST score	296
E value	2.0e-26
Match length	116
% identity	57
NCBI Description	(Y10994) acyl carrier protein [Casuarina glauca]

Seq. No.	386675
Contig ID	2146_1.R1084
5'-most EST	LIB3431-039-P1-N1-C1
Method	BLASTX
NCBI GI	g2911043
BLAST score	174
E value	4.0e-12
Match length	91
% identity	43
NCBI Description	(AL021961) putative protein [Arabidopsis thaliana]

Seq. No.	386676
Contig ID	2148_1.R1084
5'-most EST	g3761373

Seq. No.	386677
Contig ID	2149_1.R1084
5'-most EST	g5667322
Method	BLASTX
NCBI GI	g2160158
BLAST score	1421
E value	1.0e-158
Match length	416
% identity	65
NCBI Description	(AC000132) Similar to elongation factor 1-gamma (gb_EF1G_XENLA). ESTs gb_T20564,gb_T45940,gb_T04527 come from this gene. [Arabidopsis thaliana]

Seq. No.	386678
Contig ID	2156_1.R1084
5'-most EST	LIB3431-039-P1-N1-D2

Seq. No.	386679
Contig ID	2158_1.R1084
5'-most EST	LIB3431-039-P1-N1-D4
Method	BLASTX
NCBI GI	g4680193
BLAST score	295
E value	1.0e-32
Match length	119
% identity	54
NCBI Description	(AF111710) putative farnesyl pyrophosphate synthase [Oryza sativa subsp. indica]

Seq. No.	386680
Contig ID	2162_1.R1084
5'-most EST	LIB3433-040-P1-K1-B11
Method	BLASTN
NCBI GI	g5257255
BLAST score	64
E value	9.0e-27
Match length	104
% identity	90
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	386681
Contig ID	2162_3.R1084
5'-most EST	uC-osflcyp054f01b1
Method	BLASTN
NCBI GI	g1679852
BLAST score	57
E value	5.0e-23
Match length	57
% identity	100
NCBI Description	N.tabacum mRNA for caffeoyl-CoA O-methyltransferase

Seq. No.	386682
Contig ID	2165_1.R1084
5'-most EST	LIB3431-039-P1-N1-E5

Seq. No.	386683
Contig ID	2168_1.R1084
5'-most EST	LIB3431-039-P1-N1-E8

Seq. No.	386684
Contig ID	2169_1.R1084
5'-most EST	LIB3431-020-P1-N1-A11
Method	BLASTX
NCBI GI	g2244847
BLAST score	237
E value	6.0e-31
Match length	488
% identity	28
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	386685
Contig ID	2170_1.R1084

5'-most EST	LIB3431-058-P1-N1-G7
Method	BLASTX
NCBI GI	g136640
BLAST score	804
E value	9.0e-86
Match length	152
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum]

Seq. No.	386686
Contig ID	2170_2.R1084
5'-most EST	uC-osflcyp013e11b2
Method	BLASTX
NCBI GI	g136640
BLAST score	804
E value	8.0e-86
Match length	152
% identity	97
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-17 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi_170785 (M62720) ubiquitin carrier protein [Triticum aestivum]

Seq. No.	386687
Contig ID	2171_1.R1084
5'-most EST	jC-osleLIB3474037g12a1

Seq. No.	386688
Contig ID	2172_1.R1084
5'-most EST	g4714800
Method	BLASTX
NCBI GI	g2598589
BLAST score	345
E value	4.0e-32
Match length	98
% identity	60
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	386689
Contig ID	2173_1.R1084
5'-most EST	uC-osrocyp003h11a1
Method	BLASTX
NCBI GI	g5729704
BLAST score	269
E value	2.0e-23
Match length	114
% identity	44
NCBI Description	(AC007927) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	386690
Contig ID	2185_1.R1084
5'-most EST	g3761306
Method	BLASTX
NCBI GI	g4206765
BLAST score	438

E value	1.0e-42
Match length	335
% identity	33
NCBI Description	(AF104329) putative type 1 membrane protein [Arabidopsis thaliana]

Seq. No.	386691
Contig ID	2186_1.R1084
5'-most EST	g5607362
Method	BLASTX
NCBI GI	g2464852
BLAST score	268
E value	4.0e-23
Match length	150
% identity	44
NCBI Description	(Z99707) putative protein [Arabidopsis thaliana]

Seq. No.	386692
Contig ID	2186_3.R1084
5'-most EST	uC-osflcyp080g11b1

Seq. No.	386693
Contig ID	2190_1.R1084
5'-most EST	g4716392
Method	BLASTX
NCBI GI	g1708424
BLAST score	1070
E value	1.0e-117
Match length	291
% identity	68
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No.	386694
Contig ID	2190_2.R1084
5'-most EST	uC-osflcyp118d04a1
Method	BLASTX
NCBI GI	g1708424
BLAST score	267
E value	3.0e-23
Match length	61
% identity	74
NCBI Description	ISOFLAVONE REDUCTASE HOMOLOG >gi_1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]

Seq. No.	386695
Contig ID	2192_1.R1084
5'-most EST	g2798995
Method	BLASTN
NCBI GI	g4097015
BLAST score	53
E value	2.0e-20
Match length	53
% identity	100
NCBI Description	Expression vector pBRz, complete cds

Seq. No.	386696

Contig ID	2196_1.R1084
5'-most EST	uC-osroM202029f08a1
Seq. No.	386697
Contig ID	2203_1.R1084
5'-most EST	g5607621
Seq. No.	386698
Contig ID	2214_1.R1084
5'-most EST	g3762769
Method	BLASTX
NCBI GI	g2997591
BLAST score	656
E value	1.0e-68
Match length	164
% identity	76
NCBI Description	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
Seq. No.	386699
Contig ID	2215_1.R1084
5'-most EST	LIB3431-041-P1-N1-B9
Seq. No.	386700
Contig ID	2221_1.R1084
5'-most EST	LIB3433-030-P1-K1-C9
Method	BLASTX
NCBI GI	g3128177
BLAST score	178
E value	5.0e-24
Match length	114
% identity	60
NCBI Description	(AC004521) unknown protein [Arabidopsis thaliana]
Seq. No.	386701
Contig ID	2226_1.R1084
5'-most EST	g427070
Method	BLASTN
NCBI GI	g5730046
BLAST score	33
E value	1.0e-08
Match length	39
% identity	63
NCBI Description	Homo sapiens solute carrier family 17 (sodium phosphate), member 3 (SLC17A3) mRNA >gi_2062691_gb_U90545_HSU90545 Human sodium phosphate transporter (NPT4) mRNA, complete cds
Seq. No.	386702
Contig ID	2227_1.R1084
5'-most EST	g3768329
Method	BLASTN
NCBI GI	g6006355
BLAST score	113
E value	2.0e-56
Match length	199
% identity	36

NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11
Seq. No.	386703
Contig ID	2231_1.R1084
5'-most EST	LIB3431-041-P1-N1-D6
Seq. No.	386704
Contig ID	2231_2.R1084
5'-most EST	LIB3477-011-P1-K1-A12
Method	BLASTX
NCBI GI	g1172676
BLAST score	562
E value	1.0e-65
Match length	176
% identity	73
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) (CP43) >gi_1262709_dbj_BAA04424.1_ (D17510) PSII 44kDa protein [Pinus thunbergii]
Seq. No.	386705
Contig ID	2233_1.R1084
5'-most EST	LIB3431-041-P1-N1-D9
Seq. No.	386706
Contig ID	2235_1.R1084
5'-most EST	uC-osf1M2020114c01a1
Method	BLASTX
NCBI GI	g3582335
BLAST score	2062
E value	0.0e+00
Match length	464
% identity	86
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.	386707
Contig ID	2235_2.R1084
5'-most EST	uC-osflcyp140h07b1
Method	BLASTX
NCBI GI	g3582335
BLAST score	994
E value	1.0e-108
Match length	256
% identity	73
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.	386708
Contig ID	2235_3.R1084
5'-most EST	uC-osflcyp092c11b1
Method	BLASTX
NCBI GI	g3582335
BLAST score	615
E value	8.0e-64
Match length	132
% identity	84
NCBI Description	(AC005496) unknown protein [Arabidopsis thaliana]
Seq. No.	386709

Contig ID	2248_1.R1084
5'-most EST	g3761385
Method	BLASTX
NCBI GI	g4982500
BLAST score	279
E value	4.0e-27
Match length	153
% identity	50
NCBI Description	(AC000107) F17F8.6 [Arabidopsis thaliana]

Seq. No.	386710
Contig ID	2255_1.R1084
5'-most EST	g3767625
Method	BLASTX
NCBI GI	g1168537
BLAST score	1996
E value	0.0e+00
Match length	495
% identity	74
NCBI Description	ASPARTIC PROTEINASE PRECURSOR >gi_82458_pir__JS0732 aspartic proteinase (EC 3.4.23.-) - rice >gi_218143_dbj_BAA02242_ (D12777) aspartic proteinase [Oryza sativa]

Seq. No.	386711
Contig ID	2255_2.R1084
5'-most EST	uC-osf1cyp080d11a1

Seq. No.	386712
Contig ID	2263_1.R1084
5'-most EST	g1854168
Method	BLASTX
NCBI GI	g119958
BLAST score	603
E value	3.0e-62
Match length	153
% identity	77
NCBI Description	FERREDOXIN III PRECURSOR (FD III) >gi_168473 (M73831) ferredoxin [Zea mays] >gi_1864001_dbj_BAA19251_ (AB001387) Fd III [Zea mays] >gi_444686_prf__1907324C ferredoxin:ISOTYPE=III [Zea mays]

Seq. No.	386713
Contig ID	2265_1.R1084
5'-most EST	g4716817
Method	BLASTX
NCBI GI	g542200
BLAST score	535
E value	4.0e-86
Match length	239
% identity	67
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	386714
Contig ID	2267_1.R1084

5'-most EST	LIB3433-006-Q6-K6-D1
Seq. No.	386715
Contig ID	2270_1.R1084
5'-most EST	g3762399
Seq. No.	386716
Contig ID	2271_1.R1084
5'-most EST	LIB3475-005-P1-K1-D6
Method	BLASTN
NCBI GI	g5410347
BLAST score	70
E value	1.0e-30
Match length	197
% identity	88
NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence
Seq. No.	386717
Contig ID	2271_2.R1084
5'-most EST	LIB3431-041-P1-N1-H7
Method	BLASTX
NCBI GI	g1655653
BLAST score	220
E value	2.0e-17
Match length	149
% identity	37
NCBI Description	(Z81368) hypothetical protein Rv2406c [Mycobacterium tuberculosis]
Seq. No.	386718
Contig ID	2273_1.R1084
5'-most EST	uC-osrocyp037g01a1
Seq. No.	386719
Contig ID	2273_2.R1084
5'-most EST	LIB3433-049-P1-K1-B1
Seq. No.	386720
Contig ID	2277_1.R1084
5'-most EST	LIB3431-021-P1-K1-H2
Method	BLASTX
NCBI GI	g4733937
BLAST score	132
E value	3.0e-10
Match length	104
% identity	42
NCBI Description	(AF080245) sesquiterpene synthase [Elaeis oleifera]
Seq. No.	386721
Contig ID	2280_1.R1084
5'-most EST	uC-osflcyp099h09a1
Method	BLASTX
NCBI GI	g2129825
BLAST score	391
E value	1.0e-37
Match length	93
% identity	83

NCBI Description	dynamin-like protein phragmoplastin 12 - soybean >gi_1217994 (U25547) SDL [Glycine max]
Seq. No.	386722
Contig ID	2281_1.R1084
5'-most EST	LIB3431-042-P1-N1-A8
Seq. No.	386723
Contig ID	2283_1.R1084
5'-most EST	LIB3432-007-P1-K1-E1
Method	BLASTX
NCBI GI	g4972067
BLAST score	259
E value	4.0e-47
Match length	223
% identity	48
NCBI Description	(AL078467) putative protei [Arabidopsis thaliana]
Seq. No.	386724
Contig ID	2285_1.R1084
5'-most EST	LIB3431-042-P1-N1-B11
Method	BLASTN
NCBI GI	g4959460
BLAST score	36
E value	2.0e-10
Match length	36
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds
Seq. No.	386725
Contig ID	2287_1.R1084
5'-most EST	LIB3431-042-P1-N1-B2
Method	BLASTX
NCBI GI	g4582783
BLAST score	165
E value	1.0e-12
Match length	73
% identity	55
NCBI Description	(AJ006752) starch synthase, isoform V [Vigna unguiculata]
Seq. No.	386726
Contig ID	2288_1.R1084
5'-most EST	g4714883
Method	BLASTX
NCBI GI	g5733882
BLAST score	983
E value	1.0e-106
Match length	339
% identity	59
NCBI Description	(AC007932) Similar to gb_Y12465 serine/threonine kinase from Sorghum bicolor and contains a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]
Seq. No.	386727
Contig ID	2288_2.R1084
5'-most EST	LIB3431-052-P1-N1-B12
Method	BLASTX

NCBI GI	g5733882
BLAST score	299
E value	2.0e-26
Match length	136
% identity	52
NCBI Description	(AC007932) Similar to gb_Y12465 serine/threonine kinase from Sorghum bicolor and contains a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	386728
Contig ID	2288_3.R1084
5'-most EST	LIB3431-054-P1-N1-C7
Method	BLASTX
NCBI GI	g3158476
BLAST score	948
E value	1.0e-102
Match length	255
% identity	69
NCBI Description	(AF067185) aquaporin 2 [Samanea saman]

Seq. No.	386729
Contig ID	2289_1.R1084
5'-most EST	LIB3431-042-P1-N1-B4
Method	BLASTX
NCBI GI	g2065019
BLAST score	290
E value	8.0e-26
Match length	119
% identity	23
NCBI Description	(Y09823) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386730
Contig ID	2291_1.R1084
5'-most EST	g5667281
Method	BLASTX
NCBI GI	g133936
BLAST score	305
E value	3.0e-27
Match length	59
% identity	98
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_ (X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein S3 [Oryza sativa]

Seq. No.	386731
Contig ID	2299_1.R1084
5'-most EST	g3762504

Seq. No.	386732
Contig ID	2300_1.R1084
5'-most EST	g3767345
Method	BLASTX
NCBI GI	g1483563
BLAST score	1127
E value	1.0e-123

Match length	230
% identity	93
NCBI Description	(X99825) leucine aminopeptidase [Petroselinum crispum]

Seq. No.	386733
Contig ID	2308_1.R1084
5'-most EST	LIB3433-051-P1-K1-F11
Method	BLASTN
NCBI GI	g452439
BLAST score	68
E value	1.0e-29
Match length	253
% identity	87
NCBI Description	Wheat (clone p80k-34) initiation factor isozyme 4F p82 subunit mRNA, complete cds

Seq. No.	386734
Contig ID	2315_1.R1084
5'-most EST	g4716139
Method	BLASTN
NCBI GI	g5922603
BLAST score	106
E value	6.0e-52
Match length	284
% identity	91
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	386735
Contig ID	2315_3.R1084
5'-most EST	g5816513
Method	BLASTN
NCBI GI	g5922603
BLAST score	97
E value	1.0e-46
Match length	278
% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01

Seq. No.	386736
Contig ID	2315_5.R1084
5'-most EST	LIB3431-042-P1-N1-E1
Method	BLASTN
NCBI GI	g6016845
BLAST score	43
E value	1.0e-14
Match length	243
% identity	89
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	386737
Contig ID	2315_6.R1084
5'-most EST	g5816501
Method	BLASTN
NCBI GI	g6016845
BLAST score	82
E value	4.0e-38
Match length	161

% identity	93
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	386738
Contig ID	2316_1.R1084
5'-most EST	uC-osrocyp029a11a1
Method	BLASTX
NCBI GI	g6041819
BLAST score	220
E value	1.0e-17
Match length	95
% identity	47
NCBI Description	(AC009918) unknown protein [Arabidopsis thaliana]

Seq. No.	386739
Contig ID	2317_1.R1084
5'-most EST	LIB3431-042-P1-N1-E11

Seq. No.	386740
Contig ID	2331_1.R1084
5'-most EST	LIB3431-042-P1-N1-F5

Seq. No.	386741
Contig ID	2338_1.R1084
5'-most EST	LIB3431-042-P1-N1-G11
Method	BLASTN
NCBI GI	g5803242
BLAST score	86
E value	2.0e-40
Match length	157
% identity	18
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0535G04

Seq. No.	386742
Contig ID	2338_2.R1084
5'-most EST	g5455392
Method	BLASTN
NCBI GI	g5852170
BLAST score	78
E value	2.0e-35
Match length	163
% identity	27
NCBI Description	Oryza sativa indica(GLA4) genomic DNA, chromosome 4, BAC clone:t17804

Seq. No.	386743
Contig ID	2342_1.R1084
5'-most EST	g3761415
Method	BLASTX
NCBI GI	g3426051
BLAST score	284
E value	4.0e-25
Match length	82
% identity	73
NCBI Description	(AC005168) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386744

Contig ID	2343_1.R1084
5'-most EST	LIB3431-042-P1-N1-G6
Method	BLASTX
NCBI GI	g3915088
BLAST score	248
E value	5.0e-21
Match length	75
% identity	61
NCBI Description	TRANS-CINNAMATE 4-MONOOXYGENASE (CINNAMIC ACID 4-HYDROXYLASE) (CA4H) (C4H) (P450C4H) (CYTOCHROME P450 73) >gi_903872 (L38838) trans-cinnamate 4-monooxygenase [Petroselinum crispum]

Seq. No.	386745
Contig ID	2347_1.R1084
5'-most EST	uC-osrocyp010g09a1
Method	BLASTX
NCBI GI	g128191
BLAST score	371
E value	2.0e-35
Match length	78
% identity	88
NCBI Description	NITRATE REDUCTASE [NAD(P)H] >gi_66210_pir__RDBHNP nitrate reductase (NAD(P)H) (EC 1.6.6.2) - barley >gi_19065_emb_CAA42739_ (X60173) nitrate reductase (NAD(P)H) [Hordeum vulgare]

Seq. No.	386746
Contig ID	2349_1.R1084
5'-most EST	uC-osflcyp083d04a1

Seq. No.	386747
Contig ID	2352_1.R1084
5'-most EST	LIB3431-042-P1-N1-H3
Method	BLASTX
NCBI GI	g3420052
BLAST score	766
E value	2.0e-81
Match length	185
% identity	77
NCBI Description	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]

Seq. No.	386748
Contig ID	2355_1.R1084
5'-most EST	LIB3433-016-Q6-K6-H8

Seq. No.	386749
Contig ID	2361_1.R1084
5'-most EST	LIB3431-043-P1-N1-A3
Method	BLASTX
NCBI GI	g3668091
BLAST score	197
E value	1.0e-14
Match length	198
% identity	10
NCBI Description	(AC004667) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386750
Contig ID	2379_1.R1084
5'-most EST	LIB3433-008-Q6-K1-C7

Seq. No.	386751
Contig ID	2382_1.R1084
5'-most EST	LIB3431-043-P1-N1-C3

Seq. No.	386752
Contig ID	2384_1.R1084
5'-most EST	LIB3431-043-P1-N1-C5
Method	BLASTX
NCBI GI	g676884
BLAST score	289
E value	1.0e-25
Match length	77
% identity	71
NCBI Description	(D29681) The expression is induced by Pi starvation. [Nicotiana tabacum] >gi_1094819_prf__2106387C Al-induced protein [Nicotiana tabacum]

Seq. No.	386753
Contig ID	2388_1.R1084
5'-most EST	LIB3431-045-P1-N1-F8
Method	BLASTX
NCBI GI	g4587556
BLAST score	433
E value	2.0e-42
Match length	140
% identity	61
NCBI Description	(AC006577) Similar to gi_1653162 (p)ppGpp 3-pyrophosphohydrolase from Synechocystis sp genome gb_D90911. EST gb_W43807 comes from this gene. [Arabidopsis thaliana]

Seq. No.	386754
Contig ID	2391_1.R1084
5'-most EST	LIB3431-043-P1-K1-D11

Seq. No.	386755
Contig ID	2392_1.R1084
5'-most EST	uC-osrocyp014g06a1
Method	BLASTX
NCBI GI	g1718097
BLAST score	312
E value	3.0e-28
Match length	123
% identity	46
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	386756
Contig ID	2395_1.R1084

5'-most EST	g3768007
Seq. No.	386757
Contig ID	2400_1.R1084
5'-most EST	LIB3432-034-P2-K1-H10
Method	BLASTX
NCBI GI	g5734470
BLAST score	420
E value	1.0e-40
Match length	246
% identity	41
NCBI Description	(AL109832) hypothetical protein [Schizosaccharomyces pombe]
Seq. No.	386758
Contig ID	2407_1.R1084
5'-most EST	LIB3431-013-P1-K1-F3
Method	BLASTX
NCBI GI	g1777312
BLAST score	357
E value	2.0e-33
Match length	107
% identity	63
NCBI Description	(D30622) novel serine/threonine protein kinase [Arabidopsis thaliana]
Seq. No.	386759
Contig ID	2407_2.R1084
5'-most EST	LIB3431-048-P1-N1-D3
Method	BLASTX
NCBI GI	g3256035
BLAST score	954
E value	1.0e-106
Match length	377
% identity	51
NCBI Description	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]
Seq. No.	386760
Contig ID	2409_1.R1084
5'-most EST	g5455449
Method	BLASTX
NCBI GI	g128690
BLAST score	553
E value	2.0e-56
Match length	120
% identity	90
NCBI Description	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 3, CHLOROPLAST >gi_66161_pir__DERZN3 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 3 - rice chloroplast >gi_11989_emb_CAA34001_ (X15901) ndhC; NADH dehydrogenase ND3 [Oryza sativa] >gi_226610_prf__1603356AG NADH dehydrogenase ND3 [Oryza sativa]
Seq. No.	386761
Contig ID	2413_1.R1084
5'-most EST	uC-osrocyp010d11b1

Seq. No.	386762
Contig ID	2417_1.R1084
5'-most EST	LIB3431-043-P1-N1-F4

Seq. No.	386763
Contig ID	2418_1.R1084
5'-most EST	LIB3431-005-P1-N1-D8

Seq. No.	386764
Contig ID	2421_1.R1084
5'-most EST	LIB3431-018-P1-K1-C11
Method	BLASTX
NCBI GI	g2739375
BLAST score	163
E value	9.0e-11
Match length	119
% identity	37
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana]

Seq. No.	386765
Contig ID	2423_1.R1084
5'-most EST	uC-osf1cyp159c12a1
Method	BLASTX
NCBI GI	g417488
BLAST score	751
E value	1.0e-79
Match length	170
% identity	82
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No.	386766
Contig ID	2423_2.R1084
5'-most EST	g701958
Method	BLASTX
NCBI GI	g417488
BLAST score	971
E value	1.0e-105
Match length	237
% identity	78
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No.	386767
Contig ID	2423_3.R1084
5'-most EST	uC-osf1cyp139f09b1
Method	BLASTX
NCBI GI	g417488
BLAST score	867
E value	2.0e-93
Match length	226
% identity	72
NCBI Description	ALPHA-GLUCAN PHOSPHORYLASE, H ISOZYME (STARCH PHOSPHORYLASE

H) >gi_100452_pir__A40995 starch phosphorylase (EC 2.4.1.1) H - potato >gi_169473 (M69038) alpha-glucan phosphorylase type H isozyme [Solanum tuberosum]

Seq. No.	386768
Contig ID	2424_1.R1084
5'-most EST	LIB3431-043-P1-N1-G10
Method	BLASTX
NCBI GI	g4006895
BLAST score	266
E value	5.0e-24
Match length	91
% identity	57
NCBI Description	(Z99708) putative protein [Arabidopsis thaliana]

Seq. No.	386769
Contig ID	2429_1.R1084
5'-most EST	uC-osrocyp011f07a1
Method	BLASTX
NCBI GI	g5596468
BLAST score	653
E value	6.0e-68
Match length	203
% identity	61
NCBI Description	(AL096882) putative protein [Arabidopsis thaliana]

Seq. No.	386770
Contig ID	2430_1.R1084
5'-most EST	LIB3431-035-P1-N1-H6
Method	BLASTX
NCBI GI	g4454459
BLAST score	521
E value	9.0e-64
Match length	204
% identity	64
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	386771
Contig ID	2435_1.R1084
5'-most EST	LIB3431-043-P1-N1-H1
Method	BLASTX
NCBI GI	g303736
BLAST score	578
E value	2.0e-59
Match length	198
% identity	61
NCBI Description	(D12541) GTP-binding protein [Pisum sativum] >gi_738934_prf__2001457B GTP-binding protein [Pisum sativum]

Seq. No.	386772
Contig ID	2443_1.R1084
5'-most EST	LIB3431-043-P1-N1-H7
Method	BLASTX
NCBI GI	g2911072
BLAST score	700
E value	1.0e-73

Match length 236
% identity 58
NCBI Description (AL021960) putative protein [Arabidopsis thaliana]

Seq. No. 386773
Contig ID 2446_1.R1084
5'-most EST LIB3431-044-P1-N1-A10
Method BLASTX
NCBI GI g2982309
BLAST score 194
E value 8.0e-15
Match length 46
% identity 78
NCBI Description (AF051239) probable ubiquitin activating enzyme 2 [Picea mariana]

Seq. No. 386774
Contig ID 2456_1.R1084
5'-most EST LIB3431-044-P1-N1-B10

Seq. No. 386775
Contig ID 2462_1.R1084
5'-most EST LIB3434-003-P1-K1-G5
Method BLASTN
NCBI GI g6015437
BLAST score 38
E value 2.0e-11
Match length 38
% identity 100
NCBI Description Homo sapiens PEX1 mRNA, complete cds

Seq. No. 386776
Contig ID 2462_2.R1084
5'-most EST g454530

Seq. No. 386777
Contig ID 2463_1.R1084
5'-most EST g5667185

Seq. No. 386778
Contig ID 2464_1.R1084
5'-most EST g5816556
Method BLASTX
NCBI GI g2344892
BLAST score 130
E value 7.0e-12
Match length 67
% identity 60
NCBI Description (AC002388) unknown protein [Arabidopsis thaliana]

Seq. No. 386779
Contig ID 2466_1.R1084
5'-most EST LIB3432-029-P1-K1-H9
Method BLASTX
NCBI GI g1707016
BLAST score 187
E value 1.0e-13

Match length	55
% identity	60
NCBI Description	(U78721) cadmium-induced protein isolog [Arabidopsis thaliana]

Seq. No.	386780
Contig ID	2466_2.R1084
5'-most EST	uC-osroM202033b07b1
Method	BLASTX
NCBI GI	g3757515
BLAST score	571
E value	2.0e-58
Match length	290
% identity	46
NCBI Description	(AC005167) hypothetical protein [Arabidopsis thaliana] >gi_4581130_gb_AAD24620.1_AC005825_27 (AC005825) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386781
Contig ID	2471_1.R1084
5'-most EST	g3768441

Seq. No.	386782
Contig ID	2471_2.R1084
5'-most EST	LIB3431-044-P1-N1-C6

Seq. No.	386783
Contig ID	2474_1.R1084
5'-most EST	g3761290
Method	BLASTX
NCBI GI	g461753
BLAST score	1160
E value	1.0e-127
Match length	255
% identity	89
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG PRECURSOR >gi_419773_pir__S31164 ATP-dependent ClpB proteinase regulatory chain homolog precursor, chloroplast - garden pea >gi_169128 (L09547) nuclear encoded precursor to chloroplast protein [Pisum sativum]

Seq. No.	386784
Contig ID	2474_2.R1084
5'-most EST	LIB3431-044-P1-K1-D1
Method	BLASTX
NCBI GI	g399213
BLAST score	1434
E value	1.0e-159
Match length	308
% identity	91
NCBI Description	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA HOMOLOG CD4B PRECURSOR >gi_100190_pir__B35905 CD4B protein - tomato >gi_170435 (M32604) ATP-dependent protease (CD4B) [Lycopersicon esculentum]

Seq. No.	386785
Contig ID	2479_1.R1084

5'-most EST	uC-osflcyp152c03a1
Seq. No.	386786
Contig ID	2481_1.R1084
5'-most EST	g3768757
Method	BLASTX
NCBI GI	g1652164
BLAST score	558
E value	7.0e-57
Match length	223
% identity	54
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]
Seq. No.	386787
Contig ID	2482_1.R1084
5'-most EST	LIB3431-044-P1-N1-D9
Seq. No.	386788
Contig ID	2488_1.R1084
5'-most EST	LIB3431-044-P1-N1-E4
Method	BLASTX
NCBI GI	g3183094
BLAST score	291
E value	4.0e-26
Match length	81
% identity	69
NCBI Description	ORNITHINE CARBAMOYLTRANSFERASE PRECURSOR (OTCASE) (ORNITHINE TRANSCARBAMYLASE) >gi_971168 (U13684) ornithine carbamoyltransferase [Pisum sativum]
Seq. No.	386789
Contig ID	2489_1.R1084
5'-most EST	g4715292
Method	BLASTX
NCBI GI	g5042409
BLAST score	808
E value	3.0e-86
Match length	221
% identity	67
NCBI Description	(AC006193) Putative membrane related protein [Arabidopsis thaliana]
Seq. No.	386790
Contig ID	2492_1.R1084
5'-most EST	LIB3431-044-P1-N1-E9
Method	BLASTX
NCBI GI	g4567284
BLAST score	279
E value	3.0e-24
Match length	101
% identity	57
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]
Seq. No.	386791
Contig ID	2492_2.R1084
5'-most EST	g5667600
Method	BLASTX

NCBI GI	g4567284
BLAST score	173
E value	3.0e-12
Match length	64
% identity	56
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	386792
Contig ID	2494_1.R1084
5'-most EST	g4715342

Seq. No.	386793
Contig ID	2496_1.R1084
5'-most EST	g4715866
Method	BLASTX
NCBI GI	g6091733
BLAST score	219
E value	3.0e-17
Match length	65
% identity	62
NCBI Description	(AC010797) unknown protein [Arabidopsis thaliana]

Seq. No.	386794
Contig ID	2501_1.R1084
5'-most EST	g3760146
Method	BLASTX
NCBI GI	g1644427
BLAST score	515
E value	4.0e-52
Match length	148
% identity	68
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	386795
Contig ID	2501_2.R1084
5'-most EST	LIB3433-033-P1-K1-E12
Method	BLASTX
NCBI GI	g1644427
BLAST score	487
E value	6.0e-49
Match length	135
% identity	69
NCBI Description	(U74610) glyoxalase II [Arabidopsis thaliana]

Seq. No.	386796
Contig ID	2506_1.R1084
5'-most EST	uC-osflM202085b11a1
Method	BLASTX
NCBI GI	g3132476
BLAST score	596
E value	1.0e-61
Match length	169
% identity	67
NCBI Description	(AC003096) unknown protein [Arabidopsis thaliana]

Seq. No.	386797
Contig ID	2508_1.R1084

5'-most EST	LIB3431-044-P1-N1-G12
Method	BLASTX
NCBI GI	g4490728
BLAST score	299
E value	8.0e-27
Match length	69
% identity	74
NCBI Description	(AL035709) putative protein [Arabidopsis thaliana]

Seq. No.	386798
Contig ID	2509_1.R1084
5'-most EST	uC-osrocyp009a10a1
Method	BLASTX
NCBI GI	g3176664
BLAST score	178
E value	1.0e-12
Match length	65
% identity	57
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	386799
Contig ID	2509_2.R1084
5'-most EST	LIB3431-044-P1-N1-G2

Seq. No.	386800
Contig ID	2510_1.R1084
5'-most EST	g5667304

Seq. No.	386801
Contig ID	2513_1.R1084
5'-most EST	LIB3431-044-P1-N1-G8

Seq. No.	386802
Contig ID	2515_1.R1084
5'-most EST	g5056144
Method	BLASTX
NCBI GI	g2129675
BLAST score	588
E value	2.0e-60
Match length	129
% identity	88
NCBI Description	probable chlorophyll synthetase G4 - Arabidopsis thaliana >gi_972938 (U19382) putative chlorophyll synthetase [Arabidopsis thaliana] >gi_3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]

Seq. No.	386803
Contig ID	2516_1.R1084
5'-most EST	LIB3433-046-P1-K1-F9
Method	BLASTX
NCBI GI	g4531444
BLAST score	1446
E value	1.0e-160
Match length	451
% identity	63

NCBI Description	(AC006224) putative protein kinase [Arabidopsis thaliana]
Seq. No.	386804
Contig ID	2517_2.R1084
5'-most EST	g2800086
Method	BLASTX
NCBI GI	g3202024
BLAST score	913
E value	2.0e-98
Match length	277
% identity	66
NCBI Description	(AF069315) thylakoid-bound L-ascorbate peroxidase precursor [Mesembryanthemum crystallinum]
Seq. No.	386805
Contig ID	2523_1.R1084
5'-most EST	LIB3431-045-P1-N1-A1
Seq. No.	386806
Contig ID	2528_1.R1084
5'-most EST	g5771204
Method	BLASTX
NCBI GI	g4581146
BLAST score	595
E value	2.0e-61
Match length	162
% identity	74
NCBI Description	(AC006919) putative fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana]
Seq. No.	386807
Contig ID	2530_1.R1084
5'-most EST	LIB3433-034-P1-K1-D3
Method	BLASTX
NCBI GI	g4680340
BLAST score	906
E value	1.0e-97
Match length	223
% identity	55
NCBI Description	(AF128457) putative nucleolysin [Oryza sativa subsp. indica]
Seq. No.	386808
Contig ID	2530_2.R1084
5'-most EST	LIB3432-007-P1-K1-G5
Method	BLASTX
NCBI GI	g4587549
BLAST score	731
E value	2.0e-77
Match length	206
% identity	38
NCBI Description	(AC006577) Similar to gb_U55861 RNA binding protein nucleolysin (TIAR) from Mus musculus and contains several PF_00076 RNA recognition motif domains. ESTs gb_T21032 and gb_T44127 come from this gene. [Arabidopsis t
Seq. No.	386809

Contig ID	2533_1.R1084
5'-most EST	LIB3431-045-P1-N1-B10
Method	BLASTX
NCBI GI	g3549656
BLAST score	302
E value	3.0e-27
Match length	114
% identity	54
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	386810
Contig ID	2534_1.R1084
5'-most EST	uC-osflcyp174g09b1
Method	BLASTX
NCBI GI	g4056438
BLAST score	300
E value	1.0e-26
Match length	213
% identity	30
NCBI Description	(AC005990) F5O8.11 [Arabidopsis thaliana]

Seq. No.	386811
Contig ID	2534_2.R1084
5'-most EST	g2797715

Seq. No.	386812
Contig ID	2535_1.R1084
5'-most EST	g3769059
Method	BLASTX
NCBI GI	g3892058
BLAST score	532
E value	7.0e-54
Match length	231
% identity	45
NCBI Description	(AC002330) putative glutamate-/aspartate-binding peptide [Arabidopsis thaliana]

Seq. No.	386813
Contig ID	2537_1.R1084
5'-most EST	g3768240
Method	BLASTX
NCBI GI	g4914330
BLAST score	654
E value	3.0e-68
Match length	215
% identity	60
NCBI Description	(AC005489) F14N23.16 [Arabidopsis thaliana]

Seq. No.	386814
Contig ID	2539_1.R1084
5'-most EST	LIB3431-045-P1-N1-B6

Seq. No.	386815
Contig ID	2544_1.R1084
5'-most EST	g5456482
Method	BLASTX
NCBI GI	g1363484

BLAST score	371
E value	6.0e-35
Match length	168
% identity	48
NCBI Description	IAA13 protein - Arabidopsis thaliana >gi_972929 (U18415) IAA13 [Arabidopsis thaliana] >gi_2459414 (AC002332) auxin inducible protein, IAA13 [Arabidopsis thaliana]

Seq. No.	386816
Contig ID	2544_3.R1084
5'-most EST	g3761036

Seq. No.	386817
Contig ID	2547_1.R1084
5'-most EST	LIB3431-045-P1-N1-C5

Seq. No.	386818
Contig ID	2548_1.R1084
5'-most EST	LIB3431-045-P1-N1-C6

Seq. No.	386819
Contig ID	2549_1.R1084
5'-most EST	LIB3431-045-P1-N1-C7

Seq. No.	386820
Contig ID	2551_1.R1084
5'-most EST	LIB3431-018-P1-K1-E4

Seq. No.	386821
Contig ID	2559_1.R1084
5'-most EST	LIB3431-045-P1-N1-D7
Method	BLASTX
NCBI GI	g2809244
BLAST score	182
E value	4.0e-13
Match length	72
% identity	44
NCBI Description	(AC002560) F21B7.13 [Arabidopsis thaliana]

Seq. No.	386822
Contig ID	2561_1.R1084
5'-most EST	LIB3431-045-P1-N1-D9
Method	BLASTX
NCBI GI	g5803254
BLAST score	238
E value	3.0e-20
Match length	147
% identity	42
NCBI Description	(AP000399) ESTs C97429(C60159),D22427(C11106), AU078031(E31854),D15683(C1084) correspond to a region of the predicted gene; hypothetical protein [Oryza sativa]

Seq. No.	386823
Contig ID	2563_1.R1084
5'-most EST	LIB3431-045-P1-N1-E11
Method	BLASTX
NCBI GI	g2274988

BLAST score	265
E value	5.0e-23
Match length	74
% identity	72
NCBI Description	(AJ000226) partial sequence, homology to serine hydroxymethyltransferases [Hordeum vulgare]

Seq. No.	386824
Contig ID	2564_1.R1084
5'-most EST	uC-osf1M202050g01b1

Seq. No.	386825
Contig ID	2566_1.R1084
5'-most EST	LIB3431-017-P1-N1-G8
Method	BLASTX
NCBI GI	g4741942
BLAST score	752
E value	1.0e-79
Match length	211
% identity	70
NCBI Description	(AF134121) Lhca5 protein [Arabidopsis thaliana]

Seq. No.	386826
Contig ID	2568_1.R1084
5'-most EST	g3759645
Method	BLASTX
NCBI GI	g404688
BLAST score	288
E value	7.0e-34
Match length	159
% identity	45
NCBI Description	(L19074) cytochrome P450 [Catharanthus roseus]

Seq. No.	386827
Contig ID	2569_1.R1084
5'-most EST	LIB3433-039-P1-K1-C10

Seq. No.	386828
Contig ID	2569_2.R1084
5'-most EST	g4716846
Method	BLASTN
NCBI GI	g5042437
BLAST score	152
E value	1.0e-79
Match length	244
% identity	91
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	386829
Contig ID	2573_1.R1084
5'-most EST	LIB3431-045-P1-N1-F1
Method	BLASTX
NCBI GI	g3212852
BLAST score	521
E value	9.0e-53
Match length	173
% identity	61

NCBI Description (AC004005) unknown protein [Arabidopsis thaliana]

Seq. No. 386830
Contig ID 2574_1.R1084
5'-most EST g2799044
Method BLASTN
NCBI GI g310732
BLAST score 41
E value 2.0e-13
Match length 41
% identity 100
NCBI Description BlueScribe SK Minus cloning vector

Seq. No. 386831
Contig ID 2581_1.R1084
5'-most EST uC-osroM202033b12a1

Seq. No. 386832
Contig ID 2581_2.R1084
5'-most EST LIB3431-045-P1-N1-F7

Seq. No. 386833
Contig ID 2586_1.R1084
5'-most EST LIB3431-045-P1-N1-G11

Seq. No. 386834
Contig ID 2589_1.R1084
5'-most EST LIB3431-045-P1-N1-G3
Method BLASTX
NCBI GI g3928083
BLAST score 376
E value 3.0e-47
Match length 139
% identity 68
NCBI Description (AC005770) unknown protein [Arabidopsis thaliana]

Seq. No. 386835
Contig ID 2592_1.R1084
5'-most EST LIB3431-055-P1-N1-B9
Method BLASTX
NCBI GI g3914005
BLAST score 1344
E value 1.0e-149
Match length 314
% identity 87
NCBI Description MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]

Seq. No. 386836
Contig ID 2592_3.R1084
5'-most EST LIB3431-055-P2-K1-B9
Method BLASTX
NCBI GI g3914005
BLAST score 245
E value 3.0e-21
Match length 79
% identity 81

NCBI Description	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi_1816586 (U85494) LON1 protease [Zea mays]
Seq. No.	386837
Contig ID	2593_1.R1084
5'-most EST	g2428701
Method	BLASTX
NCBI GI	g1652704
BLAST score	212
E value	4.0e-30
Match length	163
% identity	50
NCBI Description	(D90907) hypothetical protein [Synechocystis sp.]
Seq. No.	386838
Contig ID	2595_1.R1084
5'-most EST	uC-osrocyp008c04a1
Seq. No.	386839
Contig ID	2595_2.R1084
5'-most EST	uC-osrocyp012e10a1
Method	BLASTX
NCBI GI	g3258575
BLAST score	304
E value	3.0e-27
Match length	100
% identity	66
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	386840
Contig ID	2595_3.R1084
5'-most EST	LIB3434-035-P1-K1-H9
Seq. No.	386841
Contig ID	2595_4.R1084
5'-most EST	uC-osrocyp037c03b1
Method	BLASTX
NCBI GI	g3258575
BLAST score	511
E value	2.0e-51
Match length	177
% identity	60
NCBI Description	(U89959) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	386842
Contig ID	2595_9.R1084
5'-most EST	uC-osroM202029a01b1
Seq. No.	386843
Contig ID	2601_1.R1084
5'-most EST	uC-osroM202032e11a1
Method	BLASTX
NCBI GI	g1172977
BLAST score	791
E value	2.0e-84
Match length	188
% identity	82

NCBI Description	60S RIBOSOMAL PROTEIN L18 >gi_606970 (U15741) cytoplasmic ribosomal protein L18 [Arabidopsis thaliana]

Seq. No.	386844
Contig ID	2607_1.R1084
5'-most EST	uC-osflM202054a06b1
Method	BLASTN
NCBI GI	g4468795
BLAST score	36
E value	2.0e-10
Match length	60
% identity	90
NCBI Description	Zea mays mRNA for glutathione transferase GST6

Seq. No.	386845
Contig ID	2607_2.R1084
5'-most EST	LIB3431-046-P1-N1-A4
Method	BLASTX
NCBI GI	g2288969
BLAST score	614
E value	2.0e-63
Match length	226
% identity	57
NCBI Description	(Y12862) glutathione transferase [Zea mays]

Seq. No.	386846
Contig ID	2616_1.R1084
5'-most EST	LIB3431-046-P1-N1-B12
Method	BLASTX
NCBI GI	g3395439
BLAST score	266
E value	7.0e-23
Match length	81
% identity	62
NCBI Description	(AC004683) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386847
Contig ID	2617_1.R1084
5'-most EST	uC-osrocyp006d02a1

Seq. No.	386848
Contig ID	2618_1.R1084
5'-most EST	LIB3431-046-P1-N1-B4

Seq. No.	386849
Contig ID	2619_1.R1084
5'-most EST	g4968997
Method	BLASTX
NCBI GI	g5932555
BLAST score	415
E value	4.0e-54
Match length	194
% identity	58
NCBI Description	(AC009465) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	386850

Contig ID	2619_2.R1084
5'-most EST	LIB3431-046-P1-N1-B5
Method	BLASTX
NCBI GI	g5932555
BLAST score	855
E value	7.0e-92
Match length	219
% identity	77
NCBI Description	(AC009465) putative ribose 5-phosphate isomerase [Arabidopsis thaliana]

Seq. No.	386851
Contig ID	2622_1.R1084
5'-most EST	LIB3431-003-P1-N1-C8

Seq. No.	386852
Contig ID	2623_1.R1084
5'-most EST	LIB3431-046-P1-N1-B9
Method	BLASTX
NCBI GI	g4680212
BLAST score	241
E value	7.0e-20
Match length	70
% identity	66
NCBI Description	(AF114171) hypothetical protein [Sorghum bicolor]

Seq. No.	386853
Contig ID	2624_1.R1084
5'-most EST	uC-osrocyp015a12a1

Seq. No.	386854
Contig ID	2634_1.R1084
5'-most EST	LIB3431-046-P1-N1-D1

Seq. No.	386855
Contig ID	2639_1.R1084
5'-most EST	LIB3431-046-P1-N1-D3
Method	BLASTX
NCBI GI	g5668608
BLAST score	269
E value	6.0e-32
Match length	161
% identity	46
NCBI Description	(AF115334) MenG [Pseudomonas fluorescens]

Seq. No.	386856
Contig ID	2643_1.R1084
5'-most EST	LIB3431-040-P1-N1-E11
Method	BLASTX
NCBI GI	g4490317
BLAST score	270
E value	2.0e-23
Match length	94
% identity	53
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	386857

Contig ID	2643_2.R1084
5'-most EST	LIB3431-040-P1-K2-E11
Method	BLASTX
NCBI GI	g4490317
BLAST score	372
E value	2.0e-35
Match length	182
% identity	42
NCBI Description	(AL035678) putative protein [Arabidopsis thaliana]

Seq. No.	386858
Contig ID	2653_1.R1084
5'-most EST	uC-osflcyp062h11a1
Method	BLASTX
NCBI GI	g11998
BLAST score	292
E value	5.0e-35
Match length	76
% identity	93
NCBI Description	(X15901) ORF85 [Oryza sativa] >gi_226619_prf__1603356AR ORF 85A [Oryza sativa]

Seq. No.	386859
Contig ID	2655_1.R1084
5'-most EST	uC-osflcyp117h09a1
Method	BLASTX
NCBI GI	g3334333
BLAST score	563
E value	1.0e-57
Match length	138
% identity	75
NCBI Description	SUPEROXIDE DISMUTASE-2 [CU-ZN] >gi_2660798 (AF034832) cytosolic copper/zinc superoxide dismutase [Mesembryanthemum crystallinum]

Seq. No.	386860
Contig ID	2661_1.R1084
5'-most EST	LIB3431-046-P1-N1-F3
Method	BLASTX
NCBI GI	g4415940
BLAST score	249
E value	6.0e-21
Match length	103
% identity	49
NCBI Description	(AC006418) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386861
Contig ID	2669_1.R1084
5'-most EST	LIB3431-007-P1-N1-C7
Method	BLASTX
NCBI GI	g3914470
BLAST score	292
E value	8.0e-26
Match length	63
% identity	81
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein

[Hordeum vulgare]

Seq. No.	386862
Contig ID	2669_2.R1084
5'-most EST	LIB3479-001-Q6-K2-C8
Method	BLASTX
NCBI GI	g3914470
BLAST score	507
E value	3.0e-51
Match length	133
% identity	73
NCBI Description	PHOTOSYSTEM II 10 KD POLYPEPTIDE PRECURSOR >gi_1321868_emb_CAA66373_ (X97771) 10kD PSII protein [Hordeum vulgare]

Seq. No.	386863
Contig ID	2669_3.R1084
5'-most EST	LIB3431-060-P1-K1-G2
Method	BLASTX
NCBI GI	g131192
BLAST score	512
E value	1.0e-51
Match length	142
% identity	72
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT V PRECURSOR (PHOTOSYSTEM I 9 KD PROTEIN) (PSI-G) >gi_100606_pir__S20937 photosystem I chain V precursor - barley >gi_19091_emb_CAA42727_ (X60158) photosystem I polypeptide PSI-G precursor [Hordeum vulgare]

Seq. No.	386864
Contig ID	2669_4.R1084
5'-most EST	g5667326
Method	BLASTN
NCBI GI	g12182
BLAST score	72
E value	5.0e-32
Match length	80
% identity	97
NCBI Description	P.sativum chloroplast DNA of the single ribosomal RNA operon

Seq. No.	386865
Contig ID	2677_1.R1084
5'-most EST	g3767985
Method	BLASTX
NCBI GI	g4680205
BLAST score	714
E value	5.0e-94
Match length	198
% identity	85
NCBI Description	(AF114171) H beta 58 homolog [Sorghum bicolor]

Seq. No.	386866
Contig ID	2685_1.R1084
5'-most EST	LIB3431-046-P1-N1-H9
Method	BLASTX

NCBI GI	g2495180
BLAST score	487
E value	8.0e-49
Match length	128
% identity	70
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418) hydroxymethylbilane synthase [Pisum sativum]

Seq. No.	386867
Contig ID	2686_1.R1084
5'-most EST	LIB3431-047-P1-N1-A10
Method	BLASTX
NCBI GI	g3393019
BLAST score	622
E value	2.0e-64
Match length	223
% identity	51
NCBI Description	(AL031174) beta-transducin [Schizosaccharomyces pombe]

Seq. No.	386868
Contig ID	2700_1.R1084
5'-most EST	LIB3431-047-P1-N1-B6

Seq. No.	386869
Contig ID	2702_1.R1084
5'-most EST	uC-osflcyp169d02a1
Method	BLASTX
NCBI GI	g5002357
BLAST score	366
E value	1.0e-34
Match length	119
% identity	61
NCBI Description	(AF150957) heat-shock protein ClpP [Azospirillum brasilense]

Seq. No.	386870
Contig ID	2706_1.R1084
5'-most EST	LIB3431-054-P1-N1-E2
Method	BLASTX
NCBI GI	g549986
BLAST score	450
E value	2.0e-44
Match length	124
% identity	70
NCBI Description	(U13149) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	386871
Contig ID	2709_1.R1084
5'-most EST	g454492
Method	BLASTX
NCBI GI	g462195

BLAST score	540
E value	7.0e-55
Match length	115
% identity	89
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	386872
Contig ID	2709_2.R1084
5'-most EST	uC-osf1cyp110a01b1
Method	BLASTX
NCBI GI	g462195
BLAST score	543
E value	2.0e-55
Match length	115
% identity	90
NCBI Description	PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG (GOS2 PROTEIN) >gi_100682_pir__S21636 GOS2 protein - rice >gi_20238_emb_CAA36190_ (X51910) GOS2 [Oryza sativa] >gi_3789950 (AF094774) translation initiation factor [Oryza sativa]

Seq. No.	386873
Contig ID	2719_1.R1084
5'-most EST	LIB3431-047-P1-N1-D4
Method	BLASTX
NCBI GI	g534982
BLAST score	264
E value	1.0e-42
Match length	148
% identity	53
NCBI Description	(X75898) phosphoglucomutase [Spinacia oleracea]

Seq. No.	386874
Contig ID	2719_2.R1084
5'-most EST	LIB3474-008-P1-K1-C11
Method	BLASTX
NCBI GI	g5902394
BLAST score	415
E value	1.0e-40
Match length	124
% identity	60
NCBI Description	(AC008148) Putative phosphoglucomutase [Arabidopsis thaliana]

Seq. No.	386875
Contig ID	2721_1.R1084
5'-most EST	LIB3432-006-P1-K1-B7
Method	BLASTX
NCBI GI	g114622
BLAST score	249
E value	1.0e-20
Match length	53
% identity	92

NCBI Description	ATP SYNTHASE B CHAIN (SUBUNIT I) >gi_67929_pir__LWRZ1 H+-transporting ATP synthase (EC 3.6.1.34) chain I - rice chloroplast >gi_669080_emb_CAA33992_ (X15901) ATPase I subunit [Oryza sativa] >gi_226695_prf__1603356W ATPase I [Oryza sativa]
Seq. No.	386876
Contig ID	2724_1.R1084
5'-most EST	LIB3431-047-P1-K1-D9
Seq. No.	386877
Contig ID	2735_1.R1084
5'-most EST	LIB3431-047-P1-N1-F1
Method	BLASTX
NCBI GI	g5541681
BLAST score	354
E value	4.0e-33
Match length	202
% identity	45
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]
Seq. No.	386878
Contig ID	2736_1.R1084
5'-most EST	g4715804
Method	BLASTX
NCBI GI	g2980777
BLAST score	501
E value	5.0e-50
Match length	232
% identity	53
NCBI Description	(AL022198) putative protein [Arabidopsis thaliana]
Seq. No.	386879
Contig ID	2742_1.R1084
5'-most EST	LIB3431-007-P1-N1-B7
Method	BLASTX
NCBI GI	g4587615
BLAST score	604
E value	2.0e-62
Match length	158
% identity	72
NCBI Description	(AC006951) putative acyl-CoA synthetase [Arabidopsis thaliana] >gi_4689469_gb_AAD27905.1_AC007213_3 (AC007213) putative acyl-CoA synthetase [Arabidopsis thaliana]
Seq. No.	386880
Contig ID	2746_1.R1084
5'-most EST	LIB3431-047-P1-N1-G1
Seq. No.	386881
Contig ID	2747_1.R1084
5'-most EST	LIB3431-047-P1-N1-G10
Seq. No.	386882
Contig ID	2753_1.R1084
5'-most EST	LIB3431-058-P1-K1-D9

Seq. No.	386883
Contig ID	2763_1.R1084
5'-most EST	LIB3433-030-P1-K1-E7
Method	BLASTN
NCBI GI	g4959460
BLAST score	37
E value	7.0e-11
Match length	38
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	386884
Contig ID	2769_1.R1084
5'-most EST	g4714142
Method	BLASTX
NCBI GI	g1663724
BLAST score	294
E value	3.0e-26
Match length	95
% identity	60
NCBI Description	(U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No.	386885
Contig ID	2769_2.R1084
5'-most EST	LIB3434-049-P1-K1-D3
Method	BLASTX
NCBI GI	g1663724
BLAST score	501
E value	1.0e-50
Match length	163
% identity	60
NCBI Description	(U50846) 4-coumarate:coenzyme A ligase [Nicotiana tabacum]

Seq. No.	386886
Contig ID	2770_1.R1084
5'-most EST	uC-osflM2020114a07a1

Seq. No.	386887
Contig ID	2772_1.R1084
5'-most EST	uC-osflcyp110a03a1

Seq. No.	386888
Contig ID	2775_1.R1084
5'-most EST	LIB3431-048-P1-N1-B1
Method	BLASTX
NCBI GI	g4982499
BLAST score	165
E value	4.0e-11
Match length	42
% identity	74
NCBI Description	(AC000107) F17F8.5 [Arabidopsis thaliana]

Seq. No.	386889
Contig ID	2789_1.R1084
5'-most EST	g425864
Method	BLASTX
NCBI GI	g1917019

BLAST score	936
E value	1.0e-101
Match length	224
% identity	84
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	386890
Contig ID	2789_3.R1084
5'-most EST	g427254
Method	BLASTX
NCBI GI	g1917019
BLAST score	695
E value	6.0e-73
Match length	241
% identity	66
NCBI Description	(U92045) ribosomal protein S6 RPS6-1 [Zea mays]

Seq. No.	386891
Contig ID	2791_1.R1084
5'-most EST	g3768107
Method	BLASTX
NCBI GI	g4678261
BLAST score	511
E value	1.0e-67
Match length	156
% identity	87
NCBI Description	(AL049657) putative proteasome regulatory subunit [Arabidopsis thaliana]

Seq. No.	386892
Contig ID	2797_2.R1084
5'-most EST	LIB3431-048-P1-N1-D1

Seq. No.	386893
Contig ID	2801_1.R1084
5'-most EST	LIB3431-048-P1-N1-D2

Seq. No.	386894
Contig ID	2804_1.R1084
5'-most EST	g3761183
Method	BLASTX
NCBI GI	g5257277
BLAST score	344
E value	4.0e-32
Match length	81
% identity	85
NCBI Description	(AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa]

Seq. No.	386895
Contig ID	2806_1.R1084
5'-most EST	uC-osflcyp173h06a1
Method	BLASTX
NCBI GI	g5882728
BLAST score	291
E value	2.0e-25

Match length	216
% identity	38
NCBI Description	(AC008263) ESTs gb_T75898, gb_R65457, gb_AA597517 and gb_AA597420 come from this gene. [Arabidopsis thaliana]

Seq. No.	386896
Contig ID	2809_1.R1084
5'-most EST	uC-osflcyp174g10a1
Method	BLASTX
NCBI GI	g5630087
BLAST score	205
E value	1.0e-15
Match length	114
% identity	41
NCBI Description	(AC004876) similar to predicted proteins AAB54240 (PID:g2088822) and S67138 (PID:g2132925) [Homo sapiens]

Seq. No.	386897
Contig ID	2822_1.R1084
5'-most EST	LIB3432-015-P1-K1-D12

Seq. No.	386898
Contig ID	2824_1.R1084
5'-most EST	LIB3434-038-P1-K1-E5

Seq. No.	386899
Contig ID	2830_1.R1084
5'-most EST	g3767930
Method	BLASTX
NCBI GI	g4938477
BLAST score	198
E value	7.0e-15
Match length	72
% identity	54
NCBI Description	(AL078464) putative protein [Arabidopsis thaliana]

Seq. No.	386900
Contig ID	2833_1.R1084
5'-most EST	g5003645
Method	BLASTX
NCBI GI	g4105794
BLAST score	388
E value	4.0e-37
Match length	116
% identity	57
NCBI Description	(AF049928) PGP224 [Petunia x hybrida]

Seq. No.	386901
Contig ID	2835_1.R1084
5'-most EST	LIB3431-048-P1-N1-G5
Method	BLASTX
NCBI GI	g4455201
BLAST score	432
E value	3.0e-42
Match length	110
% identity	76
NCBI Description	(AL035440) grpE like protein [Arabidopsis thaliana]

Seq. No.	386902
Contig ID	2837_1.R1084
5'-most EST	LIB3431-052-P1-N1-A3
Method	BLASTX
NCBI GI	g4001805
BLAST score	225
E value	5.0e-18
Match length	109
% identity	42
NCBI Description	(AF041476) BAF53a [Mus musculus]

Seq. No.	386903
Contig ID	2844_1.R1084
5'-most EST	LIB3431-017-P1-N1-G11
Method	BLASTX
NCBI GI	g3063710
BLAST score	295
E value	2.0e-26
Match length	77
% identity	66
NCBI Description	(AL022537) putative protein [Arabidopsis thaliana]

Seq. No.	386904
Contig ID	2845_1.R1084
5'-most EST	LIB3431-048-P1-N1-H7

Seq. No.	386905
Contig ID	2846_1.R1084
5'-most EST	LIB3431-048-P1-N1-H8

Seq. No.	386906
Contig ID	2849_1.R1084
5'-most EST	LIB3431-049-P1-K1-A11

Seq. No.	386907
Contig ID	2850_1.R1084
5'-most EST	g2800004

Seq. No.	386908
Contig ID	2851_1.R1084
5'-most EST	LIB3431-049-P1-N1-A2
Method	BLASTX
NCBI GI	g4510363
BLAST score	637
E value	3.0e-66
Match length	148
% identity	83
NCBI Description	(AC007017) putative DNA-binding protein [Arabidopsis thaliana]

Seq. No.	386909
Contig ID	2852_1.R1084
5'-most EST	g4715430

Seq. No.	386910
Contig ID	2857_1.R1084

5'-most EST	g5003217
Seq. No.	386911
Contig ID	2862_1.R1084
5'-most EST	LIB3431-034-P1-N1-C6
Seq. No.	386912
Contig ID	2862_2.R1084
5'-most EST	uC-osflcyp065g09a1
Method	BLASTX
NCBI GI	g5902930
BLAST score	314
E value	2.0e-29
Match length	88
% identity	78
NCBI Description	(AB029510) small GTP-binding protein OsRac3 [Oryza sativa]
Seq. No.	386913
Contig ID	2864_1.R1084
5'-most EST	uC-osflcyp172b03a1
Seq. No.	386914
Contig ID	2869_1.R1084
5'-most EST	LIB3432-043-P1-K1-G7
Method	BLASTX
NCBI GI	g5123926
BLAST score	169
E value	1.0e-11
Match length	65
% identity	48
NCBI Description	(AL079350) putative protein [Arabidopsis thaliana]
Seq. No.	386915
Contig ID	2872_1.R1084
5'-most EST	LIB3433-043-P1-K1-H1
Method	BLASTX
NCBI GI	g1805617
BLAST score	216
E value	4.0e-17
Match length	75
% identity	63
NCBI Description	(D49704) OSH44 transcript; homeobox gene [Oryza sativa]
Seq. No.	386916
Contig ID	2874_1.R1084
5'-most EST	g2796821
Method	BLASTX
NCBI GI	g5616313
BLAST score	152
E value	1.0e-09
Match length	60
% identity	12
NCBI Description	(AF160977) zinc finger protein [Pisum sativum]
Seq. No.	386917
Contig ID	2876_1.R1084
5'-most EST	LIB3431-049-P1-N1-C8

Method	BLASTX
NCBI GI	g2739360
BLAST score	330
E value	1.0e-30
Match length	123
% identity	59
NCBI Description	(AC002505) unknown protein [Arabidopsis thaliana] >gi_3075385 (AC004484) unknown protein [Arabidopsis thaliana]

Seq. No.	386918
Contig ID	2878_1.R1084
5'-most EST	g4715405
Method	BLASTX
NCBI GI	g480618
BLAST score	631
E value	3.0e-65
Match length	241
% identity	58
NCBI Description	ATAF1 protein - Arabidopsis thaliana (fragment) >gi_1345506_emb_CAA52771_ (X74755) ATAF1 [Arabidopsis thaliana]

Seq. No.	386919
Contig ID	2880_1.R1084
5'-most EST	LIB3431-049-P1-N1-D11

Seq. No.	386920
Contig ID	2882_1.R1084
5'-most EST	LIB3431-049-P1-N1-D2
Method	BLASTX
NCBI GI	g3757523
BLAST score	507
E value	7.0e-51
Match length	218
% identity	50
NCBI Description	(AC005167) putative transportin [Arabidopsis thaliana]

Seq. No.	386921
Contig ID	2883_1.R1084
5'-most EST	g3766823
Method	BLASTX
NCBI GI	g3819699
BLAST score	147
E value	6.0e-09
Match length	108
% identity	35
NCBI Description	(AJ009609) BnMAP4K alpha2 [Brassica napus]

Seq. No.	386922
Contig ID	2885_1.R1084
5'-most EST	LIB3431-049-P1-N1-D5

Seq. No.	386923
Contig ID	2896_1.R1084
5'-most EST	LIB3432-023-P1-K1-B11
Method	BLASTX

NCBI GI	g131271
BLAST score	825
E value	2.0e-88
Match length	184
% identity	84
NCBI Description	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi_72705_pir__QJRZ6A photosystem II chlorophyll a-binding protein psbB - rice chloroplast >gi_12013_emb_CAA33973_ (X15901) PSII 47kDa protein [Oryza sativa] >gi_226634_prf__1603356BH photosystem II 47kD protein [Oryza sativa]

Seq. No.	386924
Contig ID	2896_2.R1084
5'-most EST	LIB3431-020-P1-N1-B12

Seq. No.	386925
Contig ID	2905_1.R1084
5'-most EST	LIB3433-058-P1-K1-D7
Method	BLASTX
NCBI GI	g3738285
BLAST score	314
E value	2.0e-28
Match length	88
% identity	66
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	386926
Contig ID	2905_2.R1084
5'-most EST	g572190
Method	BLASTX
NCBI GI	g3738285
BLAST score	272
E value	8.0e-24
Match length	100
% identity	56
NCBI Description	(AC005309) unknown protein [Arabidopsis thaliana]

Seq. No.	386927
Contig ID	2915_1.R1084
5'-most EST	LIB3431-049-P1-N1-H2

Seq. No.	386928
Contig ID	2918_1.R1084
5'-most EST	g3769117
Method	BLASTX
NCBI GI	g4262142
BLAST score	150
E value	1.0e-09
Match length	69
% identity	51
NCBI Description	(AC005275) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	386929
Contig ID	2934_1.R1084
5'-most EST	LIB3431-050-P1-N1-B11

Seq. No.	386930
Contig ID	2936_1.R1084
5'-most EST	uC-osflcyp104a01a1
Method	BLASTX
NCBI GI	g1429226
BLAST score	228
E value	2.0e-18
Match length	47
% identity	85
NCBI Description	(X98861) TFIIA [Arabidopsis thaliana]

Seq. No.	386931
Contig ID	2939_1.R1084
5'-most EST	uC-osflcyp162g12a1
Method	BLASTX
NCBI GI	g3786409
BLAST score	145
E value	9.0e-09
Match length	78
% identity	38
NCBI Description	(AF098499) contains similarity to Saccharomyces cerevisiae MAF1 protein (GB:U19492) [Caenorhabditis elegans]

Seq. No.	386932
Contig ID	2940_1.R1084
5'-most EST	g3762706
Method	BLASTX
NCBI GI	g3236242
BLAST score	427
E value	7.0e-42
Match length	104
% identity	81
NCBI Description	(AC004684) putative ribosomal protein L36 [Arabidopsis thaliana]

Seq. No.	386933
Contig ID	2946_1.R1084
5'-most EST	LIB3431-050-P1-N1-C5

Seq. No.	386934
Contig ID	2955_1.R1084
5'-most EST	g4715137
Method	BLASTX
NCBI GI	g418594
BLAST score	400
E value	1.0e-56
Match length	200
% identity	60
NCBI Description	GTP-BINDING PROTEIN YPT7 >gi_322968_pir__A44334 GTP-binding protein YPT7 - yeast (Saccharomyces cerevisiae) >gi_5519_emb_CAA48244_ (X68144) GTP-binding protein (Ypt7p) [Saccharomyces cerevisiae] >gi_728647_emb_CAA88515_ (Z48613) Ypt7p [Saccharomyces cerevisiae] >gi_1171484_dbj_BAA10973_ (D64114) small GTP binding protein [Saccharomyces cerevisiae]

Seq. No.	386935
Contig ID	2963_1.R1084
5'-most EST	uC-osflcyp109d10a1
Method	BLASTX
NCBI GI	g2346966
BLAST score	187
E value	1.0e-13
Match length	66
% identity	53
NCBI Description	(AB004871) CPC [Arabidopsis thaliana] >gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana]

Seq. No.	386936
Contig ID	2963_2.R1084
5'-most EST	LIB3431-007-P1-N1-F1
Method	BLASTX
NCBI GI	g2346966
BLAST score	153
E value	1.0e-09
Match length	57
% identity	54
NCBI Description	(AB004871) CPC [Arabidopsis thaliana] >gi_4559383_gb_AAD23043.1_AC006526_8 (AC006526) putative DNA binding protein CPC [Arabidopsis thaliana]

Seq. No.	386937
Contig ID	2973_1.R1084
5'-most EST	LIB3431-050-P1-N1-F3
Method	BLASTX
NCBI GI	g1172556
BLAST score	548
E value	1.0e-55
Match length	262
% identity	44
NCBI Description	36 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 36) >gi_629729_pir__S46925 porin II, 36K - potato >gi_1076681_pir__B55364 porin (clone pPOM 36.2) - potato mitochondrion >gi_515360_emb_CAA56600_ (X80387) 36kDA porin II [Solanum tuberosum]

Seq. No.	386938
Contig ID	2977_1.R1084
5'-most EST	uC-osflcyp005b01b2
Method	BLASTX
NCBI GI	g6056196
BLAST score	471
E value	8.0e-47
Match length	138
% identity	68
NCBI Description	(AC009400) unknown protein [Arabidopsis thaliana]

Seq. No.	386939
Contig ID	2980_1.R1084
5'-most EST	LIB3431-050-P1-N1-G10
Method	BLASTX

NCBI GI	g4680501
BLAST score	209
E value	5.0e-21
Match length	113
% identity	56
NCBI Description	(AF119222) hypothetical protein [Oryza sativa]

Seq. No.	386940
Contig ID	2981_1.R1084
5'-most EST	LIB3431-062-P1-N1-D3
Method	BLASTX
NCBI GI	g21693
BLAST score	1371
E value	1.0e-152
Match length	308
% identity	80
NCBI Description	(X66012) cathepsin B [Triticum aestivum]

Seq. No.	386941
Contig ID	2981_2.R1084
5'-most EST	LIB3431-062-P1-K1-D3
Method	BLASTX
NCBI GI	g21699
BLAST score	366
E value	9.0e-35
Match length	110
% identity	63
NCBI Description	(X66013) cathepsin B [Triticum aestivum]

Seq. No.	386942
Contig ID	2981_4.R1084
5'-most EST	g570119
Method	BLASTX
NCBI GI	g21693
BLAST score	512
E value	6.0e-52
Match length	120
% identity	75
NCBI Description	(X66012) cathepsin B [Triticum aestivum]

Seq. No.	386943
Contig ID	2982_1.R1084
5'-most EST	LIB3431-050-P1-N1-G3

Seq. No.	386944
Contig ID	2983_1.R1084
5'-most EST	LIB3431-050-P1-N1-G5
Method	BLASTX
NCBI GI	g4507067
BLAST score	566
E value	5.0e-58
Match length	195
% identity	54
NCBI Description	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 >gi_134584_sp_P28370_SN21_HUMAN POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L1 >gi_479804_pir__S35457 SNF2

protein homolog - human >gi_292496 (M88163) transcription activator [Homo sapiens]

Seq. No.	386945
Contig ID	2986_1.R1084
5'-most EST	LIB3433-037-P1-K1-G5

Seq. No.	386946
Contig ID	2996_1.R1084
5'-most EST	g4714923
Method	BLASTX
NCBI GI	g1170606
BLAST score	509
E value	5.0e-51
Match length	218
% identity	81
NCBI Description	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) >gi_629863_pir__S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize >gi_3114421_pdb_1ZAK_A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) >gi_3114422_pdb_1ZAK_B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a)

Seq. No.	386947
Contig ID	3004_1.R1084
5'-most EST	LIB3433-052-P1-K1-G1
Method	BLASTX
NCBI GI	g4508079
BLAST score	224
E value	1.0e-46
Match length	151
% identity	61
NCBI Description	(AC005882) 66284 [Arabidopsis thaliana]

Seq. No.	386948
Contig ID	3052_1.R1084
5'-most EST	LIB3433-048-P1-K1-B3

Seq. No.	386949
Contig ID	3067_1.R1084
5'-most EST	g4714606

Seq. No.	386950
Contig ID	3071_1.R1084
5'-most EST	uC-osf1cyp065h10b1
Method	BLASTX
NCBI GI	g4091129
BLAST score	208
E value	7.0e-16
Match length	183
% identity	30
NCBI Description	(AF050165) protein phosphatase 2A regulatory subunit PR59; PP2A regulatory subunit PR59 [Mus musculus]

Seq. No. 386951

Contig ID	3073_1.R1084
5'-most EST	LIB3431-051-P1-K1-H11
Method	BLASTX
NCBI GI	g133936
BLAST score	884
E value	5.0e-95
Match length	173
% identity	99
NCBI Description	CHLOROPLAST 30S RIBOSOMAL PROTEIN S3 >gi_70867_pir__R3RZ3 ribosomal protein S3 - rice chloroplast >gi_12025_emb_CAA33934_ (X15901) ribosomal protein S3 [Oryza sativa] >gi_226646_prf__1603356BW ribosomal protein S3 [Oryza sativa]

Seq. No.	386952
Contig ID	3079_1.R1084
5'-most EST	g2801044
Method	BLASTX
NCBI GI	g1174778
BLAST score	536
E value	2.0e-54
Match length	105
% identity	98
NCBI Description	TRYPTOPHAN SYNTHASE BETA CHAIN 1 (ORANGE PERICARP 1) >gi_320136_pir__PQ0449 tryptophan synthase (EC 4.2.1.20) beta-1 chain - maize (fragment) >gi_168572 (M76684) tryptophan synthase beta-subunit [Zea mays]

Seq. No.	386953
Contig ID	3080_1.R1084
5'-most EST	LIB3475-002-P1-K2-E9
Method	BLASTX
NCBI GI	g4678947
BLAST score	353
E value	8.0e-33
Match length	193
% identity	58
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	386954
Contig ID	3080_2.R1084
5'-most EST	LIB3432-024-P1-K1-A10
Method	BLASTX
NCBI GI	g4678947
BLAST score	387
E value	2.0e-37
Match length	117
% identity	62
NCBI Description	(AL049711) putative protein [Arabidopsis thaliana]

Seq. No.	386955
Contig ID	3084_1.R1084
5'-most EST	g6012798
Method	BLASTX
NCBI GI	g2498465
BLAST score	247
E value	1.0e-20

Match length	142
% identity	49
NCBI Description	28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN) >gi_2143777_pir__S62782 heat and acid-stable phosphoprotein, 28K - rat >gi_847785 (U26541) HASPP28 [Rattus norvegicus] >gi_1588241_prf__2208261A casein kinase II substrate [Rattus norvegicus]

Seq. No.	386956
Contig ID	3087_1.R1084
5'-most EST	g5803495
Method	BLASTX
NCBI GI	g5824531
BLAST score	399
E value	3.0e-38
Match length	243
% identity	37
NCBI Description	(AL024499) cDNA EST EMBL:C10123 comes from this gene [Caenorhabditis elegans]

Seq. No.	386957
Contig ID	3091_1.R1084
5'-most EST	g5004965
Method	BLASTX
NCBI GI	g1181331
BLAST score	439
E value	4.0e-43
Match length	110
% identity	80
NCBI Description	(X77569) calnexin [Zea mays]

Seq. No.	386958
Contig ID	3094_1.R1084
5'-most EST	LIB3431-017-P1-N1-A9
Method	BLASTX
NCBI GI	g4337192
BLAST score	289
E value	9.0e-26
Match length	90
% identity	67
NCBI Description	(AC006403) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386959
Contig ID	3103_1.R1084
5'-most EST	LIB3431-017-P1-N1-B6

Seq. No.	386960
Contig ID	3113_1.R1084
5'-most EST	LIB3431-059-P1-N1-C3

Seq. No.	386961
Contig ID	3116_3.R1084
5'-most EST	LIB3431-017-P1-N1-C8
Method	BLASTX
NCBI GI	g4678346
BLAST score	646
E value	2.0e-67

Match length	150
% identity	84
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	386962
Contig ID	3117_1.R1084
5'-most EST	LIB3431-017-P1-N1-C9
Method	BLASTX
NCBI GI	g3341699
BLAST score	229
E value	1.0e-18
Match length	129
% identity	40
NCBI Description	(AC003672) putative giberellin beta-hydroxylase [Arabidopsis thaliana]

Seq. No.	386963
Contig ID	3118_1.R1084
5'-most EST	uC-osflcyp151d06a1

Seq. No.	386964
Contig ID	3124_1.R1084
5'-most EST	LIB3431-017-P1-N1-D4
Method	BLASTX
NCBI GI	g3927836
BLAST score	320
E value	4.0e-29
Match length	162
% identity	39
NCBI Description	(AC005727) unknown protein [Arabidopsis thaliana]

Seq. No.	386965
Contig ID	3133_1.R1084
5'-most EST	LIB3434-059-P1-K1-C8
Method	BLASTX
NCBI GI	g5903092
BLAST score	719
E value	8.0e-76
Match length	205
% identity	76
NCBI Description	(AC008017) Highly similar to developmental protein DG1118 [Arabidopsis thaliana]

Seq. No.	386966
Contig ID	3134_1.R1084
5'-most EST	LIB3434-046-P1-K1-C8

Seq. No.	386967
Contig ID	3135_1.R1084
5'-most EST	uC-osflcyp160f11a1
Method	BLASTX
NCBI GI	g2911280
BLAST score	194
E value	7.0e-22
Match length	83
% identity	70
NCBI Description	(U73937) PK12 protein kinase [Nicotiana tabacum]

Seq. No.	386968
Contig ID	3137_1.R1084
5'-most EST	LIB3431-017-P1-N1-E5
Method	BLASTX
NCBI GI	g5902387
BLAST score	282
E value	9.0e-25
Match length	160
% identity	38
NCBI Description	(AC009322) Similar to polygalacturonases [Arabidopsis thaliana]

Seq. No.	386969
Contig ID	3138_1.R1084
5'-most EST	LIB3431-017-P1-N1-E6
Method	BLASTX
NCBI GI	g128186
BLAST score	254
E value	1.0e-21
Match length	50
% identity	92
NCBI Description	NITRATE REDUCTASE 1 (NR1) >gi_82490_pir__S07554 nitrate reductase (NADH) (EC 1.6.6.1) - rice

Seq. No.	386970
Contig ID	3147_1.R1084
5'-most EST	uC-osroM202033g09a1
Method	BLASTX
NCBI GI	g2960216
BLAST score	574
E value	6.0e-59
Match length	138
% identity	80
NCBI Description	(AJ223384) 26S proteasome regulatory ATPase subunit 10b (S10b) [Manduca sexta]

Seq. No.	386971
Contig ID	3159_1.R1084
5'-most EST	LIB3431-017-P1-N1-G7

Seq. No.	386972
Contig ID	3161_1.R1084
5'-most EST	g3761660
Method	BLASTX
NCBI GI	g1236961
BLAST score	325
E value	6.0e-30
Match length	107
% identity	53
NCBI Description	(U50201) prunasin hydrolase precursor [Prunus serotina]

Seq. No.	386973
Contig ID	3162_1.R1084
5'-most EST	uC-osflcyp174h11a1
Method	BLASTX
NCBI GI	g5919219

BLAST score	278
E value	4.0e-24
Match length	190
% identity	7
NCBI Description	(AF186273) leucine-rich repeats containing F-box protein FBL3 [Homo sapiens]

Seq. No.	386974
Contig ID	3163_1.R1084
5'-most EST	uC-osrocyp028g07a1

Seq. No.	386975
Contig ID	3170_1.R1084
5'-most EST	uC-osflcyp003e04b1
Method	BLASTN
NCBI GI	g487317
BLAST score	77
E value	2.0e-34
Match length	544
% identity	69
NCBI Description	Rice mRNA EN56, partial sequence

Seq. No.	386976
Contig ID	3170_4.R1084
5'-most EST	uC-osflcyp173b09b1
Method	BLASTN
NCBI GI	g4966303
BLAST score	45
E value	7.0e-16
Match length	211
% identity	15
NCBI Description	Caenorhabditis elegans cosmid F16B3

Seq. No.	386977
Contig ID	3180_1.R1084
5'-most EST	g3768407
Method	BLASTX
NCBI GI	g4836912
BLAST score	870
E value	2.0e-93
Match length	241
% identity	70
NCBI Description	(AC007153) 60811 [Arabidopsis thaliana]

Seq. No.	386978
Contig ID	3180_2.R1084
5'-most EST	uC-osflcyp121a09b1
Method	BLASTX
NCBI GI	g4836912
BLAST score	610
E value	2.0e-63
Match length	155
% identity	77
NCBI Description	(AC007153) 60811 [Arabidopsis thaliana]

Seq. No.	386979
Contig ID	3183_1.R1084

5'-most EST	LIB3431-018-P1-N1-B10
Method	BLASTX
NCBI GI	g2088647
BLAST score	1027
E value	1.0e-112
Match length	298
% identity	66
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana] >gi_3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]

Seq. No.	386980
Contig ID	3184_1.R1084
5'-most EST	uC-osflcyp160e04a1

Seq. No.	386981
Contig ID	3185_1.R1084
5'-most EST	LIB3431-018-P1-N1-B12

Seq. No.	386982
Contig ID	3193_1.R1084
5'-most EST	uC-osroM202023d06b1
Method	BLASTX
NCBI GI	g2501578
BLAST score	1300
E value	1.0e-144
Match length	307
% identity	84
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	386983
Contig ID	3193_3.R1084
5'-most EST	LIB3432-028-P1-K1-G2
Method	BLASTX
NCBI GI	g2501578
BLAST score	642
E value	4.0e-67
Match length	142
% identity	89
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047 ethylene-responsive protein 1 - Para rubber tree >gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	386984
Contig ID	3193_4.R1084
5'-most EST	g4715419
Method	BLASTX
NCBI GI	g2501578
BLAST score	517
E value	2.0e-52
Match length	127
% identity	81
NCBI Description	ETHYLENE-INDUCIBLE PROTEIN HEVER >gi_2129913_pir__S60047

ethylene-responsive protein 1 - Para rubber tree
>gi_1209317 (M88254) ethylene-inducible protein [Hevea brasiliensis]

Seq. No.	386985
Contig ID	3194_1.R1084
5'-most EST	LIB3431-018-P1-N1-C2

Seq. No.	386986
Contig ID	3212_1.R1084
5'-most EST	g5038814

Seq. No.	386987
Contig ID	3213_1.R1084
5'-most EST	uC-osflcyp009d11b2
Method	BLASTX
NCBI GI	g3831441
BLAST score	185
E value	2.0e-13
Match length	69
% identity	70
NCBI Description	(AC005819) hypothetical protein [Arabidopsis thaliana]

Seq. No.	386988
Contig ID	3222_1.R1084
5'-most EST	LIB3431-018-P1-N1-E6

Seq. No.	386989
Contig ID	3229_1.R1084
5'-most EST	LIB3431-018-P1-N1-F3

Seq. No.	386990
Contig ID	3235_1.R1084
5'-most EST	uC-osroM202036c07b1
Method	BLASTX
NCBI GI	g4376158
BLAST score	783
E value	2.0e-83
Match length	205
% identity	78
NCBI Description	(X98873) aspartate kinase [Arabidopsis thaliana]

Seq. No.	386991
Contig ID	3241_1.R1084
5'-most EST	LIB3431-035-P1-N1-D3
Method	BLASTX
NCBI GI	g6014904
BLAST score	683
E value	2.0e-71
Match length	157
% identity	81
NCBI Description	DAG PROTEIN, CHLOROPLAST PRECURSOR >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]

Seq. No.	386992
Contig ID	3244_1.R1084
5'-most EST	LIB3431-018-P1-N1-G8

Method	BLASTX
NCBI GI	g5262756
BLAST score	221
E value	7.0e-30
Match length	98
% identity	70
NCBI Description	(AL080283) putative protein [Arabidopsis thaliana]

Seq. No.	386993
Contig ID	3250_1.R1084
5'-most EST	LI[illegible]-Q16-P1-K1-H3
Method	BL[illegible] X
NCBI GI	g113466
BLAST score	271
E value	2.0e-23
Match length	82
% identity	63
NCBI Description	ADP,ATP CARRIER PROTEIN (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_72020_pir__XWNC ADP,ATP carrier protein - Neurospora crassa >gi_2977_emb_CAA25104_ (X00363) ADP/ATP carrier protein [Neurospora crassa]

Seq. No.	386994
Contig ID	3253_1.R1084
5'-most EST	g4716112
Method	BLASTX
NCBI GI	g50 [illegible]09
BLAST score	63[illegible]
E value	9.0e-6[illegible]
Match length	186
% identity	67
NCBI Description	(AC006193) Puta[illegible] membrane related protein [A[illegible]abidopsis thaliana]

Seq. No.	386995
Contig ID	3255_1.R1084
5'-most EST	g3760941
Method	BLASTN
NCBI GI	g4206065
BLAST score	34
E value	2.0e-09
Match length	34
% identity	100
NCBI Description	Homo sapiens map 7qter; 41.64cR from WI-8540 repeat region, complete sequence

Seq. No.	386996
Contig ID	3266_1.R1084
5'-most EST	g2801174
Method	BLASTX
NCBI GI	g2809245
BLAST score	427
E value	1.0e-41
Match length	107
% identity	76
NCBI Description	(AC002560) F21B7.14 [Arabidopsis thaliana]

Seq. No.	386997
Contig ID	3268_1.R1084
5'-most EST	g2801322
Method	BLASTX
NCBI GI	g4038594
BLAST score	118
E value	2.0e-14
Match length	66
% identity	62
NCBI Description	(AJ222798) tDET1 protein [Lycopersicon esculentum] >gi_4454332_emb_CAA11914_ (AJ224356) tDET1 protein [Lycopersicon esculentum]

Seq. No.	386998
Contig ID	3271_1.R1084
5'-most EST	LIB3431-019-P1-N1-C6

Seq. No.	386999
Contig ID	3273_1.R1084
5'-most EST	g3762880
Method	BLASTX
NCBI GI	g2199574
BLAST score	150
E value	3.0e-09
Match length	113
% identity	33
NCBI Description	(AF004293) aquaporin [Brassica rapa]

Seq. No.	387000
Contig ID	3278_1.R1084
5'-most EST	LIB3431-019-P1-K1-C10

Seq. No.	387001
Contig ID	3279_1.R1084
5'-most EST	uC-osf1cyp173c08a1
Method	BLASTX
NCBI GI	g5031281
BLAST score	328
E value	5.0e-30
Match length	92
% identity	67
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	387002
Contig ID	3279_2.R1084
5'-most EST	uC-osf1cyp018c01b2
Method	BLASTX
NCBI GI	g5031281
BLAST score	561
E value	3.0e-57
Match length	173
% identity	62
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	387003
Contig ID	3279_4.R1084
5'-most EST	uC-osrocyp015e02b1

Method	BLASTX
NCBI GI	g5031281
BLAST score	552
E value	2.0e-56
Match length	158
% identity	66
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	387004
Contig ID	3279_5.R1084
5'-most EST	g4969026
Method	BLASTX
NCBI GI	g5031281
BLAST score	197
E value	5.0e-15
Match length	72
% identity	39
NCBI Description	(AF139499) unknown [Prunus armeniaca]

Seq. No.	387005
Contig ID	3284_1.R1084
5'-most EST	LIB3431-019-P1-N1-C5
Method	BLASTX
NCBI GI	g3776005
BLAST score	423
E value	2.0e-41
Match length	91
% identity	91
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	387006
Contig ID	3303_1.R1084
5'-most EST	g5056032
Method	BLASTX
NCBI GI	g2623298
BLAST score	1643
E value	0.0e+00
Match length	581
% identity	72
NCBI Description	(AC002409) putative 4-alpha-glucanotransferase [Arabidopsis thaliana]

Seq. No.	387007
Contig ID	3303_2.R1084
5'-most EST	g3763307

Seq. No.	387008
Contig ID	3304_1.R1084
5'-most EST	LIB3431-019-P1-N1-E3

Seq. No.	387009
Contig ID	3305_1.R1084
5'-most EST	LIB3431-019-P1-N1-E4
Method	BLASTX
NCBI GI	g5764049
BLAST score	358
E value	1.0e-33

Match length	186
% identity	32
NCBI Description	(Y16832) alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Nicotiana tabacum]

Seq. No.	387010
Contig ID	3313_1.R1084
5'-most EST	g1037034

Seq. No.	387011
Contig ID	3323_1.R1084
5'-most EST	uC-osflcyp029h07a1
Method	BLASTX
NCBI GI	g1652203
BLAST score	150
E value	1.0e-09
Match length	78
% identity	38
NCBI Description	(D90903) hypothetical protein [Synechocystis sp.]

Seq. No.	387012
Contig ID	3328_1.R1084
5'-most EST	g3445003
Method	BLASTX
NCBI GI	g4506221
BLAST score	434
E value	2.0e-42
Match length	220
% identity	41
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	387013
Contig ID	3328_2.R1084
5'-most EST	g4715023
Method	BLASTX
NCBI GI	g4506221
BLAST score	266
E value	7.0e-23
Match length	146
% identity	40
NCBI Description	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 >gi_1945611_dbj_BAA19749_ (AB003103) 26S proteasome subunit p55 [Homo sapiens]

Seq. No.	387014
Contig ID	3329_1.R1084
5'-most EST	LIB3431-019-P1-N1-G9

Seq. No.	387015
Contig ID	3332_2.R1084
5'-most EST	uC-osflcyp141d10a1

Seq. No.	387016
Contig ID	3337_1.R1084

5'-most EST	LIB3431-019-P1-N1-H6
Seq. No.	387017
Contig ID	3338_1.R1084
5'-most EST	g3762544
Method	BLASTX
NCBI GI	g2132068
BLAST score	489
E value	1.0e-50
Match length	197
% identity	55
NCBI Description	hypothetical protein YOR145c - yeast (Saccharomyces cerevisiae) >gi_1293706 (U55020) O3513p [Saccharomyces cerevisiae] >gi_1420368_emb_CAA99349_ (Z75053) ORF YOR145c [Saccharomyces cerevisiae]
Seq. No.	387018
Contig ID	3338_2.R1084
5'-most EST	g426764
Method	BLASTX
NCBI GI	g1164988
BLAST score	151
E value	1.0e-09
Match length	64
% identity	42
NCBI Description	(X94335) YOR3513c [Saccharomyces cerevisiae]
Seq. No.	387019
Contig ID	3342_1.R1084
5'-most EST	g4714844
Seq. No.	387020
Contig ID	3344_1.R1084
5'-most EST	g3767235
Seq. No.	387021
Contig ID	3356_1.R1084
5'-most EST	uC-osflcyp157f05a1
Method	BLASTX
NCBI GI	g710626
BLAST score	195
E value	2.0e-14
Match length	153
% identity	34
NCBI Description	(D30719) ERD15 protein [Arabidopsis thaliana] >gi_3241941 (AC004625) dehydration-induced protein ERD15 [Arabidopsis thaliana] >gi_3894181 (AC005662) ERD15 protein [Arabidopsis thaliana]
Seq. No.	387022
Contig ID	3357_1.R1084
5'-most EST	LIB3431-020-P1-N1-B4
Seq. No.	387023
Contig ID	3359_1.R1084
5'-most EST	uC-osflcyp161e02a1
Method	BLASTX

NCBI GI	g4063821
BLAST score	1659
E value	0.0e+00
Match length	332
% identity	96
NCBI Description	(AB015204) plastidic ATP sulfurylase [Oryza sativa]

Seq. No.	387024
Contig ID	3359_2.R1084
5'-most EST	uC-osflcyp013f06b1
Method	BLASTX
NCBI GI	g4063821
BLAST score	231
E value	6.0e-19
Match length	45
% identity	98
NCBI Description	(AB015204) plastidic ATP sulfurylase [Oryza sativa]

Seq. No.	387025
Contig ID	3359_4.R1084
5'-most EST	uC-osflcyp013d10b1
Method	BLASTN
NCBI GI	g3986152
BLAST score	258
E value	1.0e-143
Match length	326
% identity	96
NCBI Description	Oryza sativa gene for plastidic ATP sulfurylase, complete cds

Seq. No.	387026
Contig ID	3361_1.R1084
5'-most EST	LIB3431-020-P1-N1-B9
Method	BLASTX
NCBI GI	g2673912
BLAST score	409
E value	1.0e-39
Match length	144
% identity	56
NCBI Description	(AC002561) unknown protein [Arabidopsis thaliana]

Seq. No.	387027
Contig ID	3376_1.R1084
5'-most EST	LIB3479-001-Q6-K1-F3
Method	BLASTX
NCBI GI	g3695005
BLAST score	988
E value	1.0e-129
Match length	267
% identity	90
NCBI Description	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]

Seq. No.	387028
Contig ID	3376_2.R1084
5'-most EST	LIB3474-007-P1-K1-C2
Method	BLASTX

NCBI GI	g3695005
BLAST score	386
E value	2.0e-76
Match length	172
% identity	91
NCBI Description	(AF038586) pyruvate dehydrogenase kinase isoform 2; PDK2 [Zea mays]

Seq. No.	387029
Contig ID	3376_3.R1084
5'-most EST	LIB3431-020-P1-N1-D3
Method	BLASTN
NCBI GI	g3695004
BLAST score	38
E value	2.0e-11
Match length	54
% identity	93
NCBI Description	Zea mays pyruvate dehydrogenase kinase isoform 2 mRNA, nuclear gene encoding mitochondrial protein, complete cds

Seq. No.	387030
Contig ID	3377_1.R1084
5'-most EST	LIB3431-020-P1-N1-D4
Method	BLASTN
NCBI GI	g2264310
BLAST score	45
E value	1.0e-15
Match length	201
% identity	84
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKP11, complete sequence

Seq. No.	387031
Contig ID	3379_1.R1084
5'-most EST	LIB3431-020-P1-N1-D6
Method	BLASTX
NCBI GI	g3047117
BLAST score	654
E value	7.0e-85
Match length	163
% identity	95
NCBI Description	(AF058919) similar to ATP-dependent RNA helicases [Arabidopsis thaliana]

Seq. No.	387032
Contig ID	3380_1.R1084
5'-most EST	LIB3431-020-P1-N1-D7

Seq. No.	387033
Contig ID	3387_1.R1084
5'-most EST	g4715006
Method	BLASTX
NCBI GI	g4886307
BLAST score	1153
E value	1.0e-127
Match length	234
% identity	93

NCBI Description	(AJ242588) 1-deoxy-d-xylulose-5-phosphate reductoisomerase [Arabidopsis thaliana]

Seq. No.	387034
Contig ID	3389_1.R1084
5'-most EST	g3107270

Seq. No.	387035
Contig ID	3390_1.R1084
5'-most EST	LIB3431-020-P1-N1-E5
Method	BLASTX
NCBI GI	g5916444
BLAST score	459
E value	2.0e-45
Match length	166
% identity	52
NCBI Description	(AC007633) putative protein [Arabidopsis thaliana]

Seq. No.	387036
Contig ID	3395_1.R1084
5'-most EST	g2798245

Seq. No.	387037
Contig ID	3400_1.R1084
5'-most EST	LIB3431-020-P1-N1-F5
Method	BLASTX
NCBI GI	g6002055
BLAST score	468
E value	5.0e-87
Match length	274
% identity	62
NCBI Description	(AJ249794) lipoxygenase [Arabidopsis thaliana]

Seq. No.	387038
Contig ID	3408_1.R1084
5'-most EST	LIB3431-001-P1-N1-C8
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	1.0e-09
Match length	37
% identity	39
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	387039
Contig ID	3409_1.R1084
5'-most EST	LIB3431-020-P1-N1-G4

Seq. No.	387040
Contig ID	3411_1.R1084
5'-most EST	LIB3433-011-Q6-K1-C2
Method	BLASTX
NCBI GI	g3236247
BLAST score	533
E value	4.0e-54
Match length	150
% identity	63

NCBI Description	(AC004684) SCARECROW-like protein [Arabidopsis thaliana]

Seq. No.	387041
Contig ID	3421_1.R1084
5'-most EST	uC-osrocyp033a08a1
Method	BLASTX
NCBI GI	g4097587
BLAST score	388
E value	4.0e-37
Match length	114
% identity	66
NCBI Description	(U64926) NTGP5 [Nicotiana tabacum]

Seq. No.	387042
Contig ID	3424_1.R1084
5'-most EST	g3762045

Seq. No.	387043
Contig ID	3433_1.R1084
5'-most EST	uC-osflcyp023e06b2

Seq. No.	387044
Contig ID	3447_1.R1084
5'-most EST	g2799603
Method	BLASTX
NCBI GI	g5091509
BLAST score	2535
E value	0.0e+00
Match length	536
% identity	96
NCBI Description	(AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No.	387045
Contig ID	3447_3.R1084
5'-most EST	g1854131
Method	BLASTX
NCBI GI	g5091509
BLAST score	329
E value	2.0e-30
Match length	65
% identity	91
NCBI Description	(AB023482) EST AU065533(C2174) corresponds to a region of the predicted gene.; Similar to Homo sapiens splicing factor Prp8 mRNA, complete cds.(AF092565) [Oryza sativa]

Seq. No.	387046
Contig ID	3450_1.R1084
5'-most EST	g3762545
Method	BLASTX
NCBI GI	g464705
BLAST score	493
E value	1.0e-73
Match length	150
% identity	97
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal

	protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.	387047
Contig ID	3450_2.R1084
5'-most EST	g3761079
Method	BLASTX
NCBI GI	g464705
BLAST score	729
E value	4.0e-77
Match length	148
% identity	95
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.	387048
Contig ID	3450_3.R1084
5'-most EST	g3759892
Method	BLASTX
NCBI GI	g464705
BLAST score	253
E value	1.0e-21
Match length	58
% identity	86
NCBI Description	40S RIBOSOMAL PROTEIN S13 >gi_419802_pir__S30146 ribosomal protein S13.e - maize >gi_288059_emb_CAA44311_ (X62455) cytoplasmatic ribosomal protein S13 [Zea mays]
Seq. No.	387049
Contig ID	3456_1.R1084
5'-most EST	LIB3431-034-P1-N1-D10
Method	BLASTN
NCBI GI	g218218
BLAST score	81
E value	2.0e-37
Match length	112
% identity	94
NCBI Description	Oryza sativa p-SINE1-r3 gene, repeat sequence
Seq. No.	387050
Contig ID	3460_1.R1084
5'-most EST	uC-osroM202027c06a1
Method	BLASTX
NCBI GI	g3786007
BLAST score	157
E value	3.0e-10
Match length	46
% identity	48
NCBI Description	(AC005499) hypothetical protein [Arabidopsis thaliana]
Seq. No.	387051
Contig ID	3461_1.R1084
5'-most EST	g3762822
Method	BLASTX
NCBI GI	g461899
BLAST score	264

E value	5.0e-26
Match length	109
% identity	67
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	387052
Contig ID	3461_2.R1084
5'-most EST	LIB3434-047-P1-K1-F12
Method	BLASTX
NCBI GI	g461899
BLAST score	577
E value	2.0e-59
Match length	171
% identity	65
NCBI Description	PEPTIDYL-PROLYL CIS-TRANS ISOMERASE, CHLOROPLAST PRECURSOR (PPIASE) (ROTAMASE) (CYCLOPHILIN) (CYCLOSPORIN A-BINDING PROTEIN) >gi_1076368_pir__B53422 peptidylprolyl isomerase (EC 5.2.1.8) ROC4 - Arabidopsis thaliana >gi_405131 (L14845) cyclophilin [Arabidopsis thaliana] >gi_1322278 (U42724) cyclophilin [Arabidopsis thaliana]

Seq. No.	387053
Contig ID	3463_1.R1084
5'-most EST	g1944259
Method	BLASTN
NCBI GI	g3819197
BLAST score	55
E value	7.0e-22
Match length	200
% identity	82
NCBI Description	Hordeum vulgare partial mRNA; clone cMWG0676.uni

Seq. No.	387054
Contig ID	3465_1.R1084
5'-most EST	LIB3431-034-P1-N1-E1
Method	BLASTX
NCBI GI	g1723339
BLAST score	345
E value	6.0e-32
Match length	156
% identity	44
NCBI Description	HYPOTHETICAL 19.2 KD PROTEIN YCF36 (ORF165) >gi_2147559_pir__S73194 hypothetical protein 36 - Porphyra purpurea chloroplast >gi_1276739 (U38804) hypothetical chloroplast ORF 36. [Porphyra purpurea]

Seq. No.	387055
Contig ID	3468_1.R1084
5'-most EST	uC-osf1cyp086d03b1
Method	BLASTX
NCBI GI	g5902389
BLAST score	176

E value	3.0e-12
Match length	83
% identity	39
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No.	387056
Contig ID	3472_1.R1084
5'-most EST	g3767845
Method	BLASTX
NCBI GI	g927575
BLAST score	673
E value	1.0e-129
Match length	354
% identity	60
NCBI Description	(U12926) alpha galactosidase [Glycine max]

Seq. No.	387057
Contig ID	3473_1.R1084
5'-most EST	uC-osrocyp009b12b1

Seq. No.	387058
Contig ID	3490_1.R1084
5'-most EST	LIB3431-034-P1-N1-G4
Method	BLASTX
NCBI GI	g3319357
BLAST score	367
E value	6.0e-35
Match length	101
% identity	66
NCBI Description	(AF077407) contains similarity to phosphoenolpyruvate synthase (ppsA) (GB:AE001056) [Arabidopsis thaliana]

Seq. No.	387059
Contig ID	3494_1.R1084
5'-most EST	g5667623
Method	BLASTN
NCBI GI	g3241924
BLAST score	33
E value	1.0e-08
Match length	109
% identity	87
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence

Seq. No.	387060
Contig ID	3499_1.R1084
5'-most EST	LIB3431-034-P1-N1-H3
Method	BLASTX
NCBI GI	g417482
BLAST score	647
E value	1.0e-67
Match length	201
% identity	63
NCBI Description	PROTEIN FARNESYLTRANSFERASE BETA SUBUNIT (CAAX FARNESYLTRANSFERASE BETA SUBUNIT) (RAS PROTEINS PRENYLTRANSFERASE) (FTASE-BETA) >gi_541966_pir__JQ2254 farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) beta

chain - garden pea >gi_169049 (L08664) farnesyl-protein transferase beta-subunit [Pisum sativum]

Seq. No.	387061
Contig ID	3501_1.R1084
5'-most EST	LIB3431-034-P1-N1-H5
Method	BLASTX
NCBI GI	g6006429
BLAST score	383
E value	2.0e-36
Match length	179
% identity	45
NCBI Description	(AJ242958) SPL1-Related3 protein [Arabidopsis thaliana]

Seq. No.	387062
Contig ID	3503_1.R1084
5'-most EST	LIB3431-034-P1-N1-H8
Method	BLASTX
NCBI GI	g2129636
BLAST score	225
E value	2.0e-33
Match length	236
% identity	41
NCBI Description	lipase - Arabidopsis thaliana >gi_1145627 (U38916) lipase [Arabidopsis thaliana]

Seq. No.	387063
Contig ID	3506_1.R1084
5'-most EST	uC-osflcyp066h07a1

Seq. No.	387064
Contig ID	3508_1.R1084
5'-most EST	LIB3431-035-P1-N1-A5
Method	BLASTX
NCBI GI	g3786009
BLAST score	689
E value	2.0e-72
Match length	178
% identity	78
NCBI Description	(AC005499) unknown protein [Arabidopsis thaliana]

Seq. No.	387065
Contig ID	3512_1.R1084
5'-most EST	LIB3431-035-P1-N1-A9

Seq. No.	387066
Contig ID	3514_1.R1084
5'-most EST	LIB3431-035-P1-N1-B10

Seq. No.	387067
Contig ID	3515_1.R1084
5'-most EST	g3768404
Method	BLASTX
NCBI GI	g3757521
BLAST score	791
E value	5.0e-84
Match length	417

% identity	44
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	387068
Contig ID	3522_1.R1084
5'-most EST	LIB3431-035-P1-N1-C1

Seq. No.	387069
Contig ID	3527_1.R1084
5'-most EST	LIB3431-035-P1-N1-C3
Method	BLASTX
NCBI GI	g2760606
BLAST score	737
E value	5.0e-78
Match length	157
% identity	87
NCBI Description	(AB001568) phospholipid hydroperoxide glutathione peroxidase-like protein [Arabidopsis thaliana] >gi_3004869 (AF030132) glutathione peroxidase; ATGP1 [Arabidopsis thaliana] >gi_4539451_emb_CAB39931.1_ (AL049500) phospholipid hydroperoxide glutathione peroxidase [Arabidopsis thaliana]

Seq. No.	387070
Contig ID	3532_1.R1084
5'-most EST	LIB3431-040-P1-K2-D1
Method	BLASTX
NCBI GI	g5042462
BLAST score	404
E value	8.0e-39
Match length	124
% identity	69
NCBI Description	(AC007789) putative negatively light-regulated protein [Oryza sativa]

Seq. No.	387071
Contig ID	3532_2.R1084
5'-most EST	g3762581
Method	BLASTN
NCBI GI	g5042437
BLAST score	281
E value	1.0e-156
Match length	495
% identity	97
NCBI Description	Oryza sativa BAC T49B20 genomic sequence, complete sequence

Seq. No.	387072
Contig ID	3542_1.R1084
5'-most EST	g4969281
Method	BLASTX
NCBI GI	g1172874
BLAST score	233
E value	1.0e-24
Match length	168
% identity	43
NCBI Description	DEHYDRATION-RESPONSIVE PROTEIN RD22 PRECURSOR >gi_479589_pir__S34823 dehydration-induced protein RD22 -

Arabidopsis thaliana >gi_391608_dbj_BAA01546_ (D10703) rd22 [Arabidopsis thaliana] >gi_447134_prf__1913421A rd22 gene [Arabidopsis thaliana]

Seq. No.	387073
Contig ID	3552_1.R1084
5'-most EST	LIB3431-035-P1-N1-E5
Method	BLASTX
NCBI GI	g5103848
BLAST score	240
E value	6.0e-20
Match length	89
% identity	49
NCBI Description	(AC007591) F9L1.16 [Arabidopsis thaliana]

Seq. No.	387074
Contig ID	3555_1.R1084
5'-most EST	LIB3431-035-P1-K1-E8

Seq. No.	387075
Contig ID	3560_1.R1084
5'-most EST	LIB3431-035-P1-N1-F2

Seq. No.	387076
Contig ID	3561_1.R1084
5'-most EST	LIB3431-035-P1-N1-F4
Method	BLASTX
NCBI GI	g5441881
BLAST score	175
E value	3.0e-12
Match length	115
% identity	39
NCBI Description	(AP000367) Similar to putative receptor kinase. (AC002332) [Oryza sativa]

Seq. No.	387077
Contig ID	3570_1.R1084
5'-most EST	LIB3431-035-P1-N1-G12
Method	BLASTN
NCBI GI	g3063523
BLAST score	111
E value	3.0e-55
Match length	111
% identity	100
NCBI Description	Oryza sativa ribulose 1,5-bisphosphate carboxylase small subunit mRNA, complete cds

Seq. No.	387078
Contig ID	3573_1.R1084
5'-most EST	g3107022
Method	BLASTX
NCBI GI	g1616659
BLAST score	784
E value	1.0e-83
Match length	159
% identity	92
NCBI Description	(U49387) adenylosuccinate synthetase [Triticum aestivum]

Seq. No.	387079
Contig ID	3577_1.R1084
5'-most EST	g5803453
Seq. No.	387080
Contig ID	3583_1.R1084
5'-most EST	g4715662
Seq. No.	387081
Contig ID	3589_1.R1084
5'-most EST	LIB3431-035-P1-N1-H9
Seq. No.	387082
Contig ID	3591_1.R1084
5'-most EST	g4716561
Method	BLASTX
NCBI GI	g5734748
BLAST score	217
E value	4.0e-17
Match length	134
% identity	36
NCBI Description	(AC007651) Unknown protein [Arabidopsis thaliana]
Seq. No.	387083
Contig ID	3596_1.R1084
5'-most EST	LIB3431-052-P1-N1-F6
Seq. No.	387084
Contig ID	3597_1.R1084
5'-most EST	g4716165
Seq. No.	387085
Contig ID	3597_2.R1084
5'-most EST	uC-osflcyp033b02b1
Seq. No.	387086
Contig ID	3598_1.R1084
5'-most EST	LIB3431-040-P1-N1-B5
Seq. No.	387087
Contig ID	3604_1.R1084
5'-most EST	LIB3431-040-P1-N1-C2
Method	BLASTX
NCBI GI	g4995921
BLAST score	230
E value	5.0e-19
Match length	56
% identity	79
NCBI Description	(AJ006708) HMG1 protein [Zea mays]
Seq. No.	387088
Contig ID	3606_1.R1084
5'-most EST	g4716379
Method	BLASTN
NCBI GI	g5295936
BLAST score	56

E value	1.0e-22
Match length	170
% identity	51
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0681F10, complete sequence

Seq. No.	387089
Contig ID	3611_1.R1084
5'-most EST	LIB3431-040-P1-N1-D2

Seq. No.	387090
Contig ID	3613_1.R1084
5'-most EST	g5607474
Method	BLASTN
NCBI GI	g4733953
BLAST score	37
E value	6.0e-11
Match length	109
% identity	83
NCBI Description	Arabidopsis thaliana chromosome I BAC F13O11 genomic sequence, complete sequence

Seq. No.	387091
Contig ID	3625_1.R1084
5'-most EST	uC-osf1cyp157f01b1
Method	BLASTX
NCBI GI	g1174745
BLAST score	1136
E value	1.0e-124
Match length	241
% identity	90
NCBI Description	TRIOSEPHOSPHATE ISOMERASE, CHLOROPLAST PRECURSOR (TIM) >gi_1363523_pir__S53761 triose-phosphate isomerase (EC 5.3.1.1) precursor, chloroplast - rye >gi_609262_emb_CAA83533_ (Z32521) triosephosphate isomerase [Secale cereale] >gi_1095494_prf__2109226B triosephosphate isomerase [Secale cereale]

Seq. No.	387092
Contig ID	3629_1.R1084
5'-most EST	g3761292

Seq. No.	387093
Contig ID	3629_2.R1084
5'-most EST	uC-osf1cyp081g04b1

Seq. No.	387094
Contig ID	3636_1.R1084
5'-most EST	g3763739

Seq. No.	387095
Contig ID	3636_2.R1084
5'-most EST	g2280981

Seq. No.	387096
Contig ID	3636_3.R1084
5'-most EST	g3762988

Seq. No.	387097
Contig ID	3637_1.R1084
5'-most EST	uC-osflM202064g04a1
Method	BLASTX
NCBI GI	g3080420
BLAST score	175
E value	2.0e-12
Match length	43
% identity	74
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	387098
Contig ID	3648_1.R1084
5'-most EST	LIB3431-036-P1-N1-A10

Seq. No.	387099
Contig ID	3653_1.R1084
5'-most EST	uC-osrocyp030d04b1
Method	BLASTN
NCBI GI	g6016845
BLAST score	180
E value	3.0e-96
Match length	523
% identity	90
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	387100
Contig ID	3653_2.R1084
5'-most EST	uC-osroM202034b06b1
Method	BLASTN
NCBI GI	g6016845
BLAST score	429
E value	0.0e+00
Match length	574
% identity	94
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0711E10

Seq. No.	387101
Contig ID	3655_1.R1084
5'-most EST	LIB3431-036-P1-N1-A7

Seq. No.	387102
Contig ID	3667_1.R1084
5'-most EST	g5667483

Seq. No.	387103
Contig ID	3672_1.R1084
5'-most EST	LIB3431-036-P1-N1-C2
Method	BLASTX
NCBI GI	g3929323
BLAST score	369
E value	8.0e-35
Match length	158
% identity	38
NCBI Description	(AF100332) putative 21D7 protein [Dendrobium grex Madame

Thong-IN]

Seq. No.	387104
Contig ID	3676_1.R1084
5'-most EST	uC-osf1M202064b09a1

Seq. No.	387105
Contig ID	3678_1.R1084
5'-most EST	g3761046
Method	BLASTX
NCBI GI	g2511594
BLAST score	324
E value	3.0e-35
Match length	107
% identity	73
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	387106
Contig ID	3683_1.R1084
5'-most EST	g2800299
Method	BLASTN
NCBI GI	g5734616
BLAST score	95
E value	2.0e-45
Match length	119
% identity	95
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0538C01

Seq. No.	387107
Contig ID	3687_1.R1084
5'-most EST	g4716034
Method	BLASTX
NCBI GI	g4678279
BLAST score	311
E value	3.0e-28
Match length	97
% identity	67
NCBI Description	(AL049660) carboxyl terminal protease-like protein [Arabidopsis thaliana]

Seq. No.	387108
Contig ID	3690_1.R1084
5'-most EST	LIB3432-058-P1-K1-C12

Seq. No.	387109
Contig ID	3692_1.R1084
5'-most EST	LIB3431-036-P1-N1-E10

Seq. No.	387110
Contig ID	3695_1.R1084
5'-most EST	g3107069
Method	BLASTX

NCBI GI	g2244910
BLAST score	311
E value	5.0e-28
Match length	194
% identity	44
NCBI Description	(Z97339) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387111
Contig ID	3697_1.R1084
5'-most EST	uC-osroM202020a02a1

Seq. No.	387112
Contig ID	3698_1.R1084
5'-most EST	g4715753
Method	BLASTX
NCBI GI	g585452
BLAST score	583
E value	5.0e-60
Match length	167
% identity	69
NCBI Description	MALATE OXIDOREDUCTASE [NAD] 59 KD ISOFORM, MITOCHONDRIAL PRECURSOR (MALIC ENZYME) (ME) (NAD-DEPENDENT MALIC ENZYME) (NAD-ME) >gi_1076666_pir__A53318 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) 59K chain precursor, mitochondrial - potato >gi_438131_emb_CAA80547_ (Z23002) precursor of the 59kDa subunit of the mitochondrial NAD+-dependent malic enzyme [Solanum tuberosum]

Seq. No.	387113
Contig ID	3698_2.R1084
5'-most EST	g4715754
Method	BLASTX
NCBI GI	g3047125
BLAST score	810
E value	2.0e-86
Match length	245
% identity	63
NCBI Description	(AF058919) No definition line found [Arabidopsis thaliana]

Seq. No.	387114
Contig ID	3699_1.R1084
5'-most EST	g4716558
Method	BLASTX
NCBI GI	g5360595
BLAST score	677
E value	8.0e-71
Match length	207
% identity	66
NCBI Description	(AB022330) nClpP5 [Arabidopsis thaliana]

Seq. No.	387115
Contig ID	3699_2.R1084
5'-most EST	LIB3431-036-P1-K1-E7

Seq. No.	387116
Contig ID	3700_1.R1084
5'-most EST	g3761302

Method	BLASTX
NCBI GI	g3461848
BLAST score	692
E value	8.0e-73
Match length	184
% identity	75
NCBI Description	(AC005315) putative ATPase [Arabidopsis thaliana]

Seq. No.	387117
Contig ID	3701_1.R1084
5'-most EST	LIB3431-054-P1-N1-G10
Method	BLASTX
NCBI GI	g1071913
BLAST score	1092
E value	1.0e-119
Match length	344
% identity	64
NCBI Description	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach >gi_1066153_dbj_BAA07177_ (D37963) cysteine synthase [Spinacia oleracea]

Seq. No.	387118
Contig ID	3704_1.R1084
5'-most EST	uC-osflcyp172d02a1
Method	BLASTX
NCBI GI	g3426039
BLAST score	976
E value	1.0e-117
Match length	317
% identity	68
NCBI Description	(AC005168) unknown protein [Arabidopsis thaliana]

Seq. No.	387119
Contig ID	3711_1.R1084
5'-most EST	uC-osflcyp170g12a1
Method	BLASTX
NCBI GI	g4314378
BLAST score	241
E value	6.0e-20
Match length	90
% identity	53
NCBI Description	(AC006232) putative lipase [Arabidopsis thaliana] >gi_5306262_gb_AAD41994.1_AC006233_5 (AC006233) putative lipase [Arabidopsis thaliana]

Seq. No.	387120
Contig ID	3717_1.R1084
5'-most EST	g3762283
Method	BLASTX
NCBI GI	g3236258
BLAST score	153
E value	7.0e-16
Match length	67
% identity	67
NCBI Description	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana] >gi_4895208_gb_AAD32795.1_AC007661_32 (AC007661) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq. No.	387121
Contig ID	3718_1.R1084
5'-most EST	LIB3431-036-P1-N1-G7
Method	BLASTX
NCBI GI	g2695931
BLAST score	374
E value	3.0e-46
Match length	182
% identity	60
NCBI Description	(AJ222779) hypothetical protein [Hordeum vulgare]

Seq. No.	387122
Contig ID	3724_1.R1084
5'-most EST	g3766702
Method	BLASTX
NCBI GI	g729882
BLAST score	984
E value	1.0e-107
Match length	198
% identity	86
NCBI Description	CASEIN KINASE II BETA' CHAIN (CK II) >gi_1076300_pir__S47968 casein kinase II (EC 2.7.1.-) beta chain CKB2 - Arabidopsis thaliana >gi_467975 (U03984) casein kinase II beta subunit CKB2 [Arabidopsis thaliana] >gi_2245122_emb_CAB10544.1_ (Z97343) casein kinase II beta chain CKB2 [Arabidopsis thaliana]

Seq. No.	387123
Contig ID	3731_1.R1084
5'-most EST	LIB3431-037-P1-N1-A10

Seq. No.	387124
Contig ID	3732_1.R1084
5'-most EST	g3760263
Method	BLASTX
NCBI GI	g5262946
BLAST score	1258
E value	1.0e-139
Match length	282
% identity	82
NCBI Description	(Y19104) beta-alanine synthase [Lycopersicon esculentum]

Seq. No.	387125
Contig ID	3734_1.R1084
5'-most EST	LIB3431-044-P1-K1-B7
Method	BLASTX
NCBI GI	g2827150
BLAST score	893
E value	1.0e-154
Match length	360
% identity	83
NCBI Description	(AF029895) acetyl-coenzyme A carboxylase [Triticum aestivum]

Seq. No.	387126
Contig ID	3734_2.R1084

5'-most EST	uC-osflcyp179c01a1
Method	BLASTN
NCBI GI	g396278
BLAST score	37
E value	4.0e-11
Match length	89
% identity	85
NCBI Description	T.aestivum ACCase mRNA, 3' CDS

Seq. No.	387127
Contig ID	3735_1.R1084
5'-most EST	g5607305

Seq. No.	387128
Contig ID	3738_1.R1084
5'-most EST	uC-osroM202025f04a1

Seq. No.	387129
Contig ID	3740_1.R1084
5'-most EST	g3768836

Seq. No.	387130
Contig ID	3743_1.R1084
5'-most EST	g4715250

Seq. No.	387131
Contig ID	3744_1.R1084
5'-most EST	LIB3431-037-P1-N1-B12
Method	BLASTX
NCBI GI	g3688209
BLAST score	160
E value	1.0e-10
Match length	57
% identity	54
NCBI Description	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]

Seq. No.	387132
Contig ID	3750_1.R1084
5'-most EST	uC-osflcyp118a10a1
Method	BLASTX
NCBI GI	g100293
BLAST score	242
E value	6.0e-37
Match length	129
% identity	35
NCBI Description	ribonucleoprotein A, 29K - wood tobacco >gi_19754_emb_CAA43427_ (X61113) 29kD A ribonucleoprotein [Nicotiana sylvestris]

Seq. No.	387133
Contig ID	3766_1.R1084
5'-most EST	LIB3431-037-P1-N1-D2

Seq. No.	387134
Contig ID	3769_1.R1084
5'-most EST	g3768268
Method	BLASTX

NCBI GI	g3335335
BLAST score	502
E value	4.0e-67
Match length	194
% identity	61
NCBI Description	(AC004512) ESTs gb_F14113 and gb_T42122 come from this region. [Arabidopsis thaliana]

Seq. No.	387135
Contig ID	3770_1.R1084
5'-most EST	g5003508
Method	BLASTX
NCBI GI	g3435096
BLAST score	278
E value	4.0e-24
Match length	102
% identity	58
NCBI Description	(AF033587) SRZ21 [Arabidopsis thaliana]

Seq. No.	387136
Contig ID	3773_1.R1084
5'-most EST	LIB3431-037-P1-N1-E1
Method	BLASTX
NCBI GI	g1653513
BLAST score	104
E value	7.0e-10
Match length	55
% identity	64
NCBI Description	(D90914) hypothetical protein [Synechocystis sp.]

Seq. No.	387137
Contig ID	3776_1.R1084
5'-most EST	LIB3431-037-P1-N1-E12
Method	BLASTX
NCBI GI	g3894193
BLAST score	152
E value	2.0e-09
Match length	117
% identity	38
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	387138
Contig ID	3782_1.R1084
5'-most EST	LIB3431-037-P1-N1-E8
Method	BLASTX
NCBI GI	g402753
BLAST score	339
E value	1.0e-31
Match length	76
% identity	86
NCBI Description	(X71439) translation elongation factor EF-G [Glycine max]

Seq. No.	387139
Contig ID	3795_1.R1084
5'-most EST	LIB3431-037-P1-N1-G10
Method	BLASTX

NCBI GI	g2347098
BLAST score	245
E value	1.0e-20
Match length	52
% identity	85
NCBI Description	(U76845) ubiquitin-specific protease [Arabidopsis thaliana] >gi_4490742_emb_CAB38904.1_ (AL035708) ubiquitin-specific protease (AtUBP3) [Arabidopsis thaliana]

Seq. No.	387140
Contig ID	3796_1.R1084
5'-most EST	g572411

Seq. No.	387141
Contig ID	3800_1.R1084
5'-most EST	uC-osflcyp179a08a1
Method	BLASTX
NCBI GI	g1708191
BLAST score	396
E value	2.0e-38
Match length	104
% identity	68
NCBI Description	HEXOSE CARRIER PROTEIN HEX6 >gi_467319 (L08188) hexose carrier protein [Ricinus communis]

Seq. No.	387142
Contig ID	3801_1.R1084
5'-most EST	LIB3431-037-P1-N1-G6
Method	BLASTX
NCBI GI	g3540182
BLAST score	226
E value	3.0e-18
Match length	110
% identity	48
NCBI Description	(AC004122) Unknown protein [Arabidopsis thaliana]

Seq. No.	387143
Contig ID	3803_1.R1084
5'-most EST	LIB3431-037-P1-N1-G8
Method	BLASTX
NCBI GI	g3603401
BLAST score	742
E value	2.0e-88
Match length	343
% identity	52
NCBI Description	(AF083333) cinnamyl-alcohol dehydrogenase [Medicago sativa]

Seq. No.	387144
Contig ID	3805_1.R1084
5'-most EST	g3445006
Method	BLASTX
NCBI GI	g3294467
BLAST score	2360
E value	0.0e+00
Match length	582
% identity	95
NCBI Description	(U89341) phosphoglucomutase 1 [Zea mays]

Seq. No.	387145
Contig ID	3817_1.R1084
5'-most EST	LIB3431-038-P1-N1-A1
Method	BLASTX
NCBI GI	g3319341
BLAST score	276
E value	4.0e-24
Match length	49
% identity	90
NCBI Description	(AF077407) similar to Medicago sativa nucleic acid binding protein Alfin-1 (GB:L07291) [Arabidopsis thaliana]

Seq. No.	387146
Contig ID	3820_1.R1084
5'-most EST	g5455493
Method	BLASTX
NCBI GI	g729535
BLAST score	548
E value	7.0e-56
Match length	135
% identity	74
NCBI Description	FERREDOXIN-THIOREDOXIN REDUCTASE, CATALYTIC CHAIN PRECURSOR (FTR-C) (FERREDOXIN-THIOREDOXIN REDUCTASE SUBUNIT B) (FTR-B)

Seq. No.	387147
Contig ID	3822_1.R1084
5'-most EST	LIB3431-038-P1-K1-A3
Method	BLASTX
NCBI GI	g3548808
BLAST score	323
E value	6.0e-30
Match length	81
% identity	68
NCBI Description	(AC005313) unknown protein [Arabidopsis thaliana]

Seq. No.	387148
Contig ID	3825_1.R1084
5'-most EST	LIB3431-038-P1-N1-A6

Seq. No.	387149
Contig ID	3826_1.R1084
5'-most EST	LIB3431-038-P1-N1-A7
Method	BLASTX
NCBI GI	g282882
BLAST score	197
E value	6.0e-15
Match length	111
% identity	39
NCBI Description	receptor-like protein kinase precursor - Arabidopsis thaliana >gi_166848 (M84659) receptor-like protein kinase [Arabidopsis thaliana]

Seq. No.	387150
Contig ID	3827_1.R1084
5'-most EST	LIB3432-034-P2-K1-F8

Method	BLASTX
NCBI GI	g3822223
BLAST score	440
E value	2.0e-43
Match length	123
% identity	60
NCBI Description	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]

Seq. No.	387151
Contig ID	3832_1.R1084
5'-most EST	g4714797
Method	BLASTX
NCBI GI	g2497492
BLAST score	504
E value	1.0e-50
Match length	176
% identity	58
NCBI Description	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) >gi_1653646_dbj_BAA18558_ (D90915) uridine monophosphate kinase [Synechocystis sp.]

Seq. No.	387152
Contig ID	3837_1.R1084
5'-most EST	LIB3431-038-P1-N1-B8
Method	BLASTX
NCBI GI	g4539408
BLAST score	492
E value	3.0e-49
Match length	134
% identity	75
NCBI Description	(AL049524) putative alpha NAC [Arabidopsis thaliana]

Seq. No.	387153
Contig ID	3841_1.R1084
5'-most EST	LIB3431-038-P1-N1-C11
Method	BLASTX
NCBI GI	g4204263
BLAST score	439
E value	9.0e-43
Match length	191
% identity	57
NCBI Description	(AC005223) 40409 [Arabidopsis thaliana]

Seq. No.	387154
Contig ID	3847_1.R1084
5'-most EST	LIB3431-038-P1-N1-C6
Method	BLASTX
NCBI GI	g4678364
BLAST score	197
E value	1.0e-19
Match length	102
% identity	59
NCBI Description	(AL049659) putative protein [Arabidopsis thaliana]

Seq. No.	387155
Contig ID	3851_1.R1084

5'-most EST	g3763613
Method	BLASTX
NCBI GI	g4056488
BLAST score	477
E value	2.0e-47
Match length	105
% identity	76
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	387156
Contig ID	3851_2.R1084
5'-most EST	uC-osrocyp006b04a1

Seq. No.	387157
Contig ID	3851_3.R1084
5'-most EST	uC-osrocyp009c03b1
Method	BLASTX
NCBI GI	g4056488
BLAST score	244
E value	2.0e-20
Match length	65
% identity	68
NCBI Description	(AC005896) unknown protein [Arabidopsis thaliana]

Seq. No.	387158
Contig ID	3856_1.R1084
5'-most EST	LIB3431-056-P1-N1-F8

Seq. No.	387159
Contig ID	3857_1.R1084
5'-most EST	LIB3431-038-P1-N1-D4

Seq. No.	387160
Contig ID	3859_1.R1084
5'-most EST	LIB3434-046-P1-K1-D5
Method	BLASTX
NCBI GI	g3426048
BLAST score	294
E value	6.0e-26
Match length	70
% identity	79
NCBI Description	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]

Seq. No.	387161
Contig ID	3860_1.R1084
5'-most EST	g3762033
Method	BLASTX
NCBI GI	g4582445
BLAST score	276
E value	4.0e-24
Match length	64
% identity	72
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana] >gi_4589952_gb_AAD26470.1_AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	387162
Contig ID	3860_2.R1084
5'-most EST	LIB3431-038-P1-N1-D7
Method	BLASTX
NCBI GI	g4582445
BLAST score	269
E value	2.0e-23
Match length	64
% identity	70
NCBI Description	(AC007071) unknown protein [Arabidopsis thaliana] >gi_4589952_gb_AAD26470.1_AC007169_2 (AC007169) unknown protein [Arabidopsis thaliana]

Seq. No.	387163
Contig ID	3862_1.R1084
5'-most EST	g3767917
Method	BLASTX
NCBI GI	g2760334
BLAST score	294
E value	3.0e-26
Match length	76
% identity	64
NCBI Description	(AC002130) F1N21.5 [Arabidopsis thaliana]

Seq. No.	387164
Contig ID	3863_1.R1084
5'-most EST	g4715857
Method	BLASTX
NCBI GI	g4455180
BLAST score	815
E value	1.0e-118
Match length	307
% identity	72
NCBI Description	(AL035521) putative protein [Arabidopsis thaliana]

Seq. No.	387165
Contig ID	3866_1.R1084
5'-most EST	uC-osflcyp156d07a1

Seq. No.	387166
Contig ID	3869_1.R1084
5'-most EST	g5667607
Method	BLASTX
NCBI GI	g5001734
BLAST score	993
E value	1.0e-108
Match length	239
% identity	76
NCBI Description	(AF129511) very-long-chain fatty acid condensing enzyme CUT1 [Arabidopsis thaliana]

Seq. No.	387167
Contig ID	3869_2.R1084
5'-most EST	LIB3431-038-P1-K1-E6
Method	BLASTX
NCBI GI	g4544399
BLAST score	834

E value	1.0e-89
Match length	181
% identity	86
NCBI Description	(AC007047) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]

Seq. No.	387168
Contig ID	3869_3.R1084
5'-most EST	LIB3431-038-P1-N1-E6
Method	BLASTX
NCBI GI	g4115364
BLAST score	476
E value	2.0e-47
Match length	108
% identity	78
NCBI Description	(AC005957) putative fatty acid elongase [Arabidopsis thaliana]

Seq. No.	387169
Contig ID	3871_1.R1084
5'-most EST	LIB3431-023-P1-K1-G6

Seq. No.	387170
Contig ID	3872_1.R1084
5'-most EST	g3761209
Method	BLASTX
NCBI GI	g542200
BLAST score	549
E value	8.0e-56
Match length	249
% identity	45
NCBI Description	hypothetical protein - garden asparagus >gi_452714_emb_CAA54526_ (X77320) unknown [Asparagus officinalis]

Seq. No.	387171
Contig ID	3881_1.R1084
5'-most EST	g6025008

Seq. No.	387172
Contig ID	3882_1.R1084
5'-most EST	g4716832

Seq. No.	387173
Contig ID	3883_1.R1084
5'-most EST	LIB3432-050-P1-K1-D6

Seq. No.	387174
Contig ID	3896_1.R1084
5'-most EST	LIB3433-027-P1-K1-F1
Method	BLASTX
NCBI GI	g5174741
BLAST score	178
E value	1.0e-12
Match length	78
% identity	49
NCBI Description	ubiquitin carboxyl-terminal esterase L3 (ubiquitin

thiolesterase) >gi_136682_sp_P15374_UBL3_HUMAN UBIQUITIN CARBOXYL-TERMINAL HYDROLASE ISOZYME L3 (UCH-L3) (UBIQUITIN THIOLESTERASE L3) >gi_108014_pir__A40085 ubiquitin carboxyl-terminal proteinase (EC 3.4.-.-) L3 - human >gi_2914274_pdb_1UCH_ Deubiquitinating Enzyme Uch-L3 (Human) At 1.8 Angstrom Resolution >gi_340074 (M30496) ubiquitin carboxyl-terminal hydrolase [Homo sapiens]

Seq. No.	387175
Contig ID	3897_1.R1084
5'-most EST	uC-osrocyp027c01b1

Seq. No.	387176
Contig ID	3897_3.R1084
5'-most EST	uC-osrocyp027c01a1
Method	BLASTN
NCBI GI	g4959460
BLAST score	36
E value	2.0e-10
Match length	36
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	387177
Contig ID	3897_5.R1084
5'-most EST	g2431530

Seq. No.	387178
Contig ID	3898_1.R1084
5'-most EST	g3759712
Method	BLASTX
NCBI GI	g5381319
BLAST score	763
E value	5.0e-81
Match length	153
% identity	95
NCBI Description	(AF091621) ubiquitin-conjugating enzyme E2 [Catharanthus roseus]

Seq. No.	387179
Contig ID	3900_1.R1084
5'-most EST	LIB3431-038-P1-N1-H5

Seq. No.	387180
Contig ID	3902_1.R1084
5'-most EST	uC-osflcyp051f05a1
Method	BLASTN
NCBI GI	g6006355
BLAST score	39
E value	2.0e-12
Match length	87
% identity	86
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone:P0493C11

Seq. No.	387181
Contig ID	3902_2.R1084
5'-most EST	LIB3431-038-P1-K1-H7

Seq. No.	387182
Contig ID	3908_1.R1084
5'-most EST	LIB3431-062-P1-N1-A12

Seq. No.	387183
Contig ID	3911_1.R1084
5'-most EST	LIB3431-062-P1-N1-A5

Seq. No.	387184
Contig ID	3919_1.R1084
5'-most EST	LIB3431-062-P1-N1-B12
Method	BLASTX
NCBI GI	g4914411
BLAST score	366
E value	8.0e-35
Match length	105
% identity	69
NCBI Description	(AL050352) putative protein [Arabidopsis thaliana]

Seq. No.	387185
Contig ID	3923_1.R1084
5'-most EST	uC-osroM202020d06b1
Method	BLASTX
NCBI GI	g4263784
BLAST score	871
E value	2.0e-93
Match length	337
% identity	52
NCBI Description	(AC006068) putative glycogenin-2 protein [Arabidopsis thaliana]

Seq. No.	387186
Contig ID	3932_1.R1084
5'-most EST	LIB3431-062-P1-N1-C4

Seq. No.	387187
Contig ID	3934_2.R1084
5'-most EST	g4878366
Method	BLASTN
NCBI GI	g1854377
BLAST score	53
E value	1.0e-20
Match length	215
% identity	84
NCBI Description	Saccharum officinarum RNA for Sucrose-Phosphate Synthase, complete cds

Seq. No.	387188
Contig ID	3934_3.R1084
5'-most EST	g428658
Method	BLASTX
NCBI GI	g4580466
BLAST score	339
E value	5.0e-32
Match length	93
% identity	71

NCBI Description	(AC006081) putative 50S ribosomal protein L4 [Arabidopsis thaliana]

Seq. No.	387189
Contig ID	3935_1.R1084
5'-most EST	LIB3431-062-P1-N1-C7
Method	BLASTX
NCBI GI	g4972111
BLAST score	813
E value	6.0e-87
Match length	230
% identity	63
NCBI Description	(AL078579) protein phosphatase homolog (PPH1) [Arabidopsis thaliana]

Seq. No.	387190
Contig ID	3938_1.R1084
5'-most EST	LIB3431-062-P1-N1-D10
Method	BLASTX
NCBI GI	g3269295
BLAST score	151
E value	2.0e-09
Match length	45
% identity	64
NCBI Description	(AL030978) putative protein [Arabidopsis thaliana]

Seq. No.	387191
Contig ID	3941_1.R1084
5'-most EST	LIB3431-062-P1-N1-D2

Seq. No.	387192
Contig ID	3947_1.R1084
5'-most EST	LIB3431-062-P1-N1-D8
Method	BLASTX
NCBI GI	g4895187
BLAST score	254
E value	2.0e-21
Match length	178
% identity	40
NCBI Description	(AC007661) unknown protein [Arabidopsis thaliana]

Seq. No.	387193
Contig ID	3951_1.R1084
5'-most EST	LIB3431-056-P1-N1-D5
Method	BLASTN
NCBI GI	g218209
BLAST score	41
E value	1.0e-13
Match length	91
% identity	95
NCBI Description	Oryza sativa mRNA for the small subunit of ribulose-1,5-bisphosphate carboxylase, complete cds, clone pOSSS2106

Seq. No.	387194
Contig ID	3955_1.R1084
5'-most EST	LIB3431-062-P1-N1-E4

Method	BLASTX
NCBI GI	g2832606
BLAST score	214
E value	7.0e-17
Match length	90
% identity	50
NCBI Description	(AL021635) predicted protein [Arabidopsis thaliana] >gi_3292810_emb_CAA19800.1_ (AL031018) putative protein [Arabidopsis thaliana]

Seq. No.	387195
Contig ID	3960_1.R1084
5'-most EST	g4715782

Seq. No.	387196
Contig ID	3963_1.R1084
5'-most EST	g6012788
Method	BLASTX
NCBI GI	g100535
BLAST score	224
E value	8.0e-18
Match length	82
% identity	55
NCBI Description	hypothetical protein - swollen duckweed >gi_1929057_emb_CAA32236_ (X14075) longest ORF (1) [Lemna gibba]

Seq. No.	387197
Contig ID	3972_1.R1084
5'-most EST	LIB3431-062-P1-N1-G1
Method	BLASTX
NCBI GI	g2462834
BLAST score	293
E value	5.0e-26
Match length	144
% identity	52
NCBI Description	(AF000657) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387198
Contig ID	3978_1.R1084
5'-most EST	LIB3431-062-P1-N1-G4
Method	BLASTX
NCBI GI	g5123711
BLAST score	472
E value	4.0e-47
Match length	149
% identity	62
NCBI Description	(AL079347) putative protein [Arabidopsis thaliana]

Seq. No.	387199
Contig ID	3980_1.R1084
5'-most EST	LIB3431-062-P1-N1-G6
Method	BLASTX
NCBI GI	g4973264
BLAST score	376
E value	4.0e-36
Match length	93

% identity	73
NCBI Description	(AF144391) thioredoxin-like 5 [Arabidopsis thaliana]
Seq. No.	387200
Contig ID	3994_1.R1084
5'-most EST	LIB3431-052-P1-N1-A1
Seq. No.	387201
Contig ID	3995_1.R1084
5'-most EST	uC-osflcyp157a10a1
Seq. No.	387202
Contig ID	3997_1.R1084
5'-most EST	LIB3431-052-P1-N1-A8
Method	BLASTX
NCBI GI	g2245004
BLAST score	216
E value	5.0e-17
Match length	107
% identity	43
NCBI Description	(Z97341) membrane transporter like protein [Arabidopsis thaliana]
Seq. No.	387203
Contig ID	4001_1.R1084
5'-most EST	LIB3431-052-P1-N1-A7
Method	BLASTX
NCBI GI	g2289010
BLAST score	389
E value	2.0e-37
Match length	86
% identity	86
NCBI Description	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
Seq. No.	387204
Contig ID	4001_2.R1084
5'-most EST	g3762429
Seq. No.	387205
Contig ID	4001_3.R1084
5'-most EST	g4879972
Method	BLASTX
NCBI GI	g2289010
BLAST score	159
E value	1.0e-10
Match length	34
% identity	91
NCBI Description	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
Seq. No.	387206
Contig ID	4005_1.R1084
5'-most EST	g3769036
Method	BLASTX
NCBI GI	g2088648
BLAST score	174

E value	5.0e-12
Match length	118
% identity	38
NCBI Description	(AF002109) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387207
Contig ID	4009_1.R1084
5'-most EST	LIB3432-006-P1-K1-E3
Method	BLASTX
NCBI GI	g5929964
BLAST score	743
E value	1.0e-78
Match length	200
% identity	80
NCBI Description	(AF180335) malate dehydrogenase [Glycine max]

Seq. No.	387208
Contig ID	4009_2.R1084
5'-most EST	LIB3433-028-P1-K1-B11
Method	BLASTX
NCBI GI	g5929964
BLAST score	519
E value	5.0e-85
Match length	213
% identity	74
NCBI Description	(AF180335) malate dehydrogenase [Glycine max]

Seq. No.	387209
Contig ID	4014_1.R1084
5'-most EST	LIB3431-052-P1-N1-C1
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	45
% identity	63
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387210
Contig ID	4016_1.R1084
5'-most EST	g3761520
Method	BLASTX
NCBI GI	g4972114
BLAST score	165
E value	2.0e-14
Match length	78
% identity	49
NCBI Description	(AL078579) putative beta-glucosidase [Arabidopsis thaliana]

Seq. No.	387211
Contig ID	4021_1.R1084
5'-most EST	g5038625
Method	BLASTX
NCBI GI	g4566614
BLAST score	565
E value	8.0e-58
Match length	137

% identity	79
NCBI Description	(AF112887) actin depolymerizing factor [Populus alba x Populus tremula]

Seq. No.	387212
Contig ID	4025_1.R1084
5'-most EST	g4878960
Method	BLASTN
NCBI GI	g2739216
BLAST score	72
E value	4.0e-32
Match length	84
% identity	96
NCBI Description	Hordeum vulgare L41 ribosomal protein

Seq. No.	387213
Contig ID	4026_1.R1084
5'-most EST	LIB3433-047-P1-K1-H8

Seq. No.	387214
Contig ID	4027_1.R1084
5'-most EST	LIB3431-052-P1-N1-D10
Method	BLASTX
NCBI GI	g6041792
BLAST score	224
E value	1.0e-23
Match length	104
% identity	58
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]

Seq. No.	387215
Contig ID	4028_1.R1084
5'-most EST	g2800016

Seq. No.	387216
Contig ID	4033_1.R1084
5'-most EST	g5038821
Method	BLASTX
NCBI GI	g4335763
BLAST score	167
E value	2.0e-11
Match length	75
% identity	45
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	387217
Contig ID	4034_1.R1084
5'-most EST	g4715076
Method	BLASTX
NCBI GI	g4239845
BLAST score	225
E value	8.0e-18
Match length	156
% identity	37
NCBI Description	(AB015855) transcription factor TEIL [Nicotiana tabacum]

Seq. No.	387218

Contig ID	4034_2.R1084
5'-most EST	g4715460

Seq. No.	387219
Contig ID	4040_1.R1084
5'-most EST	LIB3431-052-P1-N1-E2
Method	BLASTX
NCBI GI	g2947060
BLAST score	225
E value	3.0e-18
Match length	56
% identity	77
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	387220
Contig ID	4054_1.R1084
5'-most EST	g5816539
Method	BLASTX
NCBI GI	g2129622
BLAST score	558
E value	6.0e-57
Match length	134
% identity	78
NCBI Description	immunophilin FKBP15-1 - Arabidopsis thaliana >gi_1272406 (U52046) immunophilin [Arabidopsis thaliana]

Seq. No.	387221
Contig ID	4060_1.R1084
5'-most EST	g3761291

Seq. No.	387222
Contig ID	4064_1.R1084
5'-most EST	LIB3431-052-P1-N1-G6

Seq. No.	387223
Contig ID	4087_1.R1084
5'-most EST	g5038700
Method	BLASTX
NCBI GI	g6006848
BLAST score	109
E value	4.0e-12
Match length	45
% identity	67
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	387224
Contig ID	4093_1.R1084
5'-most EST	LIB3431-011-P1-N1-B11
Method	BLASTX
NCBI GI	g4982478
BLAST score	476
E value	2.0e-47
Match length	153
% identity	63
NCBI Description	(AF069441) putative leucyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	387225
Contig ID	4095_1.R1084
5'-most EST	g5055960
Method	BLASTX
NCBI GI	g431154
BLAST score	623
E value	2.0e-64
Match length	189
% identity	65
NCBI Description	(D21813) ORF [Lilium longiflorum]

Seq. No.	387226
Contig ID	4097_1.R1084
5'-most EST	LIB3432-016-P1-K1-E1
Method	BLASTX
NCBI GI	g400983
BLAST score	250
E value	3.0e-21
Match length	70
% identity	69
NCBI Description	50S RIBOSOMAL PROTEIN L11, CHLOROPLAST PRECURSOR (CL11) >gi_279648_pir__R5SP11 ribosomal protein L11 precursor - spinach >gi_21313_emb_CAA39950_ (X56615) ribosomal protein L11 [Spinacia oleracea]

Seq. No.	387227
Contig ID	4108_1.R1084
5'-most EST	g3763036

Seq. No.	387228
Contig ID	4110_1.R1084
5'-most EST	g4715810
Method	BLASTX
NCBI GI	g2130082
BLAST score	704
E value	9.0e-74
Match length	512
% identity	18
NCBI Description	protein kinase Xa21 (EC 2.7.1.-) - rice >gi_1122443 (U37133) receptor kinase-like protein [Oryza sativa] >gi_2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] >gi_1586408_prf__2203451A receptor kinase-like protein [Oryza sativa]

Seq. No.	387229
Contig ID	4114_1.R1084
5'-most EST	LIB3432-024-P1-K1-A1

Seq. No.	387230
Contig ID	4117_1.R1084
5'-most EST	LIB3431-053-P1-N1-E11
Method	BLASTX
NCBI GI	g4544390
BLAST score	510
E value	4.0e-51
Match length	377

% identity	30
NCBI Description	(AC007047) hypothetical protein [Arabidopsis thaliana]
Seq. No.	387231
Contig ID	4122_1.R1084
5'-most EST	LIB3431-053-P1-N1-E7
Method	BLASTX
NCBI GI	g4417296
BLAST score	678
E value	6.0e-82
Match length	212
% identity	72
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana] >gi_4587592_gb_AAD25820.1_AC007232_10 (AC007232) unknown protein [Arabidopsis thaliana]
Seq. No.	387232
Contig ID	4123_1.R1084
5'-most EST	g4714865
Method	BLASTX
NCBI GI	g4417289
BLAST score	197
E value	5.0e-16
Match length	98
% identity	46
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]
Seq. No.	387233
Contig ID	4128_1.R1084
5'-most EST	LIB3431-053-P1-N1-F12
Seq. No.	387234
Contig ID	4131_1.R1084
5'-most EST	g4716250
Method	BLASTX
NCBI GI	g1076812
BLAST score	202
E value	2.0e-15
Match length	40
% identity	100
NCBI Description	initiator-binding protein - maize >gi_483490_emb_CAA55691_ (X79085) initiator binding protein [Zea mays]
Seq. No.	387235
Contig ID	4137_1.R1084
5'-most EST	uC-osflcyp137a02a1
Method	BLASTX
NCBI GI	g3047064
BLAST score	220
E value	1.0e-17
Match length	51
% identity	76
NCBI Description	(AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [Arabidopsis thaliana]
Seq. No.	387236

Contig ID	4144_1.R1084
5'-most EST	g4716428
Method	BLASTX
NCBI GI	g4530591
BLAST score	847
E value	1.0e-90
Match length	210
% identity	75
NCBI Description	(AF132475) heme oxygenase 1 [Arabidopsis thaliana] >gi_4530593_gb_AAD22108.1_ (AF132476) heme oxygenase 1 [Arabidopsis thaliana] >gi_4877362_dbj_BAA77758.1_ (AB021857) plastid heme oxygenase [Arabidopsis thaliana] >gi_4877397_dbj_BAA77759.1_ (AB021858) plastid heme oxygenase [Arabidopsis thaliana] >gi_4883666_gb_AAB95301.2_ (AC003105) heme oxygenase 1 (HO1) [Arabidopsis thaliana]

Seq. No.	387237
Contig ID	4146_1.R1084
5'-most EST	LIB3432-020-P1-K1-A5

Seq. No.	387238
Contig ID	4151_1.R1084
5'-most EST	LIB3431-053-P1-N1-H12
Method	BLASTX
NCBI GI	g2384956
BLAST score	331
E value	2.0e-30
Match length	157
% identity	41
NCBI Description	(AF022985) No definition line found [Caenorhabditis elegans]

Seq. No.	387239
Contig ID	4151_2.R1084
5'-most EST	g2428756

Seq. No.	387240
Contig ID	4153_1.R1084
5'-most EST	LIB3431-053-P1-N1-H3
Method	BLASTX
NCBI GI	g4582459
BLAST score	230
E value	1.0e-18
Match length	70
% identity	66
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	387241
Contig ID	4160_1.R1084
5'-most EST	g2800196

Seq. No.	387242
Contig ID	4165_1.R1084
5'-most EST	g701067
Method	BLASTN
NCBI GI	g3241924

BLAST score	47
E value	7.0e-17
Match length	203
% identity	81
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNC6, complete sequence

Seq. No.	387243
Contig ID	4171_1.R1084
5'-most EST	g5003006
Method	BLASTX
NCBI GI	g6016696
BLAST score	323
E value	2.0e-31
Match length	128
% identity	59
NCBI Description	(AC009991) unknown protein [Arabidopsis thaliana]

Seq. No.	387244
Contig ID	4175_1.R1084
5'-most EST	uC-osflcyp118g02a1
Method	BLASTX
NCBI GI	g2435519
BLAST score	388
E value	4.0e-37
Match length	117
% identity	64
NCBI Description	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]

Seq. No.	387245
Contig ID	4184_1.R1084
5'-most EST	LIB3431-054-P1-N1-C11
Method	BLASTX
NCBI GI	g2651310
BLAST score	241
E value	3.0e-20
Match length	92
% identity	49
NCBI Description	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq. No.	387246
Contig ID	4194_1.R1084
5'-most EST	g4714369
Method	BLASTX
NCBI GI	g4371282
BLAST score	771
E value	5.0e-82
Match length	164
% identity	90
NCBI Description	(AC006260) putative 60S ribosomal protein L12 [Arabidopsis thaliana]

Seq. No.	387247
Contig ID	4194_2.R1084

5'-most EST	LIB3474-009-P1-K1-C6
Method	BLASTX
NCBI GI	g6094002
BLAST score	760
E value	9.0e-81
Match length	164
% identity	91
NCBI Description	60S RIBOSOMAL PROTEIN L12 >gi_2677830 (U93168) ribosomal protein L12 [Prunus armeniaca]

Seq. No.	387248
Contig ID	4195_1.R1084
5'-most EST	uC-osflcyp178b07a1
Method	BLASTX
NCBI GI	g4678209
BLAST score	456
E value	6.0e-45
Match length	179
% identity	52
NCBI Description	(AC007134) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	387249
Contig ID	4196_1.R1084
5'-most EST	uC-osflcyp109g03a1

Seq. No.	387250
Contig ID	4197_1.R1084
5'-most EST	g3107267
Method	BLASTX
NCBI GI	g2982991
BLAST score	147
E value	1.0e-08
Match length	117
% identity	32
NCBI Description	(AE000682) hypothetical protein [Aquifex aeolicus]

Seq. No.	387251
Contig ID	4201_1.R1084
5'-most EST	LIB3431-054-P1-N1-D6

Seq. No.	387252
Contig ID	4208_1.R1084
5'-most EST	LIB3431-054-P1-K1-E12

Seq. No.	387253
Contig ID	4215_1.R1084
5'-most EST	LIB3431-054-P1-N1-E8

Seq. No.	387254
Contig ID	4215_2.R1084
5'-most EST	uC-osflcyp087f03a1
Method	BLASTX
NCBI GI	g4220527
BLAST score	175
E value	5.0e-12
Match length	66

% identity	48
NCBI Description	(AL035356) putative protein [Arabidopsis thaliana]

Seq. No.	387255
Contig ID	4215_4.R1084
5'-most EST	uC-osroM202036f08a1

Seq. No.	387256
Contig ID	4216_1.R1084
5'-most EST	LIB3431-004-P1-N1-H3

Seq. No.	387257
Contig ID	4217_1.R1084
5'-most EST	uC-osrocyp026e10a1
Method	BLASTX
NCBI GI	g4758714
BLAST score	287
E value	3.0e-25
Match length	130
% identity	45
NCBI Description	microsomal glutathione S-transferase 3 >gi_2583081 (AF026977) microsomal glutathione S-transferase 3 [Homo sapiens]

Seq. No.	387258
Contig ID	4219_1.R1084
5'-most EST	g5455446
Method	BLASTX
NCBI GI	g4490321
BLAST score	152
E value	2.0e-09
Match length	34
% identity	85
NCBI Description	(AJ011604) nitrate transporter [Arabidopsis thaliana]

Seq. No.	387259
Contig ID	4227_1.R1084
5'-most EST	LIB3431-054-P1-N1-F8
Method	BLASTX
NCBI GI	g4982480
BLAST score	185
E value	1.0e-13
Match length	44
% identity	73
NCBI Description	(AF069441) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387260
Contig ID	4231_1.R1084
5'-most EST	uC-osroM202027b07a1
Method	BLASTX
NCBI GI	g3757521
BLAST score	658
E value	1.0e-68
Match length	200
% identity	56
NCBI Description	(AC005167) unknown protein [Arabidopsis thaliana]

Seq. No.	387261
Contig ID	4234_1.R1084
5'-most EST	LIB3474-007-P1-K1-E8
Method	BLASTX
NCBI GI	g1707657
BLAST score	592
E value	7.0e-61
Match length	200
% identity	65
NCBI Description	(Z71640) DnaJ homologue [Pisum sativum]

Seq. No.	387262
Contig ID	4239_1.R1084
5'-most EST	LIB3431-054-P1-N1-H1
Method	BLASTX
NCBI GI	g2104816
BLAST score	172
E value	1.0e-11
Match length	123
% identity	30
NCBI Description	(Y13092) alpha-adaptin [Drosophila melanogaster]

Seq. No.	387263
Contig ID	4245_1.R1084
5'-most EST	LIB3431-054-P1-N1-H6
Method	BLASTX
NCBI GI	g22380
BLAST score	663
E value	3.0e-69
Match length	167
% identity	79
NCBI Description	(X59714) CAAT-box DNA binding protein subunit B (NF-YB) [Zea mays]

Seq. No.	387264
Contig ID	4254_1.R1084
5'-most EST	LIB3431-055-P1-N1-F12
Method	BLASTX
NCBI GI	g1651865
BLAST score	193
E value	4.0e-14
Match length	98
% identity	47
NCBI Description	(D90900) hypothetical protein [Synechocystis sp.]

Seq. No.	387265
Contig ID	4257_1.R1084
5'-most EST	LIB3431-055-P1-N1-A9
Method	BLASTX
NCBI GI	g3650033
BLAST score	319
E value	4.0e-43
Match length	179
% identity	57
NCBI Description	(AC005396) unknown protein [Arabidopsis thaliana]

Seq. No.	387266

Contig ID	4261_1.R1084
5'-most EST	uC-osrocyp027h01a1
Seq. No.	387267
Contig ID	4265_1.R1084
5'-most EST	g700053
Seq. No.	387268
Contig ID	4265_2.R1084
5'-most EST	uC-osflcyp003f05b1
Method	BLASTX
NCBI GI	g4559384
BLAST score	226
E value	3.0e-18
Match length	97
% identity	54
NCBI Description	(AC006526) unknown protein [Arabidopsis thaliana]
Seq. No.	387269
Contig ID	4273_1.R1084
5'-most EST	g3760425
Seq. No.	387270
Contig ID	4276_1.R1084
5'-most EST	LIB3431-055-P1-N1-C8
Method	BLASTX
NCBI GI	g4115925
BLAST score	720
E value	8.0e-79
Match length	207
% identity	37
NCBI Description	(AF118222) contains similarity to RNA recognition motifs (Pfam: PF00076, Score=5.5e-23, N=2) [Arabidopsis thaliana] >gi_4539439_emb_CAB40027.1_ (AL049523) RNA-binding protein [Arabidopsis thaliana] >gi_4959384_gb_AAD34325.1_ (AF109721) RNA-binding protein [Arabidopsis thaliana]
Seq. No.	387271
Contig ID	4279_1.R1084
5'-most EST	g2798285
Method	BLASTN
NCBI GI	g5922603
BLAST score	478
E value	0.0e+00
Match length	522
% identity	100
NCBI Description	Oryza sativa genomic DNA, chromosome 1, clone:P0705D01
Seq. No.	387272
Contig ID	4280_1.R1084
5'-most EST	uC-osrocyp015h03b1
Seq. No.	387273
Contig ID	4284_1.R1084
5'-most EST	g3767349
Seq. No.	387274

Contig ID	4287_1.R1084
5'-most EST	g3766541
Seq. No.	387275
Contig ID	4288_1.R1084
5'-most EST	g3760243
Method	BLASTX
NCBI GI	g5802955
BLAST score	377
E value	2.0e-55
Match length	216
% identity	51
NCBI Description	(AF178990) stress related protein [Vitis riparia]
Seq. No.	387276
Contig ID	4293_1.R1084
5'-most EST	uC-osflm202113a08b1
Method	BLASTX
NCBI GI	g6041808
BLAST score	832
E value	1.0e-164
Match length	396
% identity	70
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	387277
Contig ID	4293_2.R1084
5'-most EST	g701701
Method	BLASTX
NCBI GI	g6041808
BLAST score	321
E value	3.0e-29
Match length	91
% identity	57
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	387278
Contig ID	4293_3.R1084
5'-most EST	uC-osflcyp086h01b1
Method	BLASTX
NCBI GI	g6041808
BLAST score	384
E value	5.0e-91
Match length	235
% identity	69
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	387279
Contig ID	4294_1.R1084
5'-most EST	g4716284
Seq. No.	387280
Contig ID	4295_1.R1084
5'-most EST	LIB3431-055-P1-N1-E7
Method	BLASTX
NCBI GI	g6041855
BLAST score	399

E value	3.0e-38
Match length	185
% identity	50
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]

Seq. No.	387281
Contig ID	4297_1.R1084
5'-most EST	LIB3431-055-P1-N1-E9
Method	BLASTX
NCBI GI	g4335763
BLAST score	413
E value	4.0e-40
Match length	161
% identity	51
NCBI Description	(AC006284) unknown protein [Arabidopsis thaliana]

Seq. No.	387282
Contig ID	4298_1.R1084
5'-most EST	uC-osflcyp127g09a1

Seq. No.	387283
Contig ID	4299_1.R1084
5'-most EST	g3762816
Method	BLASTX
NCBI GI	g4337175
BLAST score	332
E value	2.0e-30
Match length	122
% identity	56
NCBI Description	(AC006416) ESTs gb_T20589, gb_T04648, gb_AA597906, gb_T04111, gb_R84180, gb_R65428, gb_T44439, gb_T76570, gb_R90004, gb_T45020, gb_T42457, gb_T20921, gb_AA042762 and gb_AA720210 come from this gene. [Arabidopsis thaliana]

Seq. No.	387284
Contig ID	4300_1.R1084
5'-most EST	LIB3431-055-P1-N1-F11

Seq. No.	387285
Contig ID	4313_2.R1084
5'-most EST	g2428432

Seq. No.	387286
Contig ID	4313_4.R1084
5'-most EST	uC-osflcyp022c02b1

Seq. No.	387287
Contig ID	4321_1.R1084
5'-most EST	LIB3431-055-P1-N1-H10

Seq. No.	387288
Contig ID	4332_1.R1084
5'-most EST	LIB3431-056-P1-N1-A1
Method	BLASTX
NCBI GI	g5690431
BLAST score	237
E value	9.0e-20

Match length	97
% identity	48
NCBI Description	(AF165883) prefoldin subunit 2 [Homo sapiens]

Seq. No.	387289
Contig ID	4337_1.R1084
5'-most EST	g3767324

Seq. No.	387290
Contig ID	4338_1.R1084
5'-most EST	g2801023
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	7.0e-10
Match length	36
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	387291
Contig ID	4350_1.R1084
5'-most EST	LIB3431-038-P1-K1-G5

Seq. No.	387292
Contig ID	4354_1.R1084
5'-most EST	LIB3431-001-P1-N1-G9

Seq. No.	387293
Contig ID	4362_2.R1084
5'-most EST	LIB3431-056-P1-N1-C5
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	47
% identity	48
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387294
Contig ID	4368_1.R1084
5'-most EST	g3759651

Seq. No.	387295
Contig ID	4370_1.R1084
5'-most EST	uC-osf1cyp172a04a1

Seq. No.	387296
Contig ID	4371_1.R1084
5'-most EST	g4714582
Method	BLASTX
NCBI GI	g1076660
BLAST score	293
E value	5.0e-26
Match length	152
% identity	44
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator

{DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	387297
Contig ID	4380_1.R1084
5'-most EST	g5039119
Method	BLASTX
NCBI GI	g1084461
BLAST score	263
E value	2.0e-22
Match length	83
% identity	61
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	387298
Contig ID	4380_2.R1084
5'-most EST	LIB3433-055-P1-K1-A7
Method	BLASTX
NCBI GI	g1084461
BLAST score	262
E value	2.0e-22
Match length	83
% identity	64
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	387299
Contig ID	4380_3.R1084
5'-most EST	LIB3431-056-P1-N1-E12
Method	BLASTX
NCBI GI	g1084461
BLAST score	287
E value	2.0e-25
Match length	98
% identity	60
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	387300
Contig ID	4380_4.R1084
5'-most EST	g3763621

Seq. No.	387301
Contig ID	4380_10.R1084
5'-most EST	LIB3433-053-P1-K1-B8
Method	BLASTX
NCBI GI	g1084461
BLAST score	151
E value	1.0e-18
Match length	95
% identity	60
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	387302
Contig ID	4380_12.R1084
5'-most EST	LIB3434-060-P1-K1-F9

Seq. No.	387303
Contig ID	4382_1.R1084

5'-most EST	LIB3431-056-P1-N1-E3
Seq. No.	387304
Contig ID	4392_1.R1084
5'-most EST	LIB3431-056-P1-N1-F2
Method	BLASTX
NCBI GI	g585350
BLAST score	496
E value	5.0e-50
Match length	110
% identity	83
NCBI Description	CASEIN KINASE II, ALPHA CHAIN 2 (CK II) >gi_419753_pir__S31099 casein kinase II (EC 2.7.1.-) alpha-type chain (clone ATCKA2) - Arabidopsis thaliana >gi_391605_dbj_BAA01091_ (D10247) casein kinase II catalytic subunit [Arabidopsis thaliana]
Seq. No.	387305
Contig ID	4397_1.R1084
5'-most EST	LIB3431-056-P1-N1-F7
Seq. No.	387306
Contig ID	4397_2.R1084
5'-most EST	g4879332
Seq. No.	387307
Contig ID	4400_1.R1084
5'-most EST	LIB3431-056-P1-N1-G1
Method	BLASTX
NCBI GI	g3335349
BLAST score	232
E value	4.0e-19
Match length	140
% identity	39
NCBI Description	(AC004512) Similar to gb_U46691 putative chromatin structure regulator (SUPT6H) from Homo sapiens. ESTs gb_T42908, gb_AA586170 and gb_AA395125 come from this gene. [Arabidopsis thaliana]
Seq. No.	387308
Contig ID	4401_1.R1084
5'-most EST	uC-osroM202011a08a1
Method	BLASTX
NCBI GI	g5326825
BLAST score	157
E value	4.0e-10
Match length	87
% identity	32
NCBI Description	(AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]
Seq. No.	387309
Contig ID	4409_1.R1084
5'-most EST	uC-osroM202019h05a1
Method	BLASTX
NCBI GI	g4678338
BLAST score	232

E value	7.0e-19
Match length	55
% identity	75
NCBI Description	(AL049658) putative protein [Arabidopsis thaliana]

Seq. No.	387310
Contig ID	4421_1.R1084
5'-most EST	g3760362
Method	BLASTX
NCBI GI	g4455318
BLAST score	422
E value	4.0e-47
Match length	173
% identity	56
NCBI Description	(AL035528) glycine hydroxymethyltransferase-like protein [Arabidopsis thaliana]

Seq. No.	387311
Contig ID	4425_1.R1084
5'-most EST	g2310726
Method	BLASTN
NCBI GI	g1159878
BLAST score	70
E value	1.0e-30
Match length	129
% identity	90
NCBI Description	A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No.	387312
Contig ID	4425_2.R1084
5'-most EST	g2800356
Method	BLASTN
NCBI GI	g1159878
BLAST score	87
E value	6.0e-41
Match length	127
% identity	92
NCBI Description	A.fatua mRNA for DNA-binding protein (clone ABF2)

Seq. No.	387313
Contig ID	4430_1.R1084
5'-most EST	LIB3431-058-P1-N1-A8
Method	BLASTX
NCBI GI	g3046693
BLAST score	686
E value	6.0e-76
Match length	177
% identity	73
NCBI Description	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No.	387314
Contig ID	4430_2.R1084
5'-most EST	LIB3433-059-P1-K1-B6
Method	BLASTX
NCBI GI	g3046693
BLAST score	455

E value	5.0e-69
Match length	169
% identity	66
NCBI Description	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]

Seq. No.	387315
Contig ID	4431_1.R1084
5'-most EST	LIB3431-058-P1-N1-A9

Seq. No.	387316
Contig ID	4433_1.R1084
5'-most EST	LIB3431-058-P1-N1-B11
Method	BLASTX
NCBI GI	g2582381
BLAST score	476
E value	2.0e-83
Match length	249
% identity	66
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No.	387317
Contig ID	4435_1.R1084
5'-most EST	LIB3431-011-P1-N1-B5
Method	BLASTX
NCBI GI	g3924605
BLAST score	251
E value	2.0e-21
Match length	59
% identity	71
NCBI Description	(AF069442) putative inhibitor of apoptosis [Arabidopsis thaliana]

Seq. No.	387318
Contig ID	4444_1.R1084
5'-most EST	LIB3431-058-P1-N1-C10
Method	BLASTX
NCBI GI	g1001355
BLAST score	335
E value	2.0e-49
Match length	234
% identity	46
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	387319
Contig ID	4450_1.R1084
5'-most EST	uC-osf1cyp106c10a1
Method	BLASTX
NCBI GI	g4678949
BLAST score	546
E value	1.0e-55
Match length	131
% identity	79
NCBI Description	(AL049711) dihydrolipoamide S-acetyltransferase precursor [Arabidopsis thaliana]

Seq. No.	387320
Contig ID	4457_1.R1084
5'-most EST	LIB3431-001-P1-N1-A6
Method	BLASTX
NCBI GI	g4633652
BLAST score	266
E value	5.0e-23
Match length	88
% identity	56
NCBI Description	(AF124405) alliinase precursor [Allium cepa]

Seq. No.	387321
Contig ID	4460_1.R1084
5'-most EST	LIB3431-009-P1-N1-A9

Seq. No.	387322
Contig ID	4462_1.R1084
5'-most EST	LIB3431-058-P1-N1-D7
Method	BLASTX
NCBI GI	g3334150
BLAST score	207
E value	2.0e-21
Match length	63
% identity	90
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	387323
Contig ID	4464_1.R1084
5'-most EST	LIB3432-023-P1-K1-A6
Method	BLASTX
NCBI GI	g400989
BLAST score	355
E value	2.0e-54
Match length	182
% identity	61
NCBI Description	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) >gi_322771_pir__A45113 ribosomal protein L24 precursor - common tobacco >gi_170273 (M87838) ribosomal protein L24 [Nicotiana tabacum] >gi_170324 (M87839) ribosomal protein L24 [Nicotiana tabacum]

Seq. No.	387324
Contig ID	4466_1.R1084
5'-most EST	LIB3431-058-P1-N1-E11

Seq. No.	387325
Contig ID	4467_1.R1084
5'-most EST	g5667513
Method	BLASTX
NCBI GI	g82496
BLAST score	2901
E value	0.0e+00
Match length	664

% identity	93
NCBI Description	phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No.	387326
Contig ID	4467_2.R1084
5'-most EST	g3760162
Method	BLASTX
NCBI GI	g1944573
BLAST score	488
E value	7.0e-49
Match length	114
% identity	85
NCBI Description	(Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	387327
Contig ID	4467_3.R1084
5'-most EST	g1631984
Method	BLASTX
NCBI GI	g478740
BLAST score	1003
E value	1.0e-110
Match length	283
% identity	75
NCBI Description	phenylalanine ammonia-lyase (EC 4.1.3.5) - rice

Seq. No.	387328
Contig ID	4467_4.R1084
5'-most EST	g4716005
Method	BLASTX
NCBI GI	g478740
BLAST score	318
E value	3.0e-30
Match length	77
% identity	96
NCBI Description	phenylalanine ammonia-lyase (EC 4.1.3.5) - rice

Seq. No.	387329
Contig ID	4467_5.R1084
5'-most EST	g2428719
Method	BLASTX
NCBI GI	g1944573
BLAST score	859
E value	2.0e-92
Match length	191
% identity	88
NCBI Description	(Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	387330
Contig ID	4467_6.R1084
5'-most EST	g4716519
Method	BLASTX
NCBI GI	g3024363
BLAST score	1107
E value	1.0e-134
Match length	276
% identity	88
NCBI Description	PHENYLALANINE AMMONIA-LYASE >gi_1483610_emb_CAA68036_

(X99705) phenylalanine ammonia-lyase [Triticum aestivum]

Seq. No.	387331
Contig ID	4467_7.R1084
5'-most EST	uC-osroM202016d01a1
Method	BLASTX
NCBI GI	g82496
BLAST score	206
E value	2.0e-31
Match length	189
% identity	35
NCBI Description	phenylalanine ammonia-lyase (EC 4.3.1.5) - rice

Seq. No.	387332
Contig ID	4467_9.R1084
5'-most EST	LIB3434-038-P1-K1-D4
Method	BLASTX
NCBI GI	g1944573
BLAST score	377
E value	9.0e-73
Match length	179
% identity	80
NCBI Description	(Z49146) phenylalanine ammonia-lyase [Hordeum vulgare]

Seq. No.	387333
Contig ID	4467_11.R1084
5'-most EST	g700933

Seq. No.	387334
Contig ID	4467_12.R1084
5'-most EST	uC-osflm202102e06b1
Method	BLASTN
NCBI GI	g4091009
BLAST score	253
E value	1.0e-140
Match length	498
% identity	98
NCBI Description	Oryza sativa anther-specific protein gene, complete cds

Seq. No.	387335
Contig ID	4467_16.R1084
5'-most EST	g569286

Seq. No.	387336
Contig ID	4467_27.R1084
5'-most EST	uC-osrocyp002d04a1
Method	BLASTN
NCBI GI	g20280
BLAST score	194
E value	1.0e-105
Match length	281
% identity	95
NCBI Description	Rice gene for phenylalanine ammonia-lyase (EC 4.3.1.5)

Seq. No.	387337
Contig ID	4478_1.R1084
5'-most EST	g2312330

Method	BLASTX
NCBI GI	g2245107
BLAST score	528
E value	2.0e-53
Match length	157
% identity	40
NCBI Description	(Z97343) thioesterase like protein [Arabidopsis thaliana]

Seq. No.	387338
Contig ID	4481_1.R1084
5'-most EST	LIB3432-057-P1-K1-G7
Method	BLASTX
NCBI GI	g2493493
BLAST score	553
E value	2.0e-56
Match length	218
% identity	50
NCBI Description	SERINE CARBOXYPEPTIDASE II-1 PRECURSOR (CP-MII.1) >gi_619352_bbs_153538 CP-MII.1=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 324 aa] >gi_6093206_emb_CAB58992.1_ (X78876) serine carboxypeptidase II-1 [Hordeum vulgare]

Seq. No.	387339
Contig ID	4485_1.R1084
5'-most EST	LIB3431-058-P1-N1-F7
Method	BLASTX
NCBI GI	g2688094
BLAST score	149
E value	4.0e-09
Match length	60
% identity	50
NCBI Description	(AE001130) guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (spoT) [Borrelia burgdorferi]

Seq. No.	387340
Contig ID	4490_1.R1084
5'-most EST	LIB3431-058-P1-N1-G11

Seq. No.	387341
Contig ID	4490_2.R1084
5'-most EST	g2799673

Seq. No.	387342
Contig ID	4492_1.R1084
5'-most EST	LIB3431-058-P1-N1-G2

Seq. No.	387343
Contig ID	4500_1.R1084
5'-most EST	g2310624

Seq. No.	387344
Contig ID	4505_1.R1084
5'-most EST	g2800740
Method	BLASTX
NCBI GI	g4455335
BLAST score	158

E value	4.0e-10
Match length	192
% identity	11
NCBI Description	(AL035525) putative protein [Arabidopsis thaliana]

Seq. No.	387345
Contig ID	4513_1.R1084
5'-most EST	LIB3431-059-P1-N1-A11
Method	BLASTX
NCBI GI	g6006871
BLAST score	337
E value	3.0e-31
Match length	129
% identity	52
NCBI Description	(AC009540) hypothetical protein [Arabidopsis thaliana] >gi_6091753_gb_AAF03463.1_AC009327_2 (AC009327) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387346
Contig ID	4521_1.R1084
5'-most EST	g4715187
Method	BLASTX
NCBI GI	g2257756
BLAST score	394
E value	1.0e-37
Match length	192
% identity	71
NCBI Description	(U82815) nucleolar histone deacetylase HD2-p39 [Zea mays] >gi_3650466 (AF026917) histone deacetylase HD2-p39 [Zea mays]

Seq. No.	387347
Contig ID	4523_1.R1084
5'-most EST	LIB3434-018-P1-K1-A10
Method	BLASTX
NCBI GI	g3860277
BLAST score	877
E value	2.0e-94
Match length	215
% identity	80
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	387348
Contig ID	4523_2.R1084
5'-most EST	uC-osflM202039d05b1
Method	BLASTX
NCBI GI	g1709970
BLAST score	372
E value	2.0e-35
Match length	86
% identity	83
NCBI Description	60S RIBOSOMAL PROTEIN L10A

Seq. No.	387349
Contig ID	4523_3.R1084

5'-most EST	uC-osflcyp003c04b1
Method	BLASTX
NCBI GI	g3860277
BLAST score	378
E value	6.0e-36
Match length	163
% identity	54
NCBI Description	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana] >gi_4314394_gb_AAD15604_ (AC006232) putative ribosomal protein L10A [Arabidopsis thaliana]

Seq. No.	387350
Contig ID	4529_1.R1084
5'-most EST	g4716010

Seq. No.	387351
Contig ID	4533_1.R1084
5'-most EST	uC-osflcyp065g08b1
Method	BLASTX
NCBI GI	g4732091
BLAST score	272
E value	3.0e-35
Match length	100
% identity	68
NCBI Description	(AF126742) bundle sheath defective protein 2 [Zea mays]

Seq. No.	387352
Contig ID	4540_1.R1084
5'-most EST	LIB3431-059-P1-N1-C4

Seq. No.	387353
Contig ID	4544_1.R1084
5'-most EST	LIB3431-059-P1-N1-C9
Method	BLASTX
NCBI GI	g3138799
BLAST score	603
E value	2.0e-62
Match length	125
% identity	92
NCBI Description	(AB014058) beta 6 subunit of 20S proteasome [Oryza sativa]

Seq. No.	387354
Contig ID	4553_1.R1084
5'-most EST	uC-osflcyp007a10b1

Seq. No.	387355
Contig ID	4561_1.R1084
5'-most EST	LIB3431-059-P1-N1-E3

Seq. No.	387356
Contig ID	4562_1.R1084
5'-most EST	LIB3433-053-P1-K1-C6
Method	BLASTX
NCBI GI	g2198851
BLAST score	1976
E value	0.0e+00
Match length	404

% identity	95
NCBI Description	(AF007785) cystathionine gamma-synthase [Zea mays]

Seq. No.	387357
Contig ID	4570_1.R1084
5'-most EST	LIB3431-059-P1-N1-F12
Method	BLASTN
NCBI GI	g1245938
BLAST score	35
E value	8.0e-10
Match length	35
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	387358
Contig ID	4572_1.R1084
5'-most EST	LIB3431-059-P1-N1-F3

Seq. No.	387359
Contig ID	4578_1.R1084
5'-most EST	LIB3431-059-P1-N1-G10

Seq. No.	387360
Contig ID	4580_1.R1084
5'-most EST	uC-osrocyp029c10a1

Seq. No.	387361
Contig ID	4585_1.R1084
5'-most EST	g3760948
Method	BLASTX
NCBI GI	g3450889
BLAST score	280
E value	8.0e-25
Match length	70
% identity	81
NCBI Description	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]

Seq. No.	387362
Contig ID	4586_1.R1084
5'-most EST	uC-osroM202032a04a1

Seq. No.	387363
Contig ID	4588_1.R1084
5'-most EST	g3769042
Method	BLASTX
NCBI GI	g4455232
BLAST score	344
E value	4.0e-32
Match length	94
% identity	69
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	387364
Contig ID	4591_1.R1084
5'-most EST	g3768326
Method	BLASTX

NCBI GI	g4567283
BLAST score	375
E value	1.0e-35
Match length	179
% identity	47
NCBI Description	(AC006841) unknown protein [Arabidopsis thaliana]

Seq. No.	387365
Contig ID	4596_1.R1084
5'-most EST	LIB3431-059-P1-N1-H6

Seq. No.	387366
Contig ID	4597_1.R1084
5'-most EST	g4716810
Method	BLASTX
NCBI GI	g131773
BLAST score	604
E value	2.0e-62
Match length	140
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	387367
Contig ID	4597_2.R1084
5'-most EST	uC-osroM202017g04a1
Method	BLASTX
NCBI GI	g131773
BLAST score	604
E value	2.0e-62
Match length	140
% identity	90
NCBI Description	40S RIBOSOMAL PROTEIN S14 (CLONE MCH2) >gi_82724_pir__B30097 ribosomal protein S14 (clone MCH2) - maize

Seq. No.	387368
Contig ID	4604_1.R1084
5'-most EST	uC-osroM202038f11a1
Method	BLASTX
NCBI GI	g2773154
BLAST score	159
E value	3.0e-10
Match length	63
% identity	49
NCBI Description	(AF039573) abscisic acid- and stress-inducible protein [Oryza sativa]

Seq. No.	387369
Contig ID	4604_2.R1084
5'-most EST	uC-osflcyp047c07b1
Method	BLASTN
NCBI GI	g2773153
BLAST score	45
E value	7.0e-16
Match length	89

% identity	88
NCBI Description	Oryza sativa abscisic acid- and stress-inducible protein (Asr1) mRNA, complete cds

Seq. No.	387370
Contig ID	4605_1.R1084
5'-most EST	g3769010

Seq. No.	387371
Contig ID	4608_1.R1084
5'-most EST	LIB3431-060-P1-N1-A9

Seq. No.	387372
Contig ID	4616_1.R1084
5'-most EST	LIB3432-002-P1-K1-D5

Seq. No.	387373
Contig ID	4620_1.R1084
5'-most EST	g4716041
Method	BLASTX
NCBI GI	g1619300
BLAST score	688
E value	4.0e-72
Match length	190
% identity	67
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	387374
Contig ID	4620_3.R1084
5'-most EST	g701007
Method	BLASTX
NCBI GI	g5091623
BLAST score	195
E value	5.0e-15
Match length	49
% identity	69
NCBI Description	(AC007454) Similar to gb_U93048 somatic embryogenesis receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]

Seq. No.	387375
Contig ID	4627_1.R1084
5'-most EST	LIB3432-018-P1-K1-H4

Seq. No.	387376
Contig ID	4628_1.R1084
5'-most EST	uC-osroM202034a10a1
Method	BLASTX
NCBI GI	g3894178
BLAST score	211
E value	7.0e-21
Match length	62
% identity	76
NCBI Description	(AC005312) putative nucleic acid binding protein [Arabidopsis thaliana]

Seq. No.	387377
Contig ID	4632_1.R1084
5'-most EST	uC-osflM2020116e07a1
Method	BLASTX
NCBI GI	g266567
BLAST score	368
E value	5.0e-35
Match length	105
% identity	67
NCBI Description	MITOCHONDRIAL PROCESSING PEPTIDASE ALPHA SUBUNIT PRECURSOR (ALPHA-MPP) (UBIQUINOL-CYTOCHROME C REDUCTASE SUBUNIT II) >gi_421956_pir__S23558 mitochondrial processing peptidase (EC 3.4.99.41) alpha chain precursor - potato >gi_21493_emb_CAA46990_ (X66284) mitochondrial processing peptidase [Solanum tuberosum]

Seq. No.	387378
Contig ID	4633_1.R1084
5'-most EST	LIB3431-060-P1-N1-D3
Method	BLASTX
NCBI GI	g4098647
BLAST score	916
E value	1.0e-110
Match length	232
% identity	81
NCBI Description	(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]

Seq. No.	387379
Contig ID	4639_1.R1084
5'-most EST	g3762593
Method	BLASTX
NCBI GI	g4559358
BLAST score	341
E value	1.0e-31
Match length	97
% identity	63
NCBI Description	(AC006585) putative steroid binding protein [Arabidopsis thaliana]

Seq. No.	387380
Contig ID	4642_1.R1084
5'-most EST	uC-osflM202063h10a1

Seq. No.	387381
Contig ID	4647_1.R1084
5'-most EST	g4716365
Method	BLASTX
NCBI GI	g295671
BLAST score	149
E value	6.0e-09
Match length	283
% identity	12
NCBI Description	(L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]

Seq. No.	387382
Contig ID	4652_1.R1084
5'-most EST	uC-osflcyp070c10a1

Seq. No.	387383
Contig ID	4653_1.R1084
5'-most EST	LIB3431-060-P1-N1-F12

Seq. No.	387384
Contig ID	4655_1.R1084
5'-most EST	LIB3431-060-P1-N1-F3

Seq. No.	387385
Contig ID	4656_1.R1084
5'-most EST	LIB3431-060-P1-N1-F4
Method	BLASTN
NCBI GI	g1245938
BLAST score	35
E value	7.0e-10
Match length	35
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	387386
Contig ID	4671_1.R1084
5'-most EST	LIB3474-001-P1-K1-A1
Method	BLASTX
NCBI GI	g4544428
BLAST score	316
E value	7.0e-33
Match length	108
% identity	69
NCBI Description	(AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	387387
Contig ID	4673_1.R1084
5'-most EST	uC-osflcyp132h01a1
Method	BLASTX
NCBI GI	g2253411
BLAST score	301
E value	8.0e-39
Match length	191
% identity	42
NCBI Description	(AF007219) PP2A inhibitor [Tetraodon fluviatilis]

Seq. No.	387388
Contig ID	4677_1.R1084
5'-most EST	LIB3431-060-P1-N1-H2
Method	BLASTX
NCBI GI	g2344889
BLAST score	461
E value	1.0e-45
Match length	170
% identity	49
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana] >gi_4895255_gb_AAD32840.1_AC007659_22 (AC007659) unknown

protein [Arabidopsis thaliana]

Seq. No.	387389
Contig ID	4681_1.R1084
5'-most EST	g3766889

Seq. No.	387390
Contig ID	4683_1.R1084
5'-most EST	LIB3431-060-P1-N1-H8

Seq. No.	387391
Contig ID	4684_1.R1084
5'-most EST	LIB3431-060-P1-K1-H9

Seq. No.	387392
Contig ID	4685_1.R1084
5'-most EST	g3759052
Method	BLASTX
NCBI GI	g3641252
BLAST score	224
E value	5.0e-18
Match length	102
% identity	46
NCBI Description	(AF053127) leucine-rich receptor-like protein kinase [Malus domestica]

Seq. No.	387393
Contig ID	4692_1.R1084
5'-most EST	uC-osflcyp064a01b1

Seq. No.	387394
Contig ID	4692_2.R1084
5'-most EST	uC-osflcyp032d06b1

Seq. No.	387395
Contig ID	4697_1.R1084
5'-most EST	LIB3431-063-P1-N1-B10
Method	BLASTX
NCBI GI	g4544443
BLAST score	380
E value	3.0e-36
Match length	165
% identity	43
NCBI Description	(AC006592) putative mitochondrial uncoupling protein [Arabidopsis thaliana]

Seq. No.	387396
Contig ID	4700_1.R1084
5'-most EST	uC-osrocyp017a11a1
Method	BLASTX
NCBI GI	g4103987
BLAST score	1106
E value	1.0e-121
Match length	280
% identity	76
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase

[Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589) 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	387397
Contig ID	4700_2.R1084
5'-most EST	LIB3432-052-P1-K1-E5
Method	BLASTX
NCBI GI	g4103987
BLAST score	516
E value	2.0e-52
Match length	141
% identity	71
NCBI Description	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum] >gi_6002383_emb_CAB56756.1_ (AJ011589) 5,10-methylenetetrahydrofolate dehydrogenase: 5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]

Seq. No.	387398
Contig ID	4706_1.R1084
5'-most EST	g5771217
Method	BLASTX
NCBI GI	g5803266
BLAST score	274
E value	5.0e-47
Match length	114
% identity	96
NCBI Description	(AP000399) ESTs AU078063(S15496),C97608(C60475), C28255(C60475) correspond to a region of the predicted gene; similar to plastid transketolase 2 (Y15782) [Oryza sativa]

Seq. No.	387399
Contig ID	4710_1.R1084
5'-most EST	g3760899

Seq. No.	387400
Contig ID	4721_1.R1084
5'-most EST	LIB3431-063-P1-N1-D3

Seq. No.	387401
Contig ID	4722_1.R1084
5'-most EST	LIB3431-063-P1-N1-D6
Method	BLASTX
NCBI GI	g6014934
BLAST score	540
E value	4.0e-55
Match length	118
% identity	81
NCBI Description	DCL PROTEIN, CHLOROPLAST PRECURSOR (DEFECTIVE CHLOROPLASTS AND LEAVES PROTEIN) >gi_1305531 (U55219) defective chloroplasts and leaves; required for chloroplast development and palisade cell differentiation in leaves [Lycopersicon esculentum] >gi_1323698 (U55278) DCL [Solanum

lycopersicum]

Seq. No.	387402
Contig ID	4725_1.R1084
5'-most EST	LIB3431-063-P1-N1-E1

Seq. No.	387403
Contig ID	4726_1.R1084
5'-most EST	LIB3431-063-P1-N1-E10

Seq. No.	387404
Contig ID	4727_1.R1084
5'-most EST	LIB3431-063-P1-N1-E12
Method	BLASTX
NCBI GI	g3894168
BLAST score	179
E value	1.0e-12
Match length	90
% identity	46
NCBI Description	(AC005312) similar to phloem-specific lectin [Arabidopsis thaliana]

Seq. No.	387405
Contig ID	4728_1.R1084
5'-most EST	g2798822
Method	BLASTN
NCBI GI	g58066
BLAST score	53
E value	2.0e-20
Match length	53
% identity	100
NCBI Description	pBluescript SK(-) vector DNA, phagemid excised from lambda ZAP

Seq. No.	387406
Contig ID	4736_1.R1084
5'-most EST	LIB3431-063-P1-N1-F11
Method	BLASTX
NCBI GI	g2244867
BLAST score	568
E value	4.0e-58
Match length	241
% identity	45
NCBI Description	(Z97337) hydroxynitrile lyase like protein [Arabidopsis thaliana]

Seq. No.	387407
Contig ID	4738_1.R1084
5'-most EST	g2799140
Method	BLASTX
NCBI GI	g3953471
BLAST score	273
E value	9.0e-24
Match length	88
% identity	58
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	387408
Contig ID	4744_1.R1084
5'-most EST	LIB3431-063-P1-N1-F8

Seq. No.	387409
Contig ID	4756_1.R1084
5'-most EST	g2280567
Method	BLASTX
NCBI GI	g2244772
BLAST score	705
E value	7.0e-87
Match length	214
% identity	76
NCBI Description	(Z97335) transport protein [Arabidopsis thaliana]

Seq. No.	387410
Contig ID	4763_1.R1084
5'-most EST	LIB3432-031-P1-K1-G2
Method	BLASTX
NCBI GI	g3688123
BLAST score	1704
E value	0.0e+00
Match length	479
% identity	68
NCBI Description	(AJ006293) granule-bound starch synthase [Antirrhinum majus]

Seq. No.	387411
Contig ID	4774_1.R1084
5'-most EST	g3767756

Seq. No.	387412
Contig ID	4777_1.R1084
5'-most EST	LIB3431-001-P1-N1-A7
Method	BLASTX
NCBI GI	g585963
BLAST score	231
E value	5.0e-19
Match length	60
% identity	82
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	387413
Contig ID	4777_2.R1084
5'-most EST	g2280991
Method	BLASTX
NCBI GI	g585963
BLAST score	264
E value	6.0e-23
Match length	69
% identity	80
NCBI Description	PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT

Seq. No.	387414
Contig ID	4778_1.R1084
5'-most EST	LIB3431-001-P1-N1-A9

Seq. No.	387415
Contig ID	4780_1.R1084
5'-most EST	LIB3434-041-P1-K1-G4
Method	BLASTX
NCBI GI	g5738378
BLAST score	699
E value	1.0e-73
Match length	203
% identity	67
NCBI Description	(AL080253) putative protein [Arabidopsis thaliana]

Seq. No.	387416
Contig ID	4785_1.R1084
5'-most EST	g4715492
Method	BLASTX
NCBI GI	g4960024
BLAST score	419
E value	6.0e-41
Match length	114
% identity	72
NCBI Description	(AF144079) S-adenosyl-L-methionine:L-methionine S-methyltransferase [Zea mays]

Seq. No.	387417
Contig ID	4791_1.R1084
5'-most EST	uC-osroM202037d08a1

Seq. No.	387418
Contig ID	4791_2.R1084
5'-most EST	LIB3432-016-P1-K1-E10

Seq. No.	387419
Contig ID	4794_1.R1084
5'-most EST	uC-osf1cyp086c11a1
Method	BLASTX
NCBI GI	g3128168
BLAST score	424
E value	2.0e-78
Match length	188
% identity	70
NCBI Description	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]

Seq. No.	387420
Contig ID	4799_1.R1084
5'-most EST	LIB3431-001-P1-N1-C6
Method	BLASTX
NCBI GI	g4115377
BLAST score	355
E value	1.0e-33
Match length	78
% identity	81
NCBI Description	(AC005967) unknown protein [Arabidopsis thaliana]

Seq. No.	387421
Contig ID	4802_1.R1084
5'-most EST	uC-osf1cyp086h10a1

Seq. No.	387422
Contig ID	4803_1.R1084
5'-most EST	g4715592
Seq. No.	387423
Contig ID	4808_1.R1084
5'-most EST	LIB3431-001-P1-N1-D5
Seq. No.	387424
Contig ID	4811_1.R1084
5'-most EST	LIB3431-001-P1-N1-D8
Seq. No.	387425
Contig ID	4813_1.R1084
5'-most EST	g2799041
Method	BLASTN
NCBI GI	g3402815
BLAST score	54
E value	4.0e-21
Match length	54
% identity	100
NCBI Description	Cloning Vector pGreen
Seq. No.	387426
Contig ID	4813_2.R1084
5'-most EST	LIB3434-035-P1-K1-G2
Method	BLASTX
NCBI GI	g4586107
BLAST score	297
E value	1.0e-26
Match length	115
% identity	16
NCBI Description	(AL049638) putative disease resistance protein [Arabidopsis thaliana]
Seq. No.	387427
Contig ID	4814_1.R1084
5'-most EST	LIB3431-001-P1-N1-E10
Seq. No.	387428
Contig ID	4819_1.R1084
5'-most EST	uC-osflcyp138c04a1
Method	BLASTX
NCBI GI	g4539545
BLAST score	677
E value	1.0e-120
Match length	246
% identity	87
NCBI Description	(Y16644) PRCI [Nicotiana tabacum]
Seq. No.	387429
Contig ID	4827_1.R1084
5'-most EST	LIB3434-011-P1-K1-D9
Method	BLASTX
NCBI GI	g3184288
BLAST score	214

E value	6.0e-17
Match length	62
% identity	60
NCBI Description	(AC004136) unknown protein [Arabidopsis thaliana]

Seq. No.	387430
Contig ID	4830_1.R1084
5'-most EST	LIB3431-001-P1-N1-F3

Seq. No.	387431
Contig ID	4849_1.R1084
5'-most EST	LIB3431-001-P1-N1-H4

Seq. No.	387432
Contig ID	4850_1.R1084
5'-most EST	g2798658
Method	BLASTX
NCBI GI	g499099
BLAST score	305
E value	2.0e-27
Match length	63
% identity	92
NCBI Description	(U09942) beta-galactosidase alpha-peptide [Cloning vector pDB31]

Seq. No.	387433
Contig ID	4858_1.R1084
5'-most EST	uC-osflcyp106h08a1

Seq. No.	387434
Contig ID	4861_1.R1084
5'-most EST	g4716377

Seq. No.	387435
Contig ID	4863_1.R1084
5'-most EST	LIB3433-034-P1-K1-F4

Seq. No.	387436
Contig ID	4871_1.R1084
5'-most EST	g4715436

Seq. No.	387437
Contig ID	4879_1.R1084
5'-most EST	LIB3431-002-P1-N1-D3

Seq. No.	387438
Contig ID	4884_1.R1084
5'-most EST	uC-osroM202004a06a2
Method	BLASTX
NCBI GI	g3176686
BLAST score	512
E value	1.0e-51
Match length	200
% identity	53
NCBI Description	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb_U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]

Seq. No.	387439
Contig ID	4889_1.R1084
5'-most EST	g4714888
Method	BLASTX
NCBI GI	g4733973
BLAST score	304
E value	3.0e-27
Match length	177
% identity	37
NCBI Description	(AC007264) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387440
Contig ID	4889_4.R1084
5'-most EST	LIB3433-005-Q6-K1-C7
Method	BLASTX
NCBI GI	g4914402
BLAST score	258
E value	2.0e-27
Match length	105
% identity	57
NCBI Description	(AL050352) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387441
Contig ID	4903_1.R1084
5'-most EST	uC-osf1M202063d12a1

Seq. No.	387442
Contig ID	4904_1.R1084
5'-most EST	LIB3431-002-P1-N1-G5

Seq. No.	387443
Contig ID	4907_1.R1084
5'-most EST	LIB3431-002-P1-N1-H11

Seq. No.	387444
Contig ID	4908_1.R1084
5'-most EST	g2799806
Method	BLASTX
NCBI GI	g3068809
BLAST score	417
E value	1.0e-40
Match length	149
% identity	58
NCBI Description	(AF059295) Skp1 homolog [Arabidopsis thaliana]

Seq. No.	387445
Contig ID	4910_1.R1084
5'-most EST	g3762571

Seq. No.	387446
Contig ID	4916_1.R1084
5'-most EST	LIB3431-003-P1-K1-A5
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	4.0e-10

Match length	46
% identity	48
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387447
Contig ID	4920_1.R1084
5'-most EST	g5003169

Seq. No.	387448
Contig ID	4922_1.R1084
5'-most EST	g4716017
Method	BLASTX
NCBI GI	g3402817
BLAST score	216
E value	4.0e-17
Match length	61
% identity	69
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	387449
Contig ID	4929_1.R1084
5'-most EST	uC-osf1cyp003h08b1
Method	BLASTX
NCBI GI	g218179
BLAST score	475
E value	2.0e-47
Match length	117
% identity	81
NCBI Description	(D10207) H-ATPase [Oryza sativa] >gi_444339_prf__1906387A H ATPase [Oryza sativa]

Seq. No.	387450
Contig ID	4935_1.R1084
5'-most EST	LIB3434-054-P1-K1-C2

Seq. No.	387451
Contig ID	4936_1.R1084
5'-most EST	g5900721
Method	BLASTX
NCBI GI	g2911799
BLAST score	852
E value	2.0e-91
Match length	215
% identity	75
NCBI Description	(AF008184) 4-coumarate:CoA ligase 1 [Populus balsamifera subsp. trichocarpa X Populus deltoides]

Seq. No.	387452
Contig ID	4939_1.R1084
5'-most EST	LIB3431-003-P1-N1-D10
Method	BLASTX
NCBI GI	g4336610
BLAST score	675
E value	7.0e-71
Match length	157
% identity	84
NCBI Description	(AF099112) sigma factor; Sig3 [Zea mays]

Seq. No.	387453
Contig ID	4946_1.R1084
5'-most EST	g426775

Seq. No.	387454
Contig ID	4951_1.R1084
5'-most EST	LIB3431-003-P1-N1-E11
Method	BLASTX
NCBI GI	g5734720
BLAST score	456
E value	6.0e-45
Match length	246
% identity	44
NCBI Description	(AC008075) Contains PF_01426 BAH (bromo-adjacent homology) domain. ESTs gb_N96349, gb_T42710, gb_H77084, gb_AA395147 and gb_AA605500 come from this gene. [Arabidopsis thaliana]

Seq. No.	387455
Contig ID	4955_1.R1084
5'-most EST	uC-osflcyp117e11a1
Method	BLASTX
NCBI GI	g400803
BLAST score	2698
E value	0.0e+00
Match length	559
% identity	91
NCBI Description	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) (PGAM-I) >gi_283033_pir__A42807 phosphoglycerate mutase (EC 5.4.2.1), 2, 3-bisphosphoglycerate-independent - maize >gi_168588 (M80912) 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [Zea mays]

Seq. No.	387456
Contig ID	4956_1.R1084
5'-most EST	LIB3433-029-P1-K1-C12

Seq. No.	387457
Contig ID	4963_1.R1084
5'-most EST	g3768695
Method	BLASTX
NCBI GI	g5824411
BLAST score	537
E value	2.0e-54
Match length	201
% identity	54
NCBI Description	(Z68882) Similarity to Bovine inorganic pyrophosphatase (SW:IPYR_BOVIN); cDNA EST EMBL:D66533 comes from this gene; cDNA EST EMBL:D70345 comes from this gene; cDNA EST yk338a8.3 comes from this gene; cDNA EST yk338a8.5 comes

Seq. No.	387458
Contig ID	4970_1.R1084
5'-most EST	uC-osflcyp159b03a1
Method	BLASTX
NCBI GI	g4928472

BLAST score	663
E value	2.0e-69
Match length	162
% identity	75
NCBI Description	(AF133302) type 2 peroxiredoxin [Brassica rapa subsp. pekinensis]

Seq. No.	387459
Contig ID	4971_1.R1084
5'-most EST	uC-osrocyp012b07a1
Method	BLASTN
NCBI GI	g19046
BLAST score	54
E value	3.0e-21
Match length	132
% identity	89
NCBI Description	H.vulgare mRNA for seed protein B32E

Seq. No.	387460
Contig ID	4972_1.R1084
5'-most EST	LIB3431-003-P1-N1-H6
Method	BLASTX
NCBI GI	g2088650
BLAST score	342
E value	5.0e-34
Match length	113
% identity	71
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	387461
Contig ID	4973_1.R1084
5'-most EST	g5005015

Seq. No.	387462
Contig ID	4981_1.R1084
5'-most EST	g3759083
Method	BLASTX
NCBI GI	g4325369
BLAST score	625
E value	2.0e-80
Match length	263
% identity	60
NCBI Description	(AF128396) T3H13.3 gene product [Arabidopsis thaliana]

Seq. No.	387463
Contig ID	4983_1.R1084
5'-most EST	g2800100

Seq. No.	387464
Contig ID	4984_1.R1084
5'-most EST	uC-osrocyp006e03a1
Method	BLASTX
NCBI GI	g6091726
BLAST score	178
E value	2.0e-12
Match length	156

% identity	33
NCBI Description	(AC010797) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387465
Contig ID	4984_2.R1084
5'-most EST	g428603

Seq. No.	387466
Contig ID	4988_1.R1084
5'-most EST	LIB3431-004-P1-N1-B7
Method	BLASTX
NCBI GI	g3249105
BLAST score	364
E value	4.0e-34
Match length	189
% identity	40
NCBI Description	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb_X78886 from A. thaliana. [Arabidopsis thaliana]

Seq. No.	387467
Contig ID	4989_1.R1084
5'-most EST	uC-osroM202020f11a1

Seq. No.	387468
Contig ID	4992_1.R1084
5'-most EST	LIB3431-004-P1-N1-C11
Method	BLASTN
NCBI GI	g1808687
BLAST score	61
E value	2.0e-25
Match length	178
% identity	89
NCBI Description	S.stapfianus pSD.13 mRNA

Seq. No.	387469
Contig ID	4996_1.R1084
5'-most EST	g3760864
Method	BLASTX
NCBI GI	g4115934
BLAST score	600
E value	5.0e-62
Match length	125
% identity	83
NCBI Description	(AF118223) contains similarity to Methanobacterium thermoautotrophicum transcriptional regulator (GB:AE000850) [Arabidopsis thaliana]

Seq. No.	387470
Contig ID	4998_1.R1084
5'-most EST	uC-osrocyp013f06b1
Method	BLASTN
NCBI GI	g3287498
BLAST score	75
E value	9.0e-34
Match length	75
% identity	100
NCBI Description	Oryza sativa gene for importin alpha, complete cds

Seq. No.	387471
Contig ID	5008_1.R1084
5'-most EST	g3759700
Seq. No.	387472
Contig ID	5014_1.R1084
5'-most EST	LIB3431-004-P1-N1-E2
Seq. No.	387473
Contig ID	5020_1.R1084
5'-most EST	g2798751
Seq. No.	387474
Contig ID	5021_1.R1084
5'-most EST	LIB3431-004-P1-N1-F3
Seq. No.	387475
Contig ID	5030_1.R1084
5'-most EST	LIB3431-004-P1-N1-G3
Seq. No.	387476
Contig ID	5039_1.R1084
5'-most EST	g2800666
Seq. No.	387477
Contig ID	5048_1.R1084
5'-most EST	g4714653
Seq. No.	387478
Contig ID	5048_2.R1084
5'-most EST	LIB3431-005-P1-K1-A4
Seq. No.	387479
Contig ID	5052_1.R1084
5'-most EST	LIB3431-005-P1-N1-A9
Seq. No.	387480
Contig ID	5053_1.R1084
5'-most EST	g3763633
Method	BLASTX
NCBI GI	g4056487
BLAST score	406
E value	8.0e-53
Match length	199
% identity	61
NCBI Description	(AC005896) hypothetical protein [Arabidopsis thaliana]
Seq. No.	387481
Contig ID	5058_1.R1084
5'-most EST	LIB3431-005-P1-N1-B5
Seq. No.	387482
Contig ID	5061_1.R1084
5'-most EST	LIB3431-005-P1-N1-B8
Seq. No.	387483

Contig ID	5071_1.R1084
5'-most EST	g2799096
Method	BLASTX
NCBI GI	g4559339
BLAST score	258
E value	5.0e-22
Match length	54
% identity	89
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	387484
Contig ID	5071_2.R1084
5'-most EST	g5005114
Method	BLASTX
NCBI GI	g4559339
BLAST score	719
E value	4.0e-76
Match length	165
% identity	82
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	387485
Contig ID	5071_3.R1084
5'-most EST	LIB3431-005-P1-N1-D1

Seq. No.	387486
Contig ID	5082_1.R1084
5'-most EST	g4715933

Seq. No.	387487
Contig ID	5084_1.R1084
5'-most EST	LIB3431-005-P1-N1-E10

Seq. No.	387488
Contig ID	5086_1.R1084
5'-most EST	uC-osf1M202064d07a1
Method	BLASTX
NCBI GI	g4539404
BLAST score	321
E value	2.0e-29
Match length	87
% identity	70
NCBI Description	(AL049524) putative protein [Arabidopsis thaliana]

Seq. No.	387489
Contig ID	5088_1.R1084
5'-most EST	LIB3431-005-P1-N1-E4

Seq. No.	387490
Contig ID	5102_1.R1084
5'-most EST	LIB3433-013-Q6-K1-A11
Method	BLASTX
NCBI GI	g5922625
BLAST score	559
E value	2.0e-89

Match length	191
% identity	88
NCBI Description	(AP000492) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa] >gi_6016858_dbj_BAA85201.1_ (AP000570) ESTs AU065732(E51179),AU030519(E51179) correspond to a region of the predicted gene.; Similar to epoxide hydrolases; coded for by A. thaliana cDNA T04215. (AF069298) [Oryza sativa]

Seq. No.	387491
Contig ID	5104_1.R1084
5'-most EST	LIB3431-005-P1-N1-G1
Method	BLASTX
NCBI GI	g3309269
BLAST score	822
E value	1.0e-106
Match length	238
% identity	80
NCBI Description	(AF074940) ferric leghemoglobin reductase-2 precursor [Glycine max]

Seq. No.	387492
Contig ID	5109_1.R1084
5'-most EST	uC-osroM202030e04a1
Method	BLASTX
NCBI GI	g5918016
BLAST score	148
E value	3.0e-09
Match length	57
% identity	53
NCBI Description	(AL035525) myosin-like protein [Arabidopsis thaliana]

Seq. No.	387493
Contig ID	5110_1.R1084
5'-most EST	g3768817

Seq. No.	387494
Contig ID	5117_1.R1084
5'-most EST	g5667335
Method	BLASTX
NCBI GI	g3776573
BLAST score	534
E value	8.0e-62
Match length	177
% identity	64
NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]

Seq. No.	387495
Contig ID	5121_1.R1084
5'-most EST	LIB3431-005-P1-N1-H9

Seq. No.	387496

Contig ID	5123_1.R1084
5'-most EST	g5607615
Seq. No.	387497
Contig ID	5125_1.R1084
5'-most EST	LIB3431-007-P1-N1-A12
Seq. No.	387498
Contig ID	5127_1.R1084
5'-most EST	LIB3431-007-P1-N1-A5
Seq. No.	387499
Contig ID	5142_1.R1084
5'-most EST	LIB3599-001-P1-N6-D8
Method	BLASTX
NCBI GI	g4835757
BLAST score	223
E value	6.0e-18
Match length	59
% identity	73
NCBI Description	(AC007202) EST gb_AA404917 comes from this gene. [Arabidopsis thaliana]
Seq. No.	387500
Contig ID	5144_1.R1084
5'-most EST	uC-osflcyp162b08a1
Method	BLASTX
NCBI GI	g1710780
BLAST score	644
E value	4.0e-67
Match length	175
% identity	71
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]
Seq. No.	387501
Contig ID	5144_2.R1084
5'-most EST	g5607296
Method	BLASTX
NCBI GI	g1173104
BLAST score	666
E value	2.0e-69
Match length	220
% identity	51
NCBI Description	RIBONUCLEASE 2 PRECURSOR >gi_289210 (M98336) ribonuclease [Arabidopsis thaliana] >gi_2642160 (AC003000) ribonuclease, RNS2 [Arabidopsis thaliana]
Seq. No.	387502
Contig ID	5144_3.R1084
5'-most EST	uC-osflcyp109c07a1
Method	BLASTX
NCBI GI	g1710780
BLAST score	282
E value	9.0e-25
Match length	104

% identity	59
NCBI Description	40S RIBOSOMAL PROTEIN S9 (S7) >gi_1321917_emb_CAA65433_ (X96613) cytoplasmic ribosomal protein S7 [Podospora anserina]

Seq. No.	387503
Contig ID	5144_4.R1084
5'-most EST	g3763255
Method	BLASTX
NCBI GI	g1173286
BLAST score	477
E value	1.0e-47
Match length	124
% identity	74
NCBI Description	40S RIBOSOMAL PROTEIN S9 >gi_112274_pir__S21497 ribosomal protein S9 - rat >gi_57143_emb_CAA47013_ (X66370) ribosomal protein S9 [Rattus norvegicus]

Seq. No.	387504
Contig ID	5151_1.R1084
5'-most EST	g3767295
Method	BLASTX
NCBI GI	g4467116
BLAST score	182
E value	5.0e-13
Match length	118
% identity	34
NCBI Description	(AL035538) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387505
Contig ID	5153_1.R1084
5'-most EST	LIB3431-007-P1-K1-D10

Seq. No.	387506
Contig ID	5161_1.R1084
5'-most EST	LIB3431-007-P1-N1-D8
Method	BLASTX
NCBI GI	g3668080
BLAST score	722
E value	1.0e-101
Match length	262
% identity	70
NCBI Description	(AC004667) unknown protein [Arabidopsis thaliana]

Seq. No.	387507
Contig ID	5166_1.R1084
5'-most EST	LIB3431-007-P1-N1-E2

Seq. No.	387508
Contig ID	5175_1.R1084
5'-most EST	LIB3431-007-P1-K1-F11

Seq. No.	387509
Contig ID	5178_1.R1084
5'-most EST	LIB3431-007-P1-N1-F6

Seq. No.	387510

Contig ID	5179_1.R1084
5'-most EST	g3768813

Seq. No.	387511
Contig ID	5182_1.R1084
5'-most EST	g700666
Method	BLASTX
NCBI GI	g480737
BLAST score	678
E value	4.0e-71
Match length	144
% identity	92
NCBI Description	triose phosphate/3-phosphoglycerate/phosphate translocator - common tobacco >gi_629694_pir__S42583 phosphate translocator - common tobacco >gi_403023_emb_CAA52979.1_ (X75088) phosphate translocator [Nicotiana tabacum]

Seq. No.	387512
Contig ID	5205_1.R1084
5'-most EST	g4715300
Method	BLASTX
NCBI GI	g5478530
BLAST score	839
E value	1.0e-121
Match length	644
% identity	23
NCBI Description	(AF130441) UVB-resistance protein UVR8 [Arabidopsis thaliana]

Seq. No.	387513
Contig ID	5215_1.R1084
5'-most EST	LIB3431-008-P1-N1-B3

Seq. No.	387514
Contig ID	5222_1.R1084
5'-most EST	LIB3431-008-P1-N1-C1

Seq. No.	387515
Contig ID	5224_1.R1084
5'-most EST	g5003035

Seq. No.	387516
Contig ID	5226_1.R1084
5'-most EST	uC-osflcyp141g11a1
Method	BLASTX
NCBI GI	g2598049
BLAST score	422
E value	3.0e-41
Match length	110
% identity	73
NCBI Description	(Y15269) chloroplast drought-induced stress protein, 34 kD) [Solanum tuberosum]

Seq. No.	387517
Contig ID	5227_1.R1084
5'-most EST	g4715523

Seq. No. 387518
Contig ID 5232_1.R1084
5'-most EST LIB3431-008-P1-K1-C9

Seq. No. 387519
Contig ID 5234_1.R1084
5'-most EST g5056133

Seq. No. 387520
Contig ID 5239_1.R1084
5'-most EST LIB3431-008-P1-N1-D5

Seq. No. 387521
Contig ID 5241_1.R1084
5'-most EST g5667574
Method BLASTX
NCBI GI g2688828
BLAST score 523
E value 8.0e-53
Match length 222
% identity 45
NCBI Description (U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No. 387522
Contig ID 5241_2.R1084
5'-most EST g5456502

Seq. No. 387523
Contig ID 5243_1.R1084
5'-most EST LIB3432-045-P1-K1-H4

Seq. No. 387524
Contig ID 5243_3.R1084
5'-most EST LIB3431-008-P1-N1-D9

Seq. No. 387525
Contig ID 5250_1.R1084
5'-most EST LIB3477-003-P1-K1-D12
Method BLASTX
NCBI GI g5823570
BLAST score 903
E value 2.0e-97
Match length 236
% identity 75
NCBI Description (AL049730) putative protein [Arabidopsis thaliana]

Seq. No. 387526
Contig ID 5256_1.R1084
5'-most EST LIB3431-008-P1-N1-F11
Method BLASTX
NCBI GI g4544408
BLAST score 468
E value 1.0e-46
Match length 110
% identity 77
NCBI Description (AC006955) unknown protein [Arabidopsis thaliana]

Seq. No.	387527
Contig ID	5260_1.R1084
5'-most EST	g5803547
Method	BLASTX
NCBI GI	g544242
BLAST score	2513
E value	0.0e+00
Match length	812
% identity	74
NCBI Description	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) >gi_485498_pir__S33533 heat shock protein 90 homolog precursor - barley >gi_22652_emb_CAA48143_ (X67960) GRP94 homologue [Hordeum vulgare]

Seq. No.	387528
Contig ID	5262_1.R1084
5'-most EST	g2311091
Method	BLASTX
NCBI GI	g3023812
BLAST score	273
E value	1.0e-46
Match length	121
% identity	77
NCBI Description	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC >gi_435046 (L26924) glyceraldehyde-phosphate dehydrogenase [Ginkgo biloba]

Seq. No.	387529
Contig ID	5263_1.R1084
5'-most EST	g2443095

Seq. No.	387530
Contig ID	5266_1.R1084
5'-most EST	g3768114
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	1.0e-09
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387531
Contig ID	5267_1.R1084
5'-most EST	g4714826
Method	BLASTX
NCBI GI	g4587610
BLAST score	642
E value	6.0e-67
Match length	163
% identity	75
NCBI Description	(AC006951) putative indole-3-glycerol phosphate synthase precursor [Arabidopsis thaliana]

Seq. No.	387532
Contig ID	5268_1.R1084

5'-most EST	g5003233
Seq. No.	387533
Contig ID	5273_1.R1084
5'-most EST	g5002852
Method	BLASTX
NCBI GI	g4689108
BLAST score	313
E value	2.0e-28
Match length	123
% identity	53
NCBI Description	(AF077030) hypothetical 43.2 kDa protein [Homo sapiens] >gi_4929577_gb_AAD34049.1_AF151812_1 (AF151812) CGI-54 protein [Homo sapiens]
Seq. No.	387534
Contig ID	5276_1.R1084
5'-most EST	g5003588
Method	BLASTX
NCBI GI	g3288883
BLAST score	184
E value	6.0e-13
Match length	171
% identity	33
NCBI Description	(AB015431) SAR DNA binding protein [Oryza sativa]
Seq. No.	387535
Contig ID	5280_1.R1084
5'-most EST	uC-osroM202007d09a1
Method	BLASTX
NCBI GI	g4102839
BLAST score	195
E value	8.0e-15
Match length	52
% identity	69
NCBI Description	(AF016713) LeOPT1 [Lycopersicon esculentum]
Seq. No.	387536
Contig ID	5302_1.R1084
5'-most EST	LIB3431-009-P1-N1-B9
Method	BLASTX
NCBI GI	g3810596
BLAST score	189
E value	5.0e-14
Match length	100
% identity	40
NCBI Description	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
Seq. No.	387537
Contig ID	5306_1.R1084
5'-most EST	LIB3431-009-P1-N1-C12
Method	BLASTX
NCBI GI	g4006818
BLAST score	1104
E value	1.0e-121
Match length	340

% identity	62
NCBI Description	(AC005970) putative translation initiation factor eIF-2B, alpha subunit [Arabidopsis thaliana]

Seq. No.	387538
Contig ID	5311_1.R1084
5'-most EST	LIB3431-009-P1-N1-D7

Seq. No.	387539
Contig ID	5318_1.R1084
5'-most EST	uC-osrocyp037a08b1

Seq. No.	387540
Contig ID	5321_1.R1084
5'-most EST	LIB3431-009-P1-N1-D5
Method	BLASTX
NCBI GI	g3894193
BLAST score	234
E value	3.0e-19
Match length	116
% identity	39
NCBI Description	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

Seq. No.	387541
Contig ID	5324_1.R1084
5'-most EST	LIB3431-009-P1-N1-D9
Method	BLASTX
NCBI GI	g4836907
BLAST score	485
E value	1.0e-48
Match length	148
% identity	62
NCBI Description	(AC007153) Highly similar to putative callose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	387542
Contig ID	5327_1.R1084
5'-most EST	g1036984
Method	BLASTX
NCBI GI	g4210330
BLAST score	354
E value	7.0e-40
Match length	106
% identity	81
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	387543
Contig ID	5333_1.R1084
5'-most EST	g3762694
Method	BLASTX
NCBI GI	g6009909
BLAST score	391
E value	2.0e-37
Match length	102
% identity	76

NCBI Description	(AB018242) histone H2A-like protein [Solanum melongena]

Seq. No.	387544
Contig ID	5333_2.R1084
5'-most EST	g3762568
Method	BLASTN
NCBI GI	g1129083
BLAST score	165
E value	2.0e-87
Match length	349
% identity	90
NCBI Description	Wheat mRNA for protein H2A, complete cds, clone wcH2A-2

Seq. No.	387545
Contig ID	5333_3.R1084
5'-most EST	uC-osroM202019e07a1
Method	BLASTX
NCBI GI	g6009909
BLAST score	393
E value	1.0e-37
Match length	102
% identity	75
NCBI Description	(AB018242) histone H2A-like protein [Solanum melongena]

Seq. No.	387546
Contig ID	5334_1.R1084
5'-most EST	LIB3431-009-P1-N1-G3
Method	BLASTX
NCBI GI	g4204265
BLAST score	670
E value	5.0e-70
Match length	178
% identity	66
NCBI Description	(AC005223) 45643 [Arabidopsis thaliana]

Seq. No.	387547
Contig ID	5354_1.R1084
5'-most EST	uC-osflcyp131h02a1
Method	BLASTX
NCBI GI	g1350548
BLAST score	227
E value	4.0e-18
Match length	105
% identity	47
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	387548
Contig ID	5354_2.R1084
5'-most EST	uC-osflcyp092a02b1
Method	BLASTX
NCBI GI	g1350548
BLAST score	233
E value	4.0e-19
Match length	101
% identity	50
NCBI Description	(L47609) heat shock-like protein [Picea glauca]

Seq. No.	387549
Contig ID	5357_1.R1084
5'-most EST	g3766704
Method	BLASTX
NCBI GI	g6002955
BLAST score	561
E value	3.0e-57
Match length	328
% identity	38
NCBI Description	(AF171877) cleavage and polyadenylation specificity factor 73 kDa subunit [Homo sapiens]

Seq. No.	387550
Contig ID	5362_1.R1084
5'-most EST	g4714885

Seq. No.	387551
Contig ID	5400_1.R1084
5'-most EST	uC-osflcyp116d06a1

Seq. No.	387552
Contig ID	5401_1.R1084
5'-most EST	LIB3431-010-P1-N1-D4

Seq. No.	387553
Contig ID	5409_1.R1084
5'-most EST	g2800042

Seq. No.	387554
Contig ID	5412_1.R1084
5'-most EST	LIB3431-010-P1-N1-E6

Seq. No.	387555
Contig ID	5416_1.R1084
5'-most EST	LIB3431-010-P1-N1-F10

Seq. No.	387556
Contig ID	5419_1.R1084
5'-most EST	g3761959
Method	BLASTX
NCBI GI	g2181184
BLAST score	157
E value	2.0e-20
Match length	108
% identity	48
NCBI Description	(Y13577) JR3 protein [Arabidopsis thaliana]

Seq. No.	387557
Contig ID	5421_1.R1084
5'-most EST	uC-osflcyp099c07a1

Seq. No.	387558
Contig ID	5424_1.R1084
5'-most EST	LIB3431-010-P1-N1-F7

Seq. No.	387559
Contig ID	5425_1.R1084

5'-most EST	LIB3431-010-P1-N1-F8
Method	BLASTN
NCBI GI	g3821780
BLAST score	36
E value	2.0e-10
Match length	47
% identity	66
NCBI Description	Xenopus laevis cDNA clone 27A6-1

Seq. No.	387560
Contig ID	5432_1.R1084
5'-most EST	uC-osflcyp110e05a1

Seq. No.	387561
Contig ID	5439_1.R1084
5'-most EST	LIB3431-010-P1-N1-H10

Seq. No.	387562
Contig ID	5440_1.R1084
5'-most EST	g569391
Method	BLASTX
NCBI GI	g3551523
BLAST score	312
E value	4.0e-28
Match length	198
% identity	36
NCBI Description	(AB017026) oxysterol-binding protein [Mus musculus]

Seq. No.	387563
Contig ID	5444_1.R1084
5'-most EST	LIB3431-010-P1-K1-H4

Seq. No.	387564
Contig ID	5446_1.R1084
5'-most EST	g5003209
Method	BLASTX
NCBI GI	g2737973
BLAST score	438
E value	3.0e-78
Match length	160
% identity	93
NCBI Description	(U83625) protein kinase ZmMEK1 [Zea mays]

Seq. No.	387565
Contig ID	5447_1.R1084
5'-most EST	LIB3431-010-P1-N1-H8
Method	BLASTX
NCBI GI	g5123939
BLAST score	470
E value	8.0e-47
Match length	137
% identity	60
NCBI Description	(AL079349) putative protein [Arabidopsis thaliana]

Seq. No.	387566
Contig ID	5450_1.R1084
5'-most EST	g4716725

Seq. No.	387567
Contig ID	5458_1.R1084
5'-most EST	LIB3431-011-P1-N1-A7

Seq. No.	387568
Contig ID	5460_1.R1084
5'-most EST	g3768660

Seq. No.	387569
Contig ID	5461_1.R1084
5'-most EST	LIB3431-011-P1-N1-B1
Method	BLASTX
NCBI GI	g4587611
BLAST score	525
E value	3.0e-53
Match length	140
% identity	74
NCBI Description	(AC006951) putative 40S ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	387570
Contig ID	5461_2.R1084
5'-most EST	uC-osf1cyp080e09b1
Method	BLASTX
NCBI GI	g4755193
BLAST score	498
E value	3.0e-50
Match length	117
% identity	81
NCBI Description	(AC007018) putative ribosomal protein S17 [Arabidopsis thaliana]

Seq. No.	387571
Contig ID	5462_1.R1084
5'-most EST	LIB3431-011-P1-N1-B10
Method	BLASTX
NCBI GI	g3873807
BLAST score	231
E value	9.0e-19
Match length	243
% identity	31
NCBI Description	(Z49907) B0491.1 [Caenorhabditis elegans]

Seq. No.	387572
Contig ID	5471_1.R1084
5'-most EST	g4715184
Method	BLASTX
NCBI GI	g5734779
BLAST score	410
E value	9.0e-40
Match length	170
% identity	46
NCBI Description	(AC007980) 78688 [Arabidopsis thaliana]

Seq. No.	387573
Contig ID	5472_1.R1084

5'-most EST	g5607460
Method	BLASTX
NCBI GI	g6017104
BLAST score	281
E value	3.0e-24
Match length	310
% identity	34
NCBI Description	(AC009895) putative hypersensitivity-related gene [Arabidopsis thaliana]

Seq. No.	387574
Contig ID	5476_1.R1084
5'-most EST	g4715396
Method	BLASTX
NCBI GI	g1504052
BLAST score	434
E value	1.0e-42
Match length	82
% identity	61
NCBI Description	(D87042) Calcium-dependent protein kinase [Zea mays]

Seq. No.	387575
Contig ID	5480_1.R1084
5'-most EST	uC-osflcyp178e04a1
Method	BLASTX
NCBI GI	g232172
BLAST score	1330
E value	1.0e-147
Match length	294
% identity	86
NCBI Description	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT PRECURSOR (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) >gi_481816_pir__S39504 glucose-1-phosphate adenylyltransferase (EC 2.7.7.27) - wheat >gi_21687_emb_CAA46879_ (X66080) ADP-glucose pyrophosphorylase [Triticum aestivum]

Seq. No.	387576
Contig ID	5483_1.R1084
5'-most EST	uC-osflcyp172d11a1

Seq. No.	387577
Contig ID	5494_1.R1084
5'-most EST	LIB3431-011-P1-N1-E11
Method	BLASTX
NCBI GI	g4056427
BLAST score	289
E value	1.0e-25
Match length	105
% identity	53
NCBI Description	(AC005322) Contains similarity to gb_AJ006354 zinc finger protein (ZAC) from Homo sapiens. [Arabidopsis thaliana]

Seq. No.	387578
Contig ID	5500_1.R1084
5'-most EST	LIB3431-011-P1-N1-E6

Method	BLASTX
NCBI GI	g3941480
BLAST score	336
E value	8.0e-31
Match length	192
% identity	45
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	387579
Contig ID	5500_2.R1084
5'-most EST	g4881171
Method	BLASTX
NCBI GI	g3941480
BLAST score	385
E value	2.0e-51
Match length	121
% identity	81
NCBI Description	(AF062894) putative transcription factor [Arabidopsis thaliana]

Seq. No.	387580
Contig ID	5501_1.R1084
5'-most EST	g5771085
Method	BLASTX
NCBI GI	g5679336
BLAST score	413
E value	6.0e-40
Match length	161
% identity	50
NCBI Description	(AF171223) putative zinc finger protein [Oryza sativa]

Seq. No.	387581
Contig ID	5501_2.R1084
5'-most EST	g426701
Method	BLASTX
NCBI GI	g5679336
BLAST score	152
E value	3.0e-20
Match length	68
% identity	31
NCBI Description	(AF171223) putative zinc finger protein [Oryza sativa]

Seq. No.	387582
Contig ID	5502_1.R1084
5'-most EST	g5607370
Method	BLASTX
NCBI GI	g3264769
BLAST score	298
E value	2.0e-54
Match length	249
% identity	39
NCBI Description	(AF071894) late embryogenesis-like protein [Prunus armeniaca]

Seq. No.	387583
Contig ID	5502_3.R1084

09654600 - 090900

5'-most EST	g5607369
Method	BLASTX
NCBI GI	g3212877
BLAST score	250
E value	4.0e-21
Match length	56
% identity	79
NCBI Description	(AC004005) Lea-like protein [Arabidopsis thaliana]

Seq. No.	387584
Contig ID	5515_1.R1084
5'-most EST	g4715194
Method	BLASTX
NCBI GI	g4538920
BLAST score	365
E value	9.0e-48
Match length	154
% identity	50
NCBI Description	(AL049483) nitrogen fixation like protein [Arabidopsis thaliana]

Seq. No.	387585
Contig ID	5524_1.R1084
5'-most EST	g4715872
Method	BLASTX
NCBI GI	g544437
BLAST score	730
E value	3.0e-77
Match length	156
% identity	88
NCBI Description	GLUTATHIONE PEROXIDASE HOMOLOG (SALT-ASSOCIATED PROTEIN) >gi_296358_emb_CAA47018_ (X66377) CIT-SAP [Citrus sinensis]

Seq. No.	387586
Contig ID	5527_1.R1084
5'-most EST	uC-osflcyp141b06b1
Method	BLASTX
NCBI GI	g549986
BLAST score	346
E value	2.0e-34
Match length	89
% identity	85
NCBI Description	(U13149) possible apospory-associated protein [Pennisetum ciliare]

Seq. No.	387587
Contig ID	5527_2.R1084
5'-most EST	g3760233
Method	BLASTX
NCBI GI	g3478700
BLAST score	926
E value	1.0e-100
Match length	338
% identity	56
NCBI Description	(AF034387) AFT protein [Arabidopsis thaliana]

Seq. No.	387588

Contig ID	5532_1.R1084
5'-most EST	g2798587
Method	BLASTX
NCBI GI	g2131161
BLAST score	493
E value	4.0e-49
Match length	288
% identity	42
NCBI Description	4-nitrophenylphosphatase (EC 3.1.3.41) - yeast (Saccharomyces cerevisiae) >gi_1431400_emb_CAA98816_ (Z74284) ORF YDL236w [Saccharomyces cerevisiae]

Seq. No.	387589
Contig ID	5537_1.R1084
5'-most EST	g4715151
Method	BLASTX
NCBI GI	g5882728
BLAST score	252
E value	5.0e-21
Match length	146
% identity	44
NCBI Description	(AC008263) ESTs gb_T75898, gb_R65457, gb_AA597517 and gb_AA597420 come from this gene. [Arabidopsis thaliana]

Seq. No.	387590
Contig ID	5542_1.R1084
5'-most EST	LIB3431-014-P1-N1-A7
Method	BLASTX
NCBI GI	g3551958
BLAST score	193
E value	2.0e-14
Match length	89
% identity	32
NCBI Description	(AF082032) senescence-associated protein 12 [Hemerocallis hybrid cultivar]

Seq. No.	387591
Contig ID	5548_1.R1084
5'-most EST	g702918
Method	BLASTX
NCBI GI	g1001794
BLAST score	334
E value	7.0e-31
Match length	126
% identity	56
NCBI Description	(D64005) hypothetical protein [Synechocystis sp.]

Seq. No.	387592
Contig ID	5550_1.R1084
5'-most EST	uC-osflcyp118h09a1

Seq. No.	387593
Contig ID	5553_1.R1084
5'-most EST	g2796845

Seq. No.	387594
Contig ID	5555_1.R1084

5'-most EST	LIB3431-014-P1-N1-B9
Method	BLASTX
NCBI GI	g4406780
BLAST score	1039
E value	1.0e-140
Match length	339
% identity	76
NCBI Description	(AC006532) putative multispanning membrane protein [Arabidopsis thaliana]

Seq. No.	387595
Contig ID	5558_1.R1084
5'-most EST	g5055983
Method	BLASTX
NCBI GI	g3122914
BLAST score	983
E value	1.0e-106
Match length	482
% identity	55
NCBI Description	VALYL-TRNA SYNTHETASE (VALINE--TRNA LIGASE) (VALRS) >gi_1890130_gb_AAB49704.1_ (U89986) valyl tRNA synthetase [Arabidopsis thaliana]

Seq. No.	387596
Contig ID	5560_1.R1084
5'-most EST	g3766567

Seq. No.	387597
Contig ID	5564_1.R1084
5'-most EST	g5003284
Method	BLASTX
NCBI GI	g4455246
BLAST score	800
E value	4.0e-85
Match length	327
% identity	53
NCBI Description	(AL035523) putative protein [Arabidopsis thaliana]

Seq. No.	387598
Contig ID	5573_1.R1084
5'-most EST	g5803532
Method	BLASTN
NCBI GI	g168525
BLAST score	37
E value	3.0e-11
Match length	73
% identity	95
NCBI Description	Zea mays nucleic acid-binding protein (NBP)

Seq. No.	387599
Contig ID	5574_1.R1084
5'-most EST	g2800127
Method	BLASTX
NCBI GI	g80783
BLAST score	193
E value	4.0e-14
Match length	122

% identity	35
NCBI Description	hypothetical 31.7K protein (aphE region) - Streptomyces griseus >gi_153164 (M37378) streptomycin-3'-phosphotransferase [Streptomyces griseus]
Seq. No.	387600
Contig ID	5584_1.R1084
5'-most EST	uC-osflcyp033e12b1
Seq. No.	387601
Contig ID	5588_1.R1084
5'-most EST	g3760704
Method	BLASTX
NCBI GI	g3548815
BLAST score	515
E value	1.0e-51
Match length	389
% identity	38
NCBI Description	(AC005313) similar to axoneme-associated protein mst101 [Arabidopsis thaliana]
Seq. No.	387602
Contig ID	5589_1.R1084
5'-most EST	g3106905
Method	BLASTX
NCBI GI	g1903364
BLAST score	349
E value	1.0e-32
Match length	150
% identity	49
NCBI Description	(AC000104) EST gb_T45093 comes from this gene. [Arabidopsis thaliana]
Seq. No.	387603
Contig ID	5592_1.R1084
5'-most EST	LIB3431-014-P1-N1-F3
Seq. No.	387604
Contig ID	5594_1.R1084
5'-most EST	g5455459
Method	BLASTX
NCBI GI	g1346771
BLAST score	841
E value	3.0e-90
Match length	174
% identity	89
NCBI Description	PHOSPHOENOLPYRUVATE CARBOXYKINASE [ATP] >gi_1086117_pir__S52988 phosphoenolpyruvate carboxykinase (PCK1) - Urochloa panicoides >gi_607752 (U09241) phosphoenolpyruvate carboxykinase [Urochloa panicoides]
Seq. No.	387605
Contig ID	5598_1.R1084
5'-most EST	g3767940
Seq. No.	387606
Contig ID	5599_1.R1084

5'-most EST	uC-osflcyp087d10a1
Seq. No.	387607
Contig ID	5600_1.R1084
5'-most EST	LIB3431-014-P1-N1-G12
Seq. No.	387608
Contig ID	5606_1.R1084
5'-most EST	g4715912
Seq. No.	387609
Contig ID	5613_1.R1084
5'-most EST	LIB3433-042-P1-K1-H6
Method	BLASTX
NCBI GI	g4056507
BLAST score	265
E value	9.0e-23
Match length	85
% identity	62
NCBI Description	(AC005896) putative RNA binding protein [Arabidopsis thaliana]
Seq. No.	387610
Contig ID	5614_1.R1084
5'-most EST	LIB3432-028-P1-K1-H7
Seq. No.	387611
Contig ID	5628_1.R1084
5'-most EST	uC-osflcyp111c10a1
Seq. No.	387612
Contig ID	5652_1.R1084
5'-most EST	LIB3431-041-P2-K1-D6
Method	BLASTX
NCBI GI	g5903095
BLAST score	693
E value	9.0e-74
Match length	264
% identity	59
NCBI Description	(AC008017) Unknown protein [Arabidopsis thaliana]
Seq. No.	387613
Contig ID	5657_1.R1084
5'-most EST	LIB3431-041-P2-K1-E12
Method	BLASTX
NCBI GI	g3128167
BLAST score	202
E value	2.0e-15
Match length	155
% identity	20
NCBI Description	(AC004521) hypothetical protein [Arabidopsis thaliana] >gi_3212874 (AC004005) hypothetical protein [Arabidopsis thaliana]
Seq. No.	387614
Contig ID	5663_1.R1084
5'-most EST	LIB3431-041-P2-K1-E8

Method	BLASTX
NCBI GI	g3386621
BLAST score	666
E value	7.0e-70
Match length	174
% identity	72
NCBI Description	(AC004665) unknown protein [Arabidopsis thaliana]

Seq. No.	387615
Contig ID	5669_1.R1084
5'-most EST	uC-osflcyp012f02b1
Method	BLASTX
NCBI GI	g4835242
BLAST score	147
E value	7.0e-09
Match length	41
% identity	71
NCBI Description	(AL049862) putative protein [Arabidopsis thaliana]

Seq. No.	387616
Contig ID	5670_1.R1084
5'-most EST	g2310362
Method	BLASTX
NCBI GI	g2660677
BLAST score	326
E value	2.0e-33
Match length	123
% identity	62
NCBI Description	(AC002342) unknown protein [Arabidopsis thaliana]

Seq. No.	387617
Contig ID	5670_2.R1084
5'-most EST	g3761384
Method	BLASTX
NCBI GI	g4982500
BLAST score	297
E value	7.0e-48
Match length	148
% identity	62
NCBI Description	(AC000107) F17F8.6 [Arabidopsis thaliana]

Seq. No.	387618
Contig ID	5674_1.R1084
5'-most EST	g3767331
Method	BLASTX
NCBI GI	g4007792
BLAST score	344
E value	4.0e-32
Match length	224
% identity	21
NCBI Description	(AL034463) Xenopus 14s cohesin smc1 subunit homolog [Schizosaccharomyces pombe]

Seq. No.	387619
Contig ID	5685_1.R1084
5'-most EST	LIB3431-041-P2-K1-H12
Method	BLASTX

NCBI GI	g4006915
BLAST score	179
E value	3.0e-21
Match length	126
% identity	49
NCBI Description	(Z99708) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387620
Contig ID	5686_1.R1084
5'-most EST	uC-osroM202013e09b1

Seq. No.	387621
Contig ID	5705_1.R1084
5'-most EST	g5803468

Seq. No.	387622
Contig ID	5705_2.R1084
5'-most EST	LIB3431-055-P2-K1-C5

Seq. No.	387623
Contig ID	5732_1.R1084
5'-most EST	g3061238
Method	BLASTX
NCBI GI	g5732060
BLAST score	341
E value	4.0e-35
Match length	129
% identity	61
NCBI Description	(AF147263) contains similarity to Pfam families PF00106 (short chain dehydrogenase; score=151.7, E=1.3e-41, N=1) and PF00678 (Short chain dehydrogenase/reductase C-terminus; score=48.9, E=1.1e-10, N=1) [Arabidopsis t

Seq. No.	387624
Contig ID	5739_1.R1084
5'-most EST	uC-osflcyp110f08b1
Method	BLASTX
NCBI GI	g6063542
BLAST score	1722
E value	0.0e+00
Match length	361
% identity	95
NCBI Description	(AP000615) EST C74302(E30840) corresponds to a region of the predicted gene.; similar to glyceraldehyde-3-phosphate dehydrogenase. (M64118) [Oryza sativa]

Seq. No.	387625
Contig ID	5740_1.R1084
5'-most EST	g700226

Seq. No.	387626
Contig ID	5746_1.R1084
5'-most EST	g700629
Method	BLASTX
NCBI GI	g1076725
BLAST score	405
E value	2.0e-47

Match length	147
% identity	74
NCBI Description	NADPH dehydrogenase (EC 1.6.99.1) - barley >gi_683476_emb_CAA59228_ (X84738) NADPH dehydrogenase [Hordeum vulgare]

Seq. No.	387627
Contig ID	5747_1.R1084
5'-most EST	LIB3431-003-P1-K1-B7

Seq. No.	387628
Contig ID	5751_1.R1084
5'-most EST	LIB3431-003-P1-K1-C10
Method	BLASTX
NCBI GI	g4417289
BLAST score	154
E value	2.0e-13
Match length	100
% identity	50
NCBI Description	(AC007019) unknown protein [Arabidopsis thaliana]

Seq. No.	387629
Contig ID	5752_1.R1084
5'-most EST	LIB3477-005-P1-K1-B4
Method	BLASTX
NCBI GI	g633110
BLAST score	796
E value	4.0e-85
Match length	223
% identity	75
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	387630
Contig ID	5752_2.R1084
5'-most EST	uC-osflcyp041d07b1
Method	BLASTX
NCBI GI	g633110
BLAST score	574
E value	3.0e-59
Match length	152
% identity	77
NCBI Description	(D31843) plasma membrane H+-ATPase [Oryza sativa]

Seq. No.	387631
Contig ID	5758_1.R1084
5'-most EST	LIB3433-014-Q6-K1-H5
Method	BLASTX
NCBI GI	g4972778
BLAST score	157
E value	3.0e-10
Match length	130
% identity	6
NCBI Description	(AF132196) unknown [Drosophila melanogaster]

Seq. No.	387632
Contig ID	5767_1.R1084
5'-most EST	LIB3431-003-P1-K1-D5

Seq. No.	387633
Contig ID	5767_2.R1084
5'-most EST	g699858

Seq. No.	387634
Contig ID	5775_1.R1084
5'-most EST	g287163
Method	BLASTX
NCBI GI	g231509
BLAST score	508
E value	3.0e-51
Match length	138
% identity	68
NCBI Description	ACTIN DEPOLYMERIZING FACTOR (ADF) >gi_419809_pir__S30935 actin-depolymerizing factor - trumpet lily >gi_22748_emb_CAA78483_ (Z14110) actin depolymerizing factor [Lilium longiflorum]

Seq. No.	387635
Contig ID	5780_1.R1084
5'-most EST	uC-osrocyp007f08b1
Method	BLASTX
NCBI GI	g4972075
BLAST score	594
E value	2.0e-61
Match length	241
% identity	51
NCBI Description	(AL078467) proton pump interactor [Arabidopsis thaliana]

Seq. No.	387636
Contig ID	5781_1.R1084
5'-most EST	LIB3431-003-P1-K1-E7
Method	BLASTX
NCBI GI	g2262114
BLAST score	194
E value	1.0e-14
Match length	133
% identity	37
NCBI Description	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]

Seq. No.	387637
Contig ID	5783_1.R1084
5'-most EST	LIB3431-003-P1-K1-E9

Seq. No.	387638
Contig ID	5796_1.R1084
5'-most EST	LIB3431-003-P1-K1-G6
Method	BLASTX
NCBI GI	g282995
BLAST score	246
E value	1.0e-20
Match length	95
% identity	56
NCBI Description	seed protein B32E - barley (fragment) >gi_1345530_emb_CAA45538_ (X64254) B32E [Hordeum vulgare]

Seq. No.	387639
Contig ID	5806_1.R1084
5'-most EST	LIB3432-034-P2-K1-C11
Method	BLASTX
NCBI GI	g2088650
BLAST score	364
E value	3.0e-34
Match length	225
% identity	40
NCBI Description	(AF002109) peroxisomal ATP/ADP carrier protein isolog [Arabidopsis thaliana]

Seq. No.	387640
Contig ID	5807_1.R1084
5'-most EST	uC-osf1cyp140d05b1
Method	BLASTX
NCBI GI	g4105721
BLAST score	730
E value	1.0e-112
Match length	247
% identity	81
NCBI Description	(AF050129) cell wall invertase Incw1; beta-fructosidase [Zea mays]

Seq. No.	387641
Contig ID	5809_1.R1084
5'-most EST	g2427466

Seq. No.	387642
Contig ID	5809_2.R1084
5'-most EST	LIB3431-003-P1-K1-H9

Seq. No.	387643
Contig ID	5809_3.R1084
5'-most EST	g2280549

Seq. No.	387644
Contig ID	5818_1.R1084
5'-most EST	LIB3431-059-P1-K1-F3
Method	BLASTX
NCBI GI	g124036
BLAST score	338
E value	1.0e-31
Match length	99
% identity	58
NCBI Description	BOWMAN-BIRK TYPE BRAN TRYPSIN INHIBITOR (RBTI) >gi_476550_pir__TIRZBR trypsin inhibitor (Bowman-Birk) - rice >gi_359095_prf__1310273A trypsin inhibitor [Oryza sativa]

Seq. No.	387645
Contig ID	5821_1.R1084
5'-most EST	uC-osroM202018g10b1

Seq. No.	387646
Contig ID	5825_1.R1084
5'-most EST	LIB3434-005-P1-K1-G7

Method	BLASTX
NCBI GI	g4371290
BLAST score	280
E value	1.0e-24
Match length	134
% identity	55
NCBI Description	(AC006260) unknown protein [Arabidopsis thaliana]

Seq. No.	387647
Contig ID	5836_1.R1084
5'-most EST	LIB3431-004-P1-K1-D10
Method	BLASTX
NCBI GI	g4239879
BLAST score	403
E value	4.0e-54
Match length	182
% identity	58
NCBI Description	(AB016780) Glutamine:fructose-6-phosphate amidotransferase 2 [Mus musculus]

Seq. No.	387648
Contig ID	5841_1.R1084
5'-most EST	LIB3432-017-P1-K1-C12
Method	BLASTX
NCBI GI	g2253092
BLAST score	420
E value	4.0e-41
Match length	106
% identity	78
NCBI Description	(Y14198) hypothetical protein [Spinacia oleracea]

Seq. No.	387649
Contig ID	5852_1.R1084
5'-most EST	uC-osflcyp153d05b1
Method	BLASTX
NCBI GI	g4454464
BLAST score	448
E value	4.0e-44
Match length	120
% identity	68
NCBI Description	(AC006234) unknown protein [Arabidopsis thaliana]

Seq. No.	387650
Contig ID	5854_1.R1084
5'-most EST	LIB3431-004-P1-K1-E8
Method	BLASTX
NCBI GI	g4512654
BLAST score	358
E value	7.0e-38
Match length	113
% identity	69
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	387651
Contig ID	5861_1.R1084
5'-most EST	LIB3431-004-P1-K1-F4
Method	BLASTX

NCBI GI	g3702329
BLAST score	192
E value	2.0e-14
Match length	130
% identity	33
NCBI Description	(AC005397) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387652
Contig ID	5867_1.R1084
5'-most EST	LIB3474-002-P1-K1-B12

Seq. No.	387653
Contig ID	5868_1.R1084
5'-most EST	g701990

Seq. No.	387654
Contig ID	5879_1.R1084
5'-most EST	LIB3431-005-P1-K1-A1

Seq. No.	387655
Contig ID	5886_1.R1084
5'-most EST	LIB3431-005-P1-K1-A5
Method	BLASTN
NCBI GI	g11957
BLAST score	395
E value	0.0e+00
Match length	435
% identity	43
NCBI Description	Rice complete chloroplast genome

Seq. No.	387656
Contig ID	5887_1.R1084
5'-most EST	LIB3431-005-P1-K1-A6
Method	BLASTX
NCBI GI	g3329294
BLAST score	219
E value	2.0e-17
Match length	184
% identity	28
NCBI Description	(AE001355) Zinc Metalloprotease (insulinase family) [Chlamydia trachomatis]

Seq. No.	387657
Contig ID	5899_1.R1084
5'-most EST	g2312177
Method	BLASTX
NCBI GI	g6056418
BLAST score	1022
E value	1.0e-135
Match length	486
% identity	49
NCBI Description	(AC009525) Similar to beta-glucosidases [Arabidopsis thaliana]

Seq. No.	387658
Contig ID	5901_1.R1084
5'-most EST	LIB3432-052-P1-K1-F8

Method	BLASTX
NCBI GI	g1724110
BLAST score	496
E value	1.0e-49
Match length	212
% identity	47
NCBI Description	(U79770) cinnamyl-alcohol dehydrogenase Eli3 [Mesembryanthemum crystallinum]

Seq. No.	387659
Contig ID	5901_2.R1084
5'-most EST	uC-osroM202041f05b1
Method	BLASTX
NCBI GI	g3913193
BLAST score	526
E value	1.0e-56
Match length	225
% identity	52
NCBI Description	CINNAMYL-ALCOHOL DEHYDROGENASE 1 (CAD) >gi_556422 (L36823) cinnamyl-alcohol dehydrogenase [Stylosanthes humilis]

Seq. No.	387660
Contig ID	5906_1.R1084
5'-most EST	LIB3431-005-P1-K1-D1
Method	BLASTX
NCBI GI	g4559339
BLAST score	672
E value	9.0e-71
Match length	155
% identity	85
NCBI Description	(AC007087) putative ATP-dependent RNA helicase [Arabidopsis thaliana]

Seq. No.	387661
Contig ID	5921_1.R1084
5'-most EST	LIB3431-005-P1-K1-E4
Method	BLASTX
NCBI GI	g3522947
BLAST score	195
E value	5.0e-15
Match length	72
% identity	54
NCBI Description	(AC004411) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387662
Contig ID	5925_1.R1084
5'-most EST	LIB3431-042-P1-K1-F5
Method	BLASTN
NCBI GI	g6015437
BLAST score	35
E value	5.0e-10
Match length	35
% identity	42
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387663
Contig ID	5931_1.R1084

5'-most EST	LIB3432-060-P1-K1-E7
Seq. No.	387664
Contig ID	5950_1.R1084
5'-most EST	LIB3433-044-P1-K1-D9
Method	BLASTX
NCBI GI	g3776573
BLAST score	607
E value	7.0e-63
Match length	182
% identity	63
NCBI Description	(AC005388) Similar to nodulins and lipase homolog F14J9.5 gi_3482914 from Arabidopsis thaliana BAC gb_AC003970. Alternate first exon from 72258 to 72509. [Arabidopsis thaliana]
Seq. No.	387665
Contig ID	5951_1.R1084
5'-most EST	g2801302
Seq. No.	387666
Contig ID	5959_1.R1084
5'-most EST	g2427265
Method	BLASTX
NCBI GI	g5257277
BLAST score	614
E value	7.0e-64
Match length	130
% identity	93
NCBI Description	(AP000364) ESTs C98431(E0144),C71728(E0144) correspond to a region of the predicted gene.; Similar to Medicago sativa S-adenosyl-L-methionine. (U20736) [Oryza sativa]
Seq. No.	387667
Contig ID	5962_1.R1084
5'-most EST	g4715125
Seq. No.	387668
Contig ID	5962_2.R1084
5'-most EST	g1631892
Seq. No.	387669
Contig ID	5964_1.R1084
5'-most EST	LIB3434-046-P1-K1-C11
Method	BLASTX
NCBI GI	g4588906
BLAST score	887
E value	2.0e-95
Match length	192
% identity	89
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]
Seq. No.	387670
Contig ID	5964_2.R1084
5'-most EST	LIB3433-060-P1-K1-E3
Method	BLASTX
NCBI GI	g4588906

BLAST score	558
E value	2.0e-57
Match length	120
% identity	92
NCBI Description	(AF118149) ribosomal protein S7 [Secale cereale]

Seq. No.	387671
Contig ID	5971_1.R1084
5'-most EST	g3763832

Seq. No.	387672
Contig ID	5977_1.R1084
5'-most EST	g2312009
Method	BLASTX
NCBI GI	g5669894
BLAST score	199
E value	7.0e-15
Match length	196
% identity	1
NCBI Description	(AF148805) latent nuclear antigen [Kaposi's sarcoma-associated herpesvirus]

Seq. No.	387673
Contig ID	5978_1.R1084
5'-most EST	uC-osflcyp172h08b1
Method	BLASTX
NCBI GI	g1173027
BLAST score	430
E value	3.0e-42
Match length	113
% identity	74
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	387674
Contig ID	5978_2.R1084
5'-most EST	g5004940
Method	BLASTX
NCBI GI	g1173027
BLAST score	441
E value	2.0e-43
Match length	123
% identity	71
NCBI Description	60S RIBOSOMAL PROTEIN L31 >gi_915313 (U23784) ribosomal protein L31 [Nicotiana glutinosa]

Seq. No.	387675
Contig ID	5988_1.R1084
5'-most EST	LIB3433-031-P1-K1-F10
Method	BLASTX
NCBI GI	g2493318
BLAST score	219
E value	3.0e-17
Match length	88
% identity	48
NCBI Description	BLUE COPPER PROTEIN PRECURSOR >gi_562779_emb_CAA80963_ (Z25471) blue copper protein [Pisum sativum]

>gi_1098264_prf__2115352A blue Cu protein [Pisum sativum]

Seq. No.	387676
Contig ID	5990_1.R1084
5'-most EST	LIB3431-006-P1-K1-D10
Method	BLASTX
NCBI GI	g2398853
BLAST score	316
E value	6.0e-29
Match length	151
% identity	42
NCBI Description	(AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]

Seq. No.	387677
Contig ID	5994_1.R1084
5'-most EST	LIB3431-006-P1-K1-D3
Method	BLASTX
NCBI GI	g4960024
BLAST score	1375
E value	1.0e-153
Match length	325
% identity	79
NCBI Description	(AF144079) S-adenosyl-L-methionine:L-methionine S-methyltransferase [Zea mays]

Seq. No.	387678
Contig ID	6000_1.R1084
5'-most EST	LIB3431-006-P1-K1-E1
Method	BLASTN
NCBI GI	g4959460
BLAST score	35
E value	1.0e-09
Match length	35
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	387679
Contig ID	6001_1.R1084
5'-most EST	g428420

Seq. No.	387680
Contig ID	6006_1.R1084
5'-most EST	LIB3433-005-Q6-K1-A11
Method	BLASTX
NCBI GI	g3283057
BLAST score	255
E value	1.0e-21
Match length	70
% identity	81
NCBI Description	(AF054617) one helix protein [Arabidopsis thaliana]

Seq. No.	387681
Contig ID	6009_1.R1084
5'-most EST	LIB3431-021-P1-K1-H6

Seq. No.	387682

Contig ID	6012_1.R1084
5'-most EST	LIB3431-006-P1-K1-F5
Method	BLASTX
NCBI GI	g4758520
BLAST score	158
E value	3.0e-10
Match length	217
% identity	4
NCBI Description	hect domain and RLD 2 >gi_4079809_gb_AAD08657.1_ (AF071172) HERC2 [Homo sapiens]

Seq. No.	387683
Contig ID	6016_1.R1084
5'-most EST	LIB3431-006-P1-K1-F9

Seq. No.	387684
Contig ID	6017_1.R1084
5'-most EST	uC-osflcyp099d02b1
Method	BLASTX
NCBI GI	g4115938
BLAST score	170
E value	2.0e-11
Match length	87
% identity	53
NCBI Description	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]

Seq. No.	387685
Contig ID	6019_1.R1084
5'-most EST	LIB3431-017-P1-K1-D5
Method	BLASTX
NCBI GI	g3927827
BLAST score	210
E value	1.0e-16
Match length	115
% identity	43
NCBI Description	(AC005727) osmotin-like protein precursor [Arabidopsis thaliana]

Seq. No.	387686
Contig ID	6024_1.R1084
5'-most EST	LIB3432-049-P1-K1-B11
Method	BLASTX
NCBI GI	g6006360
BLAST score	742
E value	3.0e-83
Match length	162
% identity	100
NCBI Description	(AP000559) Similar to 1-aminocyclopropane-1-carboxylate synthase (U35779) [Oryza sativa]

Seq. No.	387687
Contig ID	6032_1.R1084
5'-most EST	LIB3431-006-P1-K1-H4
Method	BLASTX
NCBI GI	g2811029

BLAST score	444
E value	4.0e-50
Match length	139
% identity	73
NCBI Description	ACETYLORNITHINE AMINOTRANSFERASE PRECURSOR (ACOAT) (ACETYLORNITHINE TRANSAMINASE) (AOTA) >gi_1944511_emb_CAA69936_ (Y08680) acetylornithine aminotransferase [Alnus glutinosa]

Seq. No.	387688
Contig ID	6034_1.R1084
5'-most EST	g427188
Method	BLASTX
NCBI GI	g4894963
BLAST score	167
E value	9.0e-12
Match length	88
% identity	53
NCBI Description	(AF140553) DNA-binding protein WRKY3 [Avena sativa]

Seq. No.	387689
Contig ID	6039_1.R1084
5'-most EST	LIB3431-007-P1-K1-A11
Method	BLASTX
NCBI GI	g4972118
BLAST score	238
E value	7.0e-20
Match length	139
% identity	41
NCBI Description	(AL078579) putative protein [Arabidopsis thaliana]

Seq. No.	387690
Contig ID	6040_1.R1084
5'-most EST	LIB3431-010-P1-K1-B2
Method	BLASTX
NCBI GI	g5802955
BLAST score	222
E value	7.0e-18
Match length	103
% identity	46
NCBI Description	(AF178990) stress related protein [Vitis riparia]

Seq. No.	387691
Contig ID	6042_1.R1084
5'-most EST	g5667408
Method	BLASTX
NCBI GI	g4585901
BLAST score	455
E value	4.0e-48
Match length	170
% identity	57
NCBI Description	(AC007133) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387692
Contig ID	6044_1.R1084
5'-most EST	LIB3434-056-P1-K1-H7
Method	BLASTX

NCBI GI	g4538992
BLAST score	189
E value	4.0e-14
Match length	50
% identity	66
NCBI Description	(AL049481) putative protein [Arabidopsis thaliana]

Seq. No.	387693
Contig ID	6047_2.R1084
5'-most EST	g2443040
Method	BLASTX
NCBI GI	g1345588
BLAST score	226
E value	9.0e-19
Match length	64
% identity	78
NCBI Description	14-3-3-LIKE PROTEIN GF14-12 >gi_998432_bbs_164524 GF14-12=GRF2 product/14-3-3 protein homolog [Zea mays, XL80, Peptide, 261 aa]

Seq. No.	387694
Contig ID	6051_1.R1084
5'-most EST	g2309786
Method	BLASTX
NCBI GI	g3023945
BLAST score	517
E value	2.0e-86
Match length	206
% identity	71
NCBI Description	HISTONE DEACETYLASE (HD) >gi_2318131 (AF014824) histone deacetylase [Arabidopsis thaliana]

Seq. No.	387695
Contig ID	6055_1.R1084
5'-most EST	uC-osrocyp013c05b1
Method	BLASTX
NCBI GI	g4966352
BLAST score	516
E value	7.0e-58
Match length	233
% identity	55
NCBI Description	(AC006341) >F3O9.11 [Arabidopsis thaliana]

Seq. No.	387696
Contig ID	6055_2.R1084
5'-most EST	uC-osf1cyp109g11b1
Method	BLASTX
NCBI GI	g4835757
BLAST score	245
E value	1.0e-20
Match length	114
% identity	41
NCBI Description	(AC007202) EST gb_AA404917 comes from this gene. [Arabidopsis thaliana]

Seq. No.	387697
Contig ID	6067_1.R1084

5'-most EST	uC-osflM202088g05a1
Seq. No.	387698
Contig ID	6073_1.R1084
5'-most EST	g4715479
Method	BLASTX
NCBI GI	g3643608
BLAST score	278
E value	5.0e-24
Match length	240
% identity	32
NCBI Description	(AC005395) hypothetical protein [Arabidopsis thaliana] >gi_4874312_gb_AAD31374.1_AC006053_16 (AC006053) hypothetical protein [Arabidopsis thaliana]
Seq. No.	387699
Contig ID	6075_1.R1084
5'-most EST	LIB3431-007-P1-K1-E4
Method	BLASTN
NCBI GI	g6015437
BLAST score	33
E value	1.0e-08
Match length	37
% identity	58
NCBI Description	Homo sapiens PEX1 mRNA, complete cds
Seq. No.	387700
Contig ID	6084_1.R1084
5'-most EST	LIB3431-007-P1-K1-F2
Method	BLASTX
NCBI GI	g1617036
BLAST score	490
E value	2.0e-49
Match length	131
% identity	70
NCBI Description	(Y08624) Ted2 [Vigna unguiculata]
Seq. No.	387701
Contig ID	6089_2.R1084
5'-most EST	uC-osrocyp037a12b1
Method	BLASTX
NCBI GI	g3608137
BLAST score	176
E value	1.0e-12
Match length	90
% identity	42
NCBI Description	(AC005314) unknown protein [Arabidopsis thaliana]
Seq. No.	387702
Contig ID	6090_1.R1084
5'-most EST	uC-osflM202123e07b1
Method	BLASTX
NCBI GI	g2983997
BLAST score	249
E value	2.0e-35
Match length	147
% identity	51

NCBI Description	(AE000749) hypothetical protein [Aquifex aeolicus]

Seq. No.	387703
Contig ID	6098_1.R1084
5'-most EST	g568299
Method	BLASTX
NCBI GI	g1076660
BLAST score	204
E value	6.0e-32
Match length	106
% identity	74
NCBI Description	D13F(MYBST1) protein - potato >gi_786426_bbs_159122 (S74753) MybSt1=Myb-related transcriptional activator {DNA-binding domain repeats} [Solanum tuberosum=potatoes, leaf, Peptide, 342 aa] [Solanum tuberosum]

Seq. No.	387704
Contig ID	6099_1.R1084
5'-most EST	LIB3431-052-P1-K1-D3
Method	BLASTX
NCBI GI	g2765817
BLAST score	162
E value	4.0e-11
Match length	58
% identity	52
NCBI Description	(Z95352) AtMlo-h1 [Arabidopsis thaliana] >gi_3892049_gb_AAC78258.1_AAC78258 (AC002330) AtMlo-h1 [Arabidopsis thaliana]

Seq. No.	387705
Contig ID	6117_1.R1084
5'-most EST	g2443083
Method	BLASTX
NCBI GI	g3157949
BLAST score	161
E value	2.0e-10
Match length	61
% identity	44
NCBI Description	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb_Z28697 from Nicotiana tabacum. ESTs gb_Z18185 and gb_AA605362 come from this gene. [Arabidopsis thaliana]

Seq. No.	387706
Contig ID	6138_1.R1084
5'-most EST	LIB3431-008-P1-K1-D7
Method	BLASTX
NCBI GI	g629561
BLAST score	164
E value	4.0e-11
Match length	100
% identity	36
NCBI Description	SRG1 protein - Arabidopsis thaliana >gi_479047_emb_CAA55654_ (X79052) SRG1 [Arabidopsis thaliana] >gi_5734767_gb_AAD50032.1_AC007651_27 (AC007651) SRG1 Protein [Arabidopsis thaliana]

Seq. No.	387707

Contig ID	6161_1.R1084
5'-most EST	g701980
Method	BLASTX
NCBI GI	g6041844
BLAST score	153
E value	8.0e-10
Match length	98
% identity	33
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]

Seq. No.	387708
Contig ID	6176_1.R1084
5'-most EST	LIB3431-008-P1-K1-H9
Method	BLASTX
NCBI GI	g4567263
BLAST score	393
E value	6.0e-38
Match length	158
% identity	57
NCBI Description	(AC006841) putative cell division inhibitor [Arabidopsis thaliana]

Seq. No.	387709
Contig ID	6178_1.R1084
5'-most EST	g2310151
Method	BLASTX
NCBI GI	g5001458
BLAST score	662
E value	2.0e-69
Match length	201
% identity	39
NCBI Description	(AC006225) putative multidrug resistance protein [Arabidopsis thaliana]

Seq. No.	387710
Contig ID	6186_1.R1084
5'-most EST	g3766950

Seq. No.	387711
Contig ID	6211_1.R1084
5'-most EST	uC-osflcyp168c01b1
Method	BLASTX
NCBI GI	g4210330
BLAST score	1681
E value	0.0e+00
Match length	376
% identity	82
NCBI Description	(AJ223802) 2-oxoglutarate dehydrogenase, E1 subunit [Arabidopsis thaliana]

Seq. No.	387712
Contig ID	6218_1.R1084
5'-most EST	LIB3432-018-P1-K1-E4
Method	BLASTX
NCBI GI	g3334150
BLAST score	911
E value	1.0e-98

Match length	217
% identity	83
NCBI Description	MAGNESIUM-CHELATASE SUBUNIT CHLI PRECURSOR (MG-PROTOPORPHYRIN IX CHELATASE) >gi_2129847_pir__JC4312 chlorophyll magnesium chelatase (EC 4.99.-.-) - soybean chloroplast >gi_1732469_dbj_BAA08291_ (D45857) Mg chelatase subunit (46 kD) [Glycine max]

Seq. No.	387713
Contig ID	6239_1.R1084
5'-most EST	g4879607
Method	BLASTX
NCBI GI	g4539423
BLAST score	441
E value	2.0e-43
Match length	153
% identity	64
NCBI Description	(AL049171) pyrophosphate-dependent phosphofructo-1-kinase [Arabidopsis thaliana]

Seq. No.	387714
Contig ID	6239_2.R1084
5'-most EST	LIB3431-009-P1-K1-H3

Seq. No.	387715
Contig ID	6240_1.R1084
5'-most EST	g4714884

Seq. No.	387716
Contig ID	6241_1.R1084
5'-most EST	LIB3431-009-P1-K1-H8
Method	BLASTX
NCBI GI	g2149640
BLAST score	921
E value	1.0e-103
Match length	224
% identity	82
NCBI Description	(U91995) Argonaute protein [Arabidopsis thaliana] >gi_5733867_gb_AAD49755.1_AC007932_3 (AC007932) Identical to gb_U91995 Argonaute protein from Arabidopsis thaliana. ESTs gb_H76075, gb_AA720232, gb_N65911 and gb_AA651494 come from this gene

Seq. No.	387717
Contig ID	6248_1.R1084
5'-most EST	LIB3431-010-P1-K1-A8
Method	BLASTX
NCBI GI	g4417271
BLAST score	368
E value	7.0e-35
Match length	151
% identity	46
NCBI Description	(AC007019) putative cellulose synthase catalytic subunit [Arabidopsis thaliana]

Seq. No.	387718
Contig ID	6252_1.R1084

5'-most EST	LIB3431-010-P1-K1-B11
Seq. No.	387719
Contig ID	6255_1.R1084
5'-most EST	g4714818
Method	BLASTX
NCBI GI	g3201680
BLAST score	451
E value	3.0e-44
Match length	227
% identity	43
NCBI Description	(AF060941) extra-large G-protein [Arabidopsis thaliana]
Seq. No.	387720
Contig ID	6271_1.R1084
5'-most EST	LIB3431-010-P1-K1-D2
Method	BLASTX
NCBI GI	g5923670
BLAST score	340
E value	1.0e-31
Match length	108
% identity	59
NCBI Description	(AC009326) unknown protein [Arabidopsis thaliana]
Seq. No.	387721
Contig ID	6290_1.R1084
5'-most EST	LIB3431-010-P1-K1-F4
Seq. No.	387722
Contig ID	6292_1.R1084
5'-most EST	uC-osflcyp110e05b1
Seq. No.	387723
Contig ID	6293_1.R1084
5'-most EST	LIB3432-044-P1-K1-G10
Seq. No.	387724
Contig ID	6318_1.R1084
5'-most EST	g2800124
Seq. No.	387725
Contig ID	6319_1.R1084
5'-most EST	LIB3431-011-P1-K1-A10
Method	BLASTX
NCBI GI	g1742187
BLAST score	164
E value	3.0e-11
Match length	121
% identity	34
NCBI Description	(D90771) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1742198_dbj_BAA14933_ (D90772) ORF_ID:o260#14; similar to [SwissProt Accession Number P11666] [Escherichia coli] >gi_1787591 (AE000231) orf, hypothetical protein [Escherichia coli]
Seq. No.	387726
Contig ID	6320_1.R1084

5'-most EST	g428414
Seq. No.	387727
Contig ID	6324_1.R1084
5'-most EST	LIB3432-008-P1-K1-D3
Method	BLASTN
NCBI GI	g3821780
BLAST score	35
E value	5.0e-10
Match length	35
% identity	59
NCBI Description	Xenopus laevis cDNA clone 27A6-1
Seq. No.	387728
Contig ID	6325_1.R1084
5'-most EST	uC-osf1cyp034a11b1
Method	BLASTX
NCBI GI	g4204281
BLAST score	154
E value	7.0e-10
Match length	73
% identity	38
NCBI Description	(AC004146) Hypothetical protein [Arabidopsis thaliana]
Seq. No.	387729
Contig ID	6327_1.R1084
5'-most EST	LIB3432-009-P1-K1-B7
Method	BLASTX
NCBI GI	g2708331
BLAST score	516
E value	2.0e-52
Match length	156
% identity	63
NCBI Description	(AF038557) ligand gated channel-like protein [Arabidopsis thaliana]
Seq. No.	387730
Contig ID	6334_1.R1084
5'-most EST	LIB3431-011-P1-K1-B5
Method	BLASTX
NCBI GI	g3850566
BLAST score	252
E value	2.0e-24
Match length	163
% identity	39
NCBI Description	(AC005278) F15K9.3 [Arabidopsis thaliana]
Seq. No.	387731
Contig ID	6339_1.R1084
5'-most EST	LIB3431-011-P1-K1-C11
Seq. No.	387732
Contig ID	6351_1.R1084
5'-most EST	LIB3431-011-P1-K1-D8
Seq. No.	387733
Contig ID	6353_1.R1084

5'-most EST	g701496
Method	BLASTX
NCBI GI	g4929595
BLAST score	412
E value	4.0e-40
Match length	191
% identity	47
NCBI Description	(AF151821) CGI-63 protein [Homo sapiens]

Seq. No.	387734
Contig ID	6359_1.R1084
5'-most EST	LIB3432-056-P1-K1-D5
Method	BLASTX
NCBI GI	g1524370
BLAST score	290
E value	5.0e-26
Match length	95
% identity	60
NCBI Description	(X92491) TOM20 [Solanum tuberosum]

Seq. No.	387735
Contig ID	6361_1.R1084
5'-most EST	LIB3479-010-Q6-K1-E1
Method	BLASTX
NCBI GI	g5541681
BLAST score	606
E value	1.0e-62
Match length	253
% identity	55
NCBI Description	(AL096859) putative protein [Arabidopsis thaliana]

Seq. No.	387736
Contig ID	6387_1.R1084
5'-most EST	LIB3432-049-P1-K1-D6

Seq. No.	387737
Contig ID	6392_1.R1084
5'-most EST	LIB3434-042-P1-K1-D5

Seq. No.	387738
Contig ID	6393_1.R1084
5'-most EST	LIB3474-006-P1-K1-F5
Method	BLASTX
NCBI GI	g1297187
BLAST score	231
E value	8.0e-19
Match length	66
% identity	61
NCBI Description	(U53501) similar to protein encoded by GenBank Accession Number U41815, nucleoporin 98 [Arabidopsis thaliana]

Seq. No.	387739
Contig ID	6406_1.R1084
5'-most EST	LIB3431-012-P1-K1-B7

Seq. No.	387740
Contig ID	6409_1.R1084

5'-most EST	LIB3431-012-P1-K1-C1
Method	BLASTX
NCBI GI	g1707018
BLAST score	457
E value	2.0e-45
Match length	104
% identity	86
NCBI Description	(U78721) CutA isolog [Arabidopsis thaliana]

Seq. No.	387741
Contig ID	6410_1.R1084
5'-most EST	uC-osflm202002b11b1

Seq. No.	387742
Contig ID	6417_1.R1084
5'-most EST	g2799070
Method	BLASTX
NCBI GI	g1619300
BLAST score	200
E value	3.0e-15
Match length	62
% identity	68
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	387743
Contig ID	6417_2.R1084
5'-most EST	g702356
Method	BLASTX
NCBI GI	g1619300
BLAST score	808
E value	9.0e-88
Match length	189
% identity	84
NCBI Description	(X95269) LRR protein [Lycopersicon esculentum]

Seq. No.	387744
Contig ID	6419_1.R1084
5'-most EST	LIB3431-012-P1-K1-C8
Method	BLASTX
NCBI GI	g4585142
BLAST score	388
E value	4.0e-37
Match length	101
% identity	71
NCBI Description	(AF088276) NADPH oxidase; gp91; phox homolog [Lycopersicon esculentum]

Seq. No.	387745
Contig ID	6421_1.R1084
5'-most EST	LIB3432-023-P1-K1-F9
Method	BLASTX
NCBI GI	g5091623
BLAST score	837
E value	7.0e-90
Match length	190
% identity	86
NCBI Description	(AC007454) Similar to gb_U93048 somatic embryogenesis

	receptor-like kinase from Daucus carota, contains 4 PF_00560 Leucine Rich Repeat domains and a PF_00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]
Seq. No.	387746
Contig ID	6430_1.R1084
5'-most EST	uC-osflcyp142f04b1
Method	BLASTX
NCBI GI	g3522929
BLAST score	1283
E value	1.0e-142
Match length	260
% identity	92
NCBI Description	(AC002535) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana] >gi_3738279 (AC005309) putative dTDP-glucose 4-6-dehydratase [Arabidopsis thaliana]
Seq. No.	387747
Contig ID	6439_2.R1084
5'-most EST	LIB3433-012-Q6-K1-B9
Method	BLASTX
NCBI GI	g3914557
BLAST score	991
E value	1.0e-109
Match length	201
% identity	99
NCBI Description	RAS-RELATED PROTEIN RAB7 (POSSIBLE APOSPORY-ASSOCIATED PROTEIN) >gi_1155265 (U40219) possible apospory-associated protein [Pennisetum ciliare]
Seq. No.	387748
Contig ID	6439_3.R1084
5'-most EST	uC-osflcyp034e12b1
Method	BLASTX
NCBI GI	g4538902
BLAST score	318
E value	2.0e-38
Match length	102
% identity	81
NCBI Description	(AL049482) rab7-like protein [Arabidopsis thaliana]
Seq. No.	387749
Contig ID	6443_1.R1084
5'-most EST	g5607326
Method	BLASTX
NCBI GI	g121950
BLAST score	149
E value	3.0e-09
Match length	64
% identity	52
NCBI Description	HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea mays]
Seq. No.	387750
Contig ID	6443_2.R1084
5'-most EST	LIB3431-022-P1-K1-F4
Method	BLASTX

NCBI GI	g121950
BLAST score	177
E value	2.0e-12
Match length	119
% identity	55
NCBI Description	HISTONE H1 >gi_22321_emb_CAA40362_ (X57077) H1 histone [Zea mays]

Seq. No.	387751
Contig ID	6443_3.R1084
5'-most EST	g3761955

Seq. No.	387752
Contig ID	6443_4.R1084
5'-most EST	g2801285

Seq. No.	387753
Contig ID	6445_1.R1084
5'-most EST	g569909

Seq. No.	387754
Contig ID	6447_1.R1084
5'-most EST	LIB3431-012-P1-K1-F7
Method	BLASTX
NCBI GI	g3548810
BLAST score	178
E value	1.0e-12
Match length	51
% identity	69
NCBI Description	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]

Seq. No.	387755
Contig ID	6450_1.R1084
5'-most EST	uC-osf1cyp055e03b1
Method	BLASTN
NCBI GI	g3819359
BLAST score	53
E value	1.0e-20
Match length	85
% identity	91
NCBI Description	Hordeum vulgare genomic DNA fragment; clone MWG0829.uni

Seq. No.	387756
Contig ID	6452_1.R1084
5'-most EST	LIB3431-012-P1-K1-G2
Method	BLASTX
NCBI GI	g115525
BLAST score	469
E value	8.0e-47
Match length	129
% identity	39
NCBI Description	CALMODULIN >gi_71685_pir__MCSP calmodulin - spinach

Seq. No.	387757
Contig ID	6454_1.R1084
5'-most EST	uC-osf1M202094e02b1

Method	BLASTX
NCBI GI	g4206122
BLAST score	526
E value	2.0e-53
Match length	125
% identity	78
NCBI Description	(AF097667) protein phosphatase 2C homolog [Mesembryanthemum crystallinum]

Seq. No.	387758
Contig ID	6458_1.R1084
5'-most EST	LIB3431-012-P1-K1-G8

Seq. No.	387759
Contig ID	6459_1.R1084
5'-most EST	LIB3431-012-P1-K1-G9
Method	BLASTX
NCBI GI	g4337011
BLAST score	318
E value	4.0e-29
Match length	147
% identity	52
NCBI Description	(AF119572) zinc-binding peroxisomal integral membrane protein [Arabidopsis thaliana]

Seq. No.	387760
Contig ID	6460_1.R1084
5'-most EST	LIB3433-018-Q6-K6-B2
Method	BLASTX
NCBI GI	g3355477
BLAST score	620
E value	3.0e-64
Match length	140
% identity	45
NCBI Description	(AC004218) putative P-glycoprotein, pgp1 [Arabidopsis thaliana]

Seq. No.	387761
Contig ID	6464_1.R1084
5'-most EST	g2311233
Method	BLASTX
NCBI GI	g2653558
BLAST score	1386
E value	1.0e-154
Match length	291
% identity	90
NCBI Description	(D50679) ferredoxin-sulfite reductase precursor [Zea mays]

Seq. No.	387762
Contig ID	6464_2.R1084
5'-most EST	LIB3434-034-P1-K1-A12

Seq. No.	387763
Contig ID	6471_1.R1084
5'-most EST	g4716670

Seq. No.	387764

Contig ID	6474_1.R1084
5'-most EST	LIB3431-013-P1-K1-A6
Method	BLASTN
NCBI GI	g6015437
BLAST score	36
E value	2.0e-10
Match length	36
% identity	59
NCBI Description	Homo sapiens PEX1 mRNA, complete cds

Seq. No.	387765
Contig ID	6484_1.R1084
5'-most EST	LIB3431-013-P1-K1-B5
Method	BLASTN
NCBI GI	g1245938
BLAST score	33
E value	7.0e-09
Match length	33
% identity	61
NCBI Description	rabClC-2 beta=chloride channel ClC-2G isoform [rabbits, heart atrium, mRNA, 2998 nt]

Seq. No.	387766
Contig ID	6487_1.R1084
5'-most EST	uC-osflcyp078g05b1

Seq. No.	387767
Contig ID	6491_1.R1084
5'-most EST	LIB3431-013-P1-K1-C12

Seq. No.	387768
Contig ID	6497_1.R1084
5'-most EST	LIB3433-049-P1-K1-A5
Method	BLASTX
NCBI GI	g4512653
BLAST score	272
E value	1.0e-23
Match length	82
% identity	66
NCBI Description	(AC007048) unknown protein [Arabidopsis thaliana]

Seq. No.	387769
Contig ID	6498_1.R1084
5'-most EST	LIB3431-013-P1-K1-D1

Seq. No.	387770
Contig ID	6507_1.R1084
5'-most EST	LIB3431-013-P1-K1-D8

Seq. No.	387771
Contig ID	6515_1.R1084
5'-most EST	LIB3431-013-P1-K1-E4
Method	BLASTX
NCBI GI	g3582333
BLAST score	798
E value	7.0e-92
Match length	201

% identity	82
NCBI Description	(AC005496) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387772
Contig ID	6518_1.R1084
5'-most EST	LIB3432-023-P1-K1-D12
Method	BLASTX
NCBI GI	g1076627
BLAST score	946
E value	1.0e-102
Match length	191
% identity	97
NCBI Description	inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco >gi_790479_emb_CAA58701_ (X83730) inorganic pyrophosphatase [Nicotiana tabacum]

Seq. No.	387773
Contig ID	6519_1.R1084
5'-most EST	uC-osflcyp062c03a1
Method	BLASTX
NCBI GI	g4680190
BLAST score	211
E value	2.0e-16
Match length	54
% identity	80
NCBI Description	(AF111710) putative dnaJ-like protein [Oryza sativa subsp. indica]

Seq. No.	387774
Contig ID	6523_1.R1084
5'-most EST	uC-osflm202100d10b1
Method	BLASTX
NCBI GI	g4704762
BLAST score	427
E value	2.0e-59
Match length	253
% identity	47
NCBI Description	(AF128404) cellulase homolog [Nicotiana alata]

Seq. No.	387775
Contig ID	6525_1.R1084
5'-most EST	LIB3431-013-P1-K1-F4
Method	BLASTX
NCBI GI	g2262157
BLAST score	144
E value	9.0e-09
Match length	39
% identity	69
NCBI Description	(AC002329) putative ligand-gated ion channel protein [Arabidopsis thaliana]

Seq. No.	387776
Contig ID	6536_1.R1084
5'-most EST	uC-osroM202035b01b1

Seq. No.	387777
Contig ID	6546_1.R1084

5'-most EST	LIB3475-009-P1-K1-A11
Method	BLASTX
NCBI GI	g2226329
BLAST score	362
E value	4.0e-34
Match length	128
% identity	57
NCBI Description	(AF001634) physical impedance induced protein [Zea mays]

Seq. No.	387778
Contig ID	6546_2.R1084
5'-most EST	LIB3431-013-P1-K1-H6
Method	BLASTX
NCBI GI	g1084461
BLAST score	297
E value	1.0e-26
Match length	123
% identity	50
NCBI Description	RCc3 protein - rice >gi_786132 (L27208) RCc3 [Oryza sativa]

Seq. No.	387779
Contig ID	6547_1.R1084
5'-most EST	g569718
Method	BLASTN
NCBI GI	g5257255
BLAST score	106
E value	4.0e-52
Match length	569
% identity	59
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	387780
Contig ID	6547_2.R1084
5'-most EST	g2427356
Method	BLASTN
NCBI GI	g5257255
BLAST score	69
E value	6.0e-30
Match length	319
% identity	82
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	387781
Contig ID	6547_3.R1084
5'-most EST	uC-osflm202101a10b1
Method	BLASTN
NCBI GI	g5257255
BLAST score	328
E value	0.0e+00
Match length	830
% identity	70
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	387782
Contig ID	6547_4.R1084
5'-most EST	g2798617
Method	BLASTX

NCBI GI	g3402817
BLAST score	229
E value	1.0e-18
Match length	45
% identity	93
NCBI Description	(AJ007829) lacZ' [Cloning vector pGreen]

Seq. No.	387783
Contig ID	6547_5.R1084
5'-most EST	uC-osflM202092a10b1
Method	BLASTN
NCBI GI	g5257255
BLAST score	293
E value	1.0e-163
Match length	715
% identity	58
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	387784
Contig ID	6547_6.R1084
5'-most EST	LIB3432-006-P1-K1-F4
Method	BLASTN
NCBI GI	g5257255
BLAST score	84
E value	4.0e-39
Match length	219
% identity	75
NCBI Description	Oryza sativa genomic DNA, chromosome 8, clone:P0026F07

Seq. No.	387785
Contig ID	6551_1.R1084
5'-most EST	LIB3432-060-P1-K1-A11

Seq. No.	387786
Contig ID	6559_1.R1084
5'-most EST	LIB3431-014-P1-K1-A9

Seq. No.	387787
Contig ID	6566_1.R1084
5'-most EST	LIB3431-014-P1-K1-B4

Seq. No.	387788
Contig ID	6579_1.R1084
5'-most EST	LIB3432-018-P1-K1-F10
Method	BLASTX
NCBI GI	g1931640
BLAST score	456
E value	3.0e-45
Match length	143
% identity	57
NCBI Description	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]

Seq. No.	387789
Contig ID	6587_1.R1084
5'-most EST	LIB3432-022-P1-K1-G9
Method	BLASTX

NCBI GI	g3550467
BLAST score	157
E value	3.0e-10
Match length	34
% identity	44
NCBI Description	(AJ005286) cp31AHv protein [Hordeum vulgare]

Seq. No.	387790
Contig ID	6588_1.R1084
5'-most EST	LIB3431-039-P1-K2-F4
Method	BLASTN
NCBI GI	g4519191
BLAST score	35
E value	7.0e-10
Match length	155
% identity	89
NCBI Description	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9P8, complete sequence

Seq. No.	387791
Contig ID	6591_1.R1084
5'-most EST	LIB3431-014-P1-K1-E10
Method	BLASTX
NCBI GI	g3025189
BLAST score	662
E value	3.0e-69
Match length	227
% identity	56
NCBI Description	HYPOTHETICAL 67.1 KD PROTEIN SLL1770 >gi_1652753_dbj_BAA17672_ (D90908) ABC1-like [Synechocystis sp.]

Seq. No.	387792
Contig ID	6613_1.R1084
5'-most EST	uC-osflcyp081d06b1
Method	BLASTX
NCBI GI	g2626753
BLAST score	269
E value	2.0e-23
Match length	89
% identity	60
NCBI Description	(AB008782) sulfate transporter [Arabidopsis thaliana]

Seq. No.	387793
Contig ID	6626_1.R1084
5'-most EST	LIB3431-014-P1-K1-H2
Method	BLASTN
NCBI GI	g1808685
BLAST score	49
E value	3.0e-18
Match length	153
% identity	84
NCBI Description	S.stapfianus pSD.39 mRNA

Seq. No.	387794
Contig ID	6633_1.R1084
5'-most EST	uC-osroM202025b06b1

Method	BLASTX
NCBI GI	g5730130
BLAST score	175
E value	2.0e-12
Match length	151
% identity	31
NCBI Description	(AL109796) putative protein [Arabidopsis thaliana]

Seq. No.	387795
Contig ID	6637_1.R1084
5'-most EST	uC-osf1cyp139b01b1

Seq. No.	387796
Contig ID	6641_1.R1084
5'-most EST	g2428355

Seq. No.	387797
Contig ID	6642_1.R1084
5'-most EST	g5003025
Method	BLASTX
NCBI GI	g3142698
BLAST score	1063
E value	1.0e-116
Match length	324
% identity	61
NCBI Description	(AF064542) protein farnesyltransferase subunit A [Arabidopsis thaliana]

Seq. No.	387798
Contig ID	6658_1.R1084
5'-most EST	LIB3431-015-P1-K1-C5

Seq. No.	387799
Contig ID	6660_1.R1084
5'-most EST	LIB3477-007-P1-K1-F10

Seq. No.	387800
Contig ID	6674_1.R1084
5'-most EST	g1632634
Method	BLASTN
NCBI GI	g295500
BLAST score	50
E value	4.0e-19
Match length	102
% identity	87
NCBI Description	Triticum aestivum heat shock protein 16.9C (hsp16.9C) mRNA, 3' end

Seq. No.	387801
Contig ID	6677_1.R1084
5'-most EST	LIB3431-034-P1-K1-H10
Method	BLASTN
NCBI GI	g5410347
BLAST score	41
E value	1.0e-13
Match length	108
% identity	92

NCBI Description	Sorghum bicolor BAC clone 110K5, partial sequence

Seq. No.	387802
Contig ID	6680_1.R1084
5'-most EST	LIB3432-027-P1-K1-E7
Method	BLASTX
NCBI GI	g4262242
BLAST score	276
E value	5.0e-24
Match length	103
% identity	64
NCBI Description	(AC006200) NADC homolog [Arabidopsis thaliana]

Seq. No.	387803
Contig ID	6685_1.R1084
5'-most EST	LIB3432-040-P1-K1-E5
Method	BLASTX
NCBI GI	g4539333
BLAST score	807
E value	6.0e-86
Match length	263
% identity	60
NCBI Description	(AL035539) putative amino acid transport protein [Arabidopsis thaliana]

Seq. No.	387804
Contig ID	6691_1.R1084
5'-most EST	g4714654

Seq. No.	387805
Contig ID	6694_1.R1084
5'-most EST	LIB3434-056-P1-K1-C5
Method	BLASTX
NCBI GI	g3273202
BLAST score	532
E value	6.0e-54
Match length	153
% identity	71
NCBI Description	(AB010918) responce reactor4 [Arabidopsis thaliana]

Seq. No.	387806
Contig ID	6694_2.R1084
5'-most EST	LIB3477-006-P1-K1-F7

Seq. No.	387807
Contig ID	6696_1.R1084
5'-most EST	uC-osflcyp155e12b1
Method	BLASTX
NCBI GI	g2281089
BLAST score	371
E value	2.0e-35
Match length	79
% identity	89
NCBI Description	(AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No.	387808
Contig ID	6696_2.R1084

5'-most EST	LIB3434-018-P1-K1-C4
Method	BLASTX
NCBI GI	g2281089
BLAST score	369
E value	3.0e-35
Match length	79
% identity	89
NCBI Description	(AC002333) Sm protein F isolog [Arabidopsis thaliana]

Seq. No.	387809
Contig ID	6705_1.R1084
5'-most EST	LIB3431-015-P1-K1-G8
Method	BLASTX
NCBI GI	g166410
BLAST score	443
E value	7.0e-44
Match length	118
% identity	71
NCBI Description	(L07291) Alfin-1 [Medicago sativa]

Seq. No.	387810
Contig ID	6720_1.R1084
5'-most EST	LIB3431-016-P1-K1-A3
Method	BLASTX
NCBI GI	g4680685
BLAST score	210
E value	2.0e-20
Match length	129
% identity	40
NCBI Description	(AF132957) CGI-23 protein [Homo sapiens]

Seq. No.	387811
Contig ID	6721_1.R1084
5'-most EST	uC-osroM202011d03a1

Seq. No.	387812
Contig ID	6726_1.R1084
5'-most EST	LIB3434-023-P1-K1-E6
Method	BLASTX
NCBI GI	g3461820
BLAST score	257
E value	6.0e-22
Match length	124
% identity	45
NCBI Description	(AC004138) unknown protein [Arabidopsis thaliana]

Seq. No.	387813
Contig ID	6731_1.R1084
5'-most EST	LIB3431-016-P1-K1-B5
Method	BLASTX
NCBI GI	g5702015
BLAST score	338
E value	2.0e-31
Match length	105
% identity	65
NCBI Description	(AJ012215) GAL83 protein [Solanum tuberosum]

Seq. No.	387814
Contig ID	6741_1.R1084
5'-most EST	g2799371

Seq. No.	387815
Contig ID	6741_2.R1084
5'-most EST	LIB3434-013-P1-K1-F2

Seq. No.	387816
Contig ID	6746_1.R1084
5'-most EST	g2310206
Method	BLASTX
NCBI GI	g3327196
BLAST score	237
E value	2.0e-28
Match length	136
% identity	49
NCBI Description	(AB014591) KIAA0691 protein [Homo sapiens]

Seq. No.	387817
Contig ID	6751_1.R1084
5'-most EST	LIB3431-020-P1-K1-G7
Method	BLASTN
NCBI GI	g21810
BLAST score	38
E value	2.0e-11
Match length	38
% identity	100
NCBI Description	T.aestivum mRNA for heat shock protein 26.6B

Seq. No.	387818
Contig ID	6753_1.R1084
5'-most EST	g5004587

Seq. No.	387819
Contig ID	6753_3.R1084
5'-most EST	LIB3479-004-Q6-K1-D7

Seq. No.	387820
Contig ID	6756_1.R1084
5'-most EST	g427264
Method	BLASTX
NCBI GI	g1351357
BLAST score	280
E value	2.0e-24
Match length	87
% identity	62
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (CR14) >gi_633681_emb_CAA55863_ (X79276) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	387821
Contig ID	6756_2.R1084
5'-most EST	g4968711
Method	BLASTX
NCBI GI	g1351357
BLAST score	438

E value	5.0e-43
Match length	123
% identity	67
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (CR14) >gi_633681_emb_CAA55863_ (X79276) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	387822
Contig ID	6756_3.R1084
5'-most EST	LIB3434-024-P1-K1-G2
Method	BLASTX
NCBI GI	g1351357
BLAST score	426
E value	1.0e-41
Match length	123
% identity	68
NCBI Description	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (CR14) >gi_633681_emb_CAA55863_ (X79276) ubiquinol--cytochrome c reductase [Solanum tuberosum]

Seq. No.	387823
Contig ID	6756_5.R1084
5'-most EST	LIB3431-016-P1-K1-D8
Method	BLASTX
NCBI GI	g4049349
BLAST score	284
E value	5.0e-25
Match length	99
% identity	59
NCBI Description	(AL034567) ubiquinol-cytochrome c reductase-like protein [Arabidopsis thaliana]

Seq. No.	387824
Contig ID	6761_1.R1084
5'-most EST	LIB3431-016-P1-K1-E3
Method	BLASTX
NCBI GI	g3184559
BLAST score	311
E value	4.0e-28
Match length	128
% identity	52
NCBI Description	(AF052290) putative c-type cytochrome biogenesis protein [Synechococcus PCC7002]

Seq. No.	387825
Contig ID	6763_1.R1084
5'-most EST	LIB3431-016-P1-K1-E5
Method	BLASTX
NCBI GI	g2245120
BLAST score	555
E value	2.0e-57
Match length	208
% identity	58
NCBI Description	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387826
Contig ID	6768_1.R1084

5'-most EST	g4714410
Seq. No.	387827
Contig ID	6777_1.R1084
5'-most EST	g2442370
Seq. No.	387828
Contig ID	6782_1.R1084
5'-most EST	LIB3434-005-P1-K1-D5
Method	BLASTX
NCBI GI	g3334456
BLAST score	149
E value	2.0e-09
Match length	74
% identity	43
NCBI Description	ACTIVATOR 1 140 KD SUBUNIT (REPLICATION FACTOR C LARGE SUBUNIT) (A1 140 KD SUBUNIT) (RF-C 140 KD SUBUNIT) (ACTIVATOR 1 LARGE SUBUNIT) (DNA-BINDING PROTEIN PO-GA) >gi_422807_pir__JN0599 DNA-binding protein PO-GA - human >gi_296908_emb_CAA80355_ (Z22642) PO-GA [Homo sapiens] >gi_307338 (L14922) DNA-binding protein [Homo sapiens] >gi_2827257 (AF040250) DNA binding protein [Homo sapiens]
Seq. No.	387829
Contig ID	6786_1.R1084
5'-most EST	LIB3431-016-P1-K1-G7
Method	BLASTX
NCBI GI	g5668811
BLAST score	569
E value	3.0e-58
Match length	230
% identity	21
NCBI Description	(AC007519) Contains 3 PF_00076 RNA recognition motif domains. EST gb_T20424 comes from this gene. [Arabidopsis thaliana]
Seq. No.	387830
Contig ID	6792_1.R1084
5'-most EST	LIB3433-059-P1-K1-E5
Method	BLASTX
NCBI GI	g5306269
BLAST score	375
E value	7.0e-36
Match length	164
% identity	25
NCBI Description	(AC006233) unknown protein [Arabidopsis thaliana]
Seq. No.	387831
Contig ID	6805_1.R1084
5'-most EST	g5443720
Method	BLASTX
NCBI GI	g510907
BLAST score	1305
E value	1.0e-144
Match length	348
% identity	68
NCBI Description	(Z35108) calnexin [Helianthus tuberosus]

Seq. No.	387832
Contig ID	6813_1.R1084
5'-most EST	LIB3431-017-P1-K1-B3
Method	BLASTX
NCBI GI	g2618704
BLAST score	701
E value	4.0e-74
Match length	163
% identity	79
NCBI Description	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]

Seq. No.	387833
Contig ID	6819_1.R1084
5'-most EST	LIB3432-026-P1-K1-D5

Seq. No.	387834
Contig ID	6819_2.R1084
5'-most EST	LIB3431-017-P1-K1-B9

Seq. No.	387835
Contig ID	6819_3.R1084
5'-most EST	uC-osroM202012h01b1

Seq. No.	387836
Contig ID	6819_4.R1084
5'-most EST	LIB3433-044-P1-K1-E4

Seq. No.	387837
Contig ID	6825_1.R1084
5'-most EST	LIB3431-027-P1-K1-F10
Method	BLASTX
NCBI GI	g1777961
BLAST score	605
E value	1.0e-62
Match length	209
% identity	54
NCBI Description	(U56406) methyljasmonate-inducible lipoxygenase 2 [Hordeum vulgare]

Seq. No.	387838
Contig ID	6831_1.R1084
5'-most EST	g4879486

Seq. No.	387839
Contig ID	6833_1.R1084
5'-most EST	uC-osflM202039f09b1

Seq. No.	387840
Contig ID	6835_1.R1084
5'-most EST	LIB3431-058-P1-K1-G10
Method	BLASTX
NCBI GI	g4581207
BLAST score	687
E value	4.0e-74
Match length	222

% identity	58
NCBI Description	(Y17914) cyclic nucleotide and calmodulin-regulated ion channel [Arabidopsis thaliana]

Seq. No.	387841
Contig ID	6840_2.R1084
5'-most EST	LIB3434-038-P1-K1-F8
Method	BLASTX
NCBI GI	g5902390
BLAST score	970
E value	1.0e-105
Match length	368
% identity	55
NCBI Description	(AC008148) Unknown protein [Arabidopsis thaliana]

Seq. No.	387842
Contig ID	6848_1.R1084
5'-most EST	g569884
Method	BLASTX
NCBI GI	g1703200
BLAST score	358
E value	1.0e-33
Match length	230
% identity	51
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	387843
Contig ID	6848_2.R1084
5'-most EST	LIB3432-057-P1-K1-F1
Method	BLASTX
NCBI GI	g1703200
BLAST score	406
E value	2.0e-39
Match length	127
% identity	62
NCBI Description	PROTEIN KINASE AFC2 >gi_601789 (U16177) protein kinase [Arabidopsis thaliana] >gi_642130_dbj_BAA08214_ (D45353) protein kinase [Arabidopsis thaliana] >gi_4220516_emb_CAA22989_ (AL035356) protein kinase (AFC2) [Arabidopsis thaliana]

Seq. No.	387844
Contig ID	6852_1.R1084
5'-most EST	LIB3431-028-P1-K1-D1

Seq. No.	387845
Contig ID	6855_1.R1084
5'-most EST	uC-osroM202038a09a1

Seq. No.	387846
Contig ID	6891_1.R1084
5'-most EST	g3759801
Method	BLASTX

NCBI GI	g1769887
BLAST score	1363
E value	1.0e-151
Match length	365
% identity	70
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	387847
Contig ID	6891_2.R1084
5'-most EST	g3761639
Method	BLASTX
NCBI GI	g1769887
BLAST score	289
E value	1.0e-25
Match length	95
% identity	55
NCBI Description	(X95736) amino acid permease 6 [Arabidopsis thaliana]

Seq. No.	387848
Contig ID	6903_1.R1084
5'-most EST	g702342
Method	BLASTX
NCBI GI	g4467145
BLAST score	272
E value	6.0e-26
Match length	144
% identity	47
NCBI Description	(AL035540) farnesylated protein (ATFP6) [Arabidopsis thaliana]

Seq. No.	387849
Contig ID	6912_1.R1084
5'-most EST	g3768552

Seq. No.	387850
Contig ID	6912_2.R1084
5'-most EST	g2428269
Method	BLASTX
NCBI GI	g3510253
BLAST score	319
E value	8.0e-29
Match length	320
% identity	31
NCBI Description	(AC005310) hypothetical protein [Arabidopsis thaliana]

Seq. No.	387851
Contig ID	6912_3.R1084
5'-most EST	LIB3431-037-P1-K1-E4

Seq. No.	387852
Contig ID	6930_1.R1084
5'-most EST	LIB3431-018-P1-K1-G12
Method	BLASTX
NCBI GI	g5921185
BLAST score	558
E value	4.0e-57
Match length	224

% identity	50
NCBI Description	CYTOCHROME P450 76C1 >gi_2979548 (AC003680) putative 7-ethoxycoumarin O-deethylase [Arabidopsis thaliana]

Seq. No.	387853
Contig ID	6973_1.R1084
5'-most EST	LIB3431-030-P1-K2-D2
Method	BLASTX
NCBI GI	g1351856
BLAST score	578
E value	1.0e-59
Match length	129
% identity	82
NCBI Description	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) >gi_868003_dbj_BAA06108_ (D29629) aconitase [Cucurbita sp.]

Seq. No.	387854
Contig ID	6990_1.R1084
5'-most EST	LIB3431-030-P1-K2-F3
Method	BLASTX
NCBI GI	g4263787
BLAST score	459
E value	1.0e-45
Match length	202
% identity	49
NCBI Description	(AC006068) unknown protein [Arabidopsis thaliana]

Seq. No.	387855
Contig ID	6998_1.R1084
5'-most EST	LIB3433-049-P1-K1-C9
Method	BLASTX
NCBI GI	g2244998
BLAST score	473
E value	5.0e-47
Match length	290
% identity	41
NCBI Description	(Z97341) transcriptional adaptor like protein [Arabidopsis thaliana]

Seq. No.	387856
Contig ID	7009_1.R1084
5'-most EST	uC-osroM202023g06b1

Seq. No.	387857
Contig ID	7030_1.R1084
5'-most EST	LIB3434-042-P1-K1-F12

Seq. No.	387858
Contig ID	7033_1.R1084
5'-most EST	LIB3431-038-P1-K1-B12

Seq. No.	387859
Contig ID	7034_1.R1084
5'-most EST	LIB3431-038-P1-K1-B3
Method	BLASTN
NCBI GI	g4959460

BLAST score	35
E value	6.0e-10
Match length	35
% identity	38
NCBI Description	Zea mays RACB small GTP binding protein mRNA, complete cds

Seq. No.	387860
Contig ID	7062_2.R1084
5'-most EST	LIB3474-011-P1-K1-F2
Method	BLASTX
NCBI GI	g4581181
BLAST score	342
E value	1.0e-31
Match length	162
% identity	46
NCBI Description	(AC006220) unknown protein [Arabidopsis thaliana]

Seq. No.	387861
Contig ID	7071_1.R1084
5'-most EST	LIB3431-038-P1-K1-E8
Method	BLASTX
NCBI GI	g4455367
BLAST score	144
E value	1.0e-08
Match length	205
% identity	28
NCBI Description	(AL035524) putative protein [Arabidopsis thaliana]

Seq. No.	387862
Contig ID	7094_1.R1084
5'-most EST	LIB3431-038-P1-K1-H1
Method	BLASTX
NCBI GI	g3024440
BLAST score	372
E value	2.0e-37
Match length	98
% identity	78
NCBI Description	PROTEASOME DELTA CHAIN PRECURSOR (MULTICATALYTIC ENDOPEPTIDASE COMPLEX DELTA CHAIN) >gi_1743356_emb_CAA70699_ (Y09505) proteasome delta subunit [Nicotiana tabacum]

Seq. No.	387863
Contig ID	7094_2.R1084
5'-most EST	g571639
Method	BLASTX
NCBI GI	g2511594
BLAST score	444
E value	5.0e-44
Match length	97
% identity	88
NCBI Description	(Y13694) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_2827525_emb_CAA16533.1_ (AL021633) multicatalytic endopeptidase complex, proteasome precursor, beta subunit [Arabidopsis thaliana] >gi_3421099 (AF043529) 20S proteasome subunit PBA1 [Arabidopsis thaliana]

Seq. No.	387864
Contig ID	7132_1.R1084
5'-most EST	LIB3431-039-P1-K2-D12

Seq. No.	387865
Contig ID	7133_1.R1084
5'-most EST	LIB3431-039-P1-K2-D2

Seq. No.	387866
Contig ID	7139_1.R1084
5'-most EST	LIB3431-039-P1-K2-D8

Seq. No.	387867
Contig ID	7140_1.R1084
5'-most EST	LIB3431-039-P1-K2-E1

Seq. No.	387868
Contig ID	7143_1.R1084
5'-most EST	LIB3431-039-P1-K2-E3

Seq. No.	387869
Contig ID	7154_1.R1084
5'-most EST	LIB3431-039-P1-K2-F6
Method	BLASTX
NCBI GI	g2598589
BLAST score	414
E value	3.0e-40
Match length	158
% identity	53
NCBI Description	(Y15367) MtN19 [Medicago truncatula]

Seq. No.	387870
Contig ID	7177_1.R1084
5'-most EST	g2798350

Seq. No.	387871
Contig ID	7179_1.R1084
5'-most EST	LIB3434-032-P1-K1-F10
Method	BLASTX
NCBI GI	g2808638
BLAST score	307
E value	2.0e-47
Match length	284
% identity	48
NCBI Description	(AJ001367) small GTP-binding protein [Daucus carota]

Seq. No.	387872
Contig ID	7179_2.R1084
5'-most EST	LIB3434-048-P1-K1-A4
Method	BLASTX
NCBI GI	g1362065
BLAST score	293
E value	3.0e-26
Match length	88
% identity	69
NCBI Description	small GTP-binding protein - garden pea

>gi_871506_emb_CAA90081_ (Z49901) small GTP-binding protein [Pisum sativum]

Seq. No.	387873
Contig ID	7185_1.R1084
5'-most EST	LIB3431-040-P1-K2-B4
Method	BLASTX
NCBI GI	g2244847
BLAST score	211
E value	1.0e-16
Match length	135
% identity	40
NCBI Description	(Z97337) hydroxyproline-rich glycoprotein homolog [Arabidopsis thaliana]

Seq. No.	387874
Contig ID	7195_1.R1084
5'-most EST	LIB3431-053-P1-K1-C11
Method	BLASTX
NCBI GI	g2130042
BLAST score	658
E value	1.0e-118
Match length	234
% identity	94
NCBI Description	Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]

Seq. No.	387875
Contig ID	7195_2.R1084
5'-most EST	g2275796
Method	BLASTX
NCBI GI	g2130042
BLAST score	574
E value	5.0e-94
Match length	202
% identity	85
NCBI Description	Mg-chelatase chain Xantha-f - barley >gi_861199 (U26916) protoporphyrin IX Mg-chelatase subunit precursor [Hordeum vulgare]

Seq. No.	387876
Contig ID	7217_1.R1084
5'-most EST	LIB3431-040-P1-K2-E5
Method	BLASTX
NCBI GI	g1651459
BLAST score	489
E value	9.0e-49
Match length	275
% identity	40
NCBI Description	(D90732) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	387877
Contig ID	7217_2.R1084
5'-most EST	LIB3432-014-P1-K1-A11
Method	BLASTX

NCBI GI	g113742
BLAST score	317
E value	7.0e-29
Match length	218
% identity	34
NCBI Description	AMINOPEPTIDASE N (ALPHA-AMINOACYLPEPTIDE HYDROLASE) >gi_147142 (M15273) peptidase N [Escherichia coli] >gi_147144 (M15676) aminopeptidase N [Escherichia coli] >gi_1787163 (AE000195) aminopeptidase N [Escherichia coli] >gi_4062498_dbj_BAA35684_ (D90731) Aminopeptidase n (EC 3.4.11.2) (alpha-aminoacylpeptide hydrolase). [Escherichia coli]

Seq. No.	387878
Contig ID	7223_1.R1084
5'-most EST	g286560
Method	BLASTX
NCBI GI	g2104959
BLAST score	463
E value	4.0e-46
Match length	106
% identity	76
NCBI Description	(U96925) immunophilin [Vicia faba]

Seq. No.	387879
Contig ID	7237_1.R1084
5'-most EST	LIB3431-040-P1-K2-G7
Method	BLASTX
NCBI GI	g3080420
BLAST score	372
E value	1.0e-35
Match length	135
% identity	56
NCBI Description	(AL022604) putative sugar transporter protein [Arabidopsis thaliana]

Seq. No.	387880
Contig ID	7242_1.R1084
5'-most EST	uC-osf1M202089f04b1
Method	BLASTX
NCBI GI	g4584342
BLAST score	391
E value	1.0e-37
Match length	168
% identity	34
NCBI Description	(AC007127) putative ubiquitin protein [Arabidopsis thaliana]

Seq. No.	387881
Contig ID	7249_1.R1084
5'-most EST	LIB3431-043-P1-K1-A2
Method	BLASTX
NCBI GI	g3150410
BLAST score	277
E value	3.0e-24
Match length	96
% identity	39

NCBI Description	(AC004165) unknown protein [Arabidopsis thaliana]
Seq. No.	387882
Contig ID	7252_1.R1084
5'-most EST	LIB3431-043-P1-K1-A6
Seq. No.	387883
Contig ID	7253_1.R1084
5'-most EST	uC-osroM202014h12b1
Method	BLASTX
NCBI GI	g4581156
BLAST score	1261
E value	0.0e+00
Match length	475
% identity	79
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	387884
Contig ID	7253_2.R1084
5'-most EST	g3767016
Method	BLASTX
NCBI GI	g2245394
BLAST score	264
E value	1.0e-22
Match length	75
% identity	63
NCBI Description	(U89771) ARF1-binding protein [Arabidopsis thaliana]
Seq. No.	387885
Contig ID	7253_3.R1084
5'-most EST	g2311956
Method	BLASTX
NCBI GI	g4581156
BLAST score	296
E value	2.0e-26
Match length	71
% identity	80
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	387886
Contig ID	7253_4.R1084
5'-most EST	uC-osflcyp003f11b1
Method	BLASTX
NCBI GI	g4581156
BLAST score	355
E value	1.0e-33
Match length	78
% identity	88
NCBI Description	(AC006919) putative pyruvate kinase [Arabidopsis thaliana]
Seq. No.	387887
Contig ID	7277_1.R1084
5'-most EST	LIB3431-043-P1-K1-D12
Method	BLASTX
NCBI GI	g1718097
BLAST score	450
E value	1.0e-44

Match length	147
% identity	55
NCBI Description	VACUOLAR ATP SYNTHASE SUBUNIT AC39 (V-ATPASE AC39 SUBUNIT) (41 KD ACCESSORY PROTEIN) (DVA41) >gi_626048_pir__A55016 lysosomal membrane protein DVA41 - slime mold (Dictyostelium discoideum) >gi_532733 (U13150) vacuolar ATPase subunit DVA41 [Dictyostelium discoideum]

Seq. No.	387888
Contig ID	7286_1.R1084
5'-most EST	LIB3432-036-P2-K1-H12
Method	BLASTX
NCBI GI	g2911276
BLAST score	171
E value	5.0e-12
Match length	85
% identity	47
NCBI Description	(U63631) LMW heat shock protein [Fragaria x ananassa]

Seq. No.	387889
Contig ID	7292_1.R1084
5'-most EST	g3761152

Seq. No.	387890
Contig ID	7293_1.R1084
5'-most EST	g2309720
Method	BLASTX
NCBI GI	g1916290
BLAST score	276
E value	8.0e-24
Match length	104
% identity	52
NCBI Description	(U89876) ALY [Mus musculus]

Seq. No.	387891
Contig ID	7297_1.R1084
5'-most EST	LIB3434-040-P1-K1-B8

Seq. No.	387892
Contig ID	7319_1.R1084
5'-most EST	uC-osflM202123b08b1

Seq. No.	387893
Contig ID	7319_2.R1084
5'-most EST	uC-osflcyp125c10b1

Seq. No.	387894
Contig ID	7319_3.R1084
5'-most EST	LIB3431-029-P1-K1-B7

Seq. No.	387895
Contig ID	7324_1.R1084
5'-most EST	g3767003

Seq. No.	387896
Contig ID	7329_1.R1084
5'-most EST	LIB3431-044-P1-K1-A8

Method	BLASTX
NCBI GI	g3402711
BLAST score	310
E value	2.0e-33
Match length	141
% identity	37
NCBI Description	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]

Seq. No.	387897
Contig ID	7332_1.R1084
5'-most EST	LIB3432-048-P2-K1-G1
Method	BLASTX
NCBI GI	g1731181
BLAST score	215
E value	4.0e-17
Match length	138
% identity	38
NCBI Description	HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi_3874230_emb_CAA90107.1_ (Z49909) weak similarity with a B. Flavum translocation protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene; cDNA EST yk549e12.3 comes from this gene; cDNA EST yk618d6.3 comes from this gene

Seq. No.	387898
Contig ID	7340_1.R1084
5'-most EST	LIB3431-044-P1-K1-B8
Method	BLASTX
NCBI GI	g2344892
BLAST score	213
E value	7.0e-17
Match length	68
% identity	69
NCBI Description	(AC002388) unknown protein [Arabidopsis thaliana]

Seq. No.	387899
Contig ID	7346_1.R1084
5'-most EST	LIB3474-007-P1-K1-G7
Method	BLASTX
NCBI GI	g2829916
BLAST score	183
E value	6.0e-15
Match length	61
% identity	79
NCBI Description	(AC002291) Unknown protein [Arabidopsis thaliana]

Seq. No.	387900
Contig ID	7359_1.R1084
5'-most EST	g3766651

Seq. No.	387901
Contig ID	7360_1.R1084
5'-most EST	LIB3431-044-P1-K1-D8

Seq. No.	387902
Contig ID	7373_1.R1084

5'-most EST	LIB3431-044-P1-K1-F1
Method	BLASTX
NCBI GI	g2943792
BLAST score	769
E value	5.0e-82
Match length	182
% identity	70
NCBI Description	(AB006809) PV72 [Cucurbita sp.]

Seq. No.	387903
Contig ID	7375_1.R1084
5'-most EST	LIB3431-035-P1-K1-G6

Seq. No.	387904
Contig ID	7379_1.R1084
5'-most EST	LIB3431-044-P1-K1-F5
Method	BLASTX
NCBI GI	g2147484
BLAST score	761
E value	4.0e-81
Match length	170
% identity	85
NCBI Description	homeotic protein - Phalaenopsis sp >gi_1173622 (U34743) homeobox protein [Phalaenopsis sp. 'hybrid SM9108']

Seq. No.	387905
Contig ID	7388_1.R1084
5'-most EST	LIB3431-044-P1-K1-G2
Method	BLASTX
NCBI GI	g3176664
BLAST score	322
E value	2.0e-29
Match length	108
% identity	57
NCBI Description	(AC004393) Contains similarity to beta scruin gb_Z47541 from Limulus polyphemus. ESTs gb_T04493 and gb_AA585955 come from this gene. [Arabidopsis thaliana]

Seq. No.	387906
Contig ID	7390_1.R1084
5'-most EST	LIB3431-044-P1-K1-G4
Method	BLASTX
NCBI GI	g1684851
BLAST score	248
E value	6.0e-21
Match length	103
% identity	54
NCBI Description	(U77935) DnaJ-like protein [Phaseolus vulgaris]

Seq. No.	387907
Contig ID	7392_1.R1084
5'-most EST	LIB3431-044-P1-K1-G7

Seq. No.	387908
Contig ID	7406_1.R1084
5'-most EST	LIB3431-045-P1-K1-A10
Method	BLASTN

NCBI GI	g5441876
BLAST score	170
E value	1.0e-90
Match length	359
% identity	32
NCBI Description	Oryza sativa genomic DNA, chromosome 2, clone:P0437H03 (contig b)

Seq. No.	387909
Contig ID	7416_1.R1084
5'-most EST	g2312108
Method	BLASTX
NCBI GI	g3549656
BLAST score	283
E value	6.0e-25
Match length	172
% identity	31
NCBI Description	(AL031394) putative protein [Arabidopsis thaliana]

Seq. No.	387910
Contig ID	7422_1.R1084
5'-most EST	LIB3431-045-P1-K1-B5
Method	BLASTX
NCBI GI	g6056413
BLAST score	673
E value	9.0e-71
Match length	184
% identity	72
NCBI Description	(AC009525) Unknown protein [Arabidopsis thaliana]

Seq. No.	387911
Contig ID	7423_1.R1084
5'-most EST	LIB3433-054-P1-K1-E1
Method	BLASTX
NCBI GI	g2191152
BLAST score	307
E value	1.0e-27
Match length	140
% identity	53
NCBI Description	(AF007269) A_IG002N01.31 gene product [Arabidopsis thaliana]

Seq. No.	387912
Contig ID	7426_1.R1084
5'-most EST	LIB3431-045-P1-K1-B9
Method	BLASTX
NCBI GI	g3169012
BLAST score	472
E value	4.0e-47
Match length	123
% identity	75
NCBI Description	(AJ002610) putative calmodulin binding transporter protein [Hordeum vulgare]

Seq. No.	387913
Contig ID	7430_1.R1084
5'-most EST	uC-osflm202113f10b1

Method	BLASTX
NCBI GI	g399015
BLAST score	1313
E value	1.0e-145
Match length	375
% identity	71
NCBI Description	ADP,ATP CARRIER PROTEIN PRECURSOR (ADP/ATP TRANSLOCASE) (ADENINE NUCLEOTIDE TRANSLOCATOR) (ANT) >gi_218145_dbj_BAA02161_ (D12637) ATP/ADP translocator [Oryza sativa]

Seq. No.	387914
Contig ID	7444_1.R1084
5'-most EST	uC-osflcyp143h07b1
Method	BLASTX
NCBI GI	g1651828
BLAST score	311
E value	2.0e-37
Match length	186
% identity	53
NCBI Description	(D90900) dihydrolipoamide dehydrogenase [Synechocystis sp.]

Seq. No.	387915
Contig ID	7446_1.R1084
5'-most EST	LIB3431-045-P1-K1-E11
Method	BLASTX
NCBI GI	g2244749
BLAST score	1022
E value	1.0e-111
Match length	242
% identity	81
NCBI Description	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]

Seq. No.	387916
Contig ID	7483_1.R1084
5'-most EST	LIB3431-045-P1-K1-H9

Seq. No.	387917
Contig ID	7490_1.R1084
5'-most EST	LIB3431-046-P1-K1-A5

Seq. No.	387918
Contig ID	7498_1.R1084
5'-most EST	g4881097
Method	BLASTX
NCBI GI	g2499932
BLAST score	753
E value	6.0e-80
Match length	172
% identity	84
NCBI Description	ADENINE PHOSPHORIBOSYLTRANSFERASE 1 (APRT) >gi_726305 (U22442) adenine phosphoribosyltransferase form 1 [Triticum aestivum]

Seq. No.	387919
Contig ID	7499_1.R1084
5'-most EST	LIB3431-046-P1-K1-B4

Seq. No.	387920
Contig ID	7521_1.R1084
5'-most EST	LIB3432-014-P1-K1-B1

Seq. No.	387921
Contig ID	7528_1.R1084
5'-most EST	LIB3431-046-P1-K1-E5
Method	BLASTX
NCBI GI	g131205
BLAST score	178
E value	9.0e-13
Match length	36
% identity	100
NCBI Description	PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-I) >gi_72677_pir__A1RZI photosystem I protein psaI - rice chloroplast >gi_11996_emb_CAA33957_ (X15901) ORF36 [Oryza sativa] >gi_226617_prf__1603356AP photosystem I small peptide [Oryza sativa]

Seq. No.	387922
Contig ID	7528_2.R1084
5'-most EST	LIB3474-009-P1-K1-E6
Method	BLASTX
NCBI GI	g140291
BLAST score	649
E value	7.0e-68
Match length	144
% identity	86
NCBI Description	HYPOTHETICAL 21.5 KD PROTEIN (ORF 185) >gi_82541_pir__S05116 hypothetical protein 185 - rice chloroplast >gi_11997_emb_CAA33958_ (X15901) ORF185 [Oryza sativa] >gi_226618_prf__1603356AQ ORF 185 [Oryza sativa]

Seq. No.	387923
Contig ID	7562_1.R1084
5'-most EST	LIB3431-046-P1-K1-H9
Method	BLASTX
NCBI GI	g2495180
BLAST score	482
E value	2.0e-48
Match length	115
% identity	83
NCBI Description	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) >gi_421882_pir__S35873 hydroxymethylbilane synthase (EC 4.3.1.8) - garden pea >gi_541971_pir__JQ2278 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - garden pea chloroplast >gi_313724_emb_CAA51820_ (X73418) hydroxymethylbilane synthase [Pisum sativum]

Seq. No.	387924
Contig ID	7568_1.R1084
5'-most EST	g5900642
Method	BLASTX
NCBI GI	g6016875
BLAST score	278

E value	3.0e-24
Match length	68
% identity	79
NCBI Description	(AP000570) EST AU078302(C63241) corresponds to a region of the predicted gene.; hypothetical protein [Oryza sativa]

Seq. No.	387925
Contig ID	7573_1.R1084
5'-most EST	LIB3431-047-P1-K1-B2
Method	BLASTN
NCBI GI	g399628
BLAST score	35
E value	4.0e-10
Match length	35
% identity	100
NCBI Description	Lycopersicon esculentum (DB207) meloidogyne-induced giant cell protein mRNA, 3' end

Seq. No.	387926
Contig ID	7582_1.R1084
5'-most EST	LIB3474-001-P1-K1-B5
Method	BLASTX
NCBI GI	g4205079
BLAST score	467
E value	2.0e-46
Match length	163
% identity	56
NCBI Description	(U70425) ankyrin repeat-containing protein 2 [Arabidopsis thaliana]

Seq. No.	387927
Contig ID	7583_1.R1084
5'-most EST	g3763799
Method	BLASTX
NCBI GI	g4589726
BLAST score	962
E value	1.0e-104
Match length	278
% identity	64
NCBI Description	(AB003137) DnaJ homolog protein [Salix gilgiana] >gi_4589739_dbj_BAA76888.1_ (AB003138) DnaJ homolog protein [Salix gilgiana]

Seq. No.	387928
Contig ID	7583_2.R1084
5'-most EST	g701305
Method	BLASTX
NCBI GI	g4589726
BLAST score	1018
E value	1.0e-164
Match length	416
% identity	70
NCBI Description	(AB003137) DnaJ homolog protein [Salix gilgiana] >gi_4589739_dbj_BAA76888.1_ (AB003138) DnaJ homolog protein [Salix gilgiana]

Seq. No.	387929

Contig ID	7583_3.R1084
5'-most EST	g2799038
Method	BLASTN
NCBI GI	g2894791
BLAST score	41
E value	2.0e-13
Match length	68
% identity	97
NCBI Description	Cryptosporidium parvum heat shock protein 70 (Hsp 70) mRNA, complete cds

Seq. No.	387930
Contig ID	7587_1.R1084
5'-most EST	LIB3431-047-P1-K1-C6
Method	BLASTX
NCBI GI	g131283
BLAST score	800
E value	2.0e-85
Match length	244
% identity	69
NCBI Description	PHOTOSYSTEM II 44 KD REACTION CENTER PROTEIN (P6 PROTEIN) (CP43) >gi_72710_pir__F2RZ44 photosystem II chlorophyll a-binding protein psbC - rice chloroplast >gi_11965_emb_CAA34014_ (X15901) PSII 43kDa protein [Oryza sativa]

Seq. No.	387931
Contig ID	7595_1.R1084
5'-most EST	LIB3431-047-P1-K1-D5
Method	BLASTN
NCBI GI	g2062705
BLAST score	33
E value	8.0e-09
Match length	68
% identity	56
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	387932
Contig ID	7606_1.R1084
5'-most EST	uC-osflcyp174b12b1
Method	BLASTX
NCBI GI	g4887131
BLAST score	1276
E value	1.0e-141
Match length	384
% identity	64
NCBI Description	(AF134732) 60S ribosomal protein L1 [Prunus armeniaca]

Seq. No.	387933
Contig ID	7606_3.R1084
5'-most EST	uC-osflcyp170e01b1
Method	BLASTX
NCBI GI	g4887131
BLAST score	505
E value	3.0e-51
Match length	119
% identity	75

NCBI Description	(AF134732) 60S ribosomal protein L1 [Prunus armeniaca]

Seq. No.	387934
Contig ID	7612_1.R1084
5'-most EST	g5004758
Method	BLASTX
NCBI GI	g120510
BLAST score	431
E value	3.0e-42
Match length	93
% identity	88
NCBI Description	FERRITIN 2 PRECURSOR >gi_82688_pir__S24057 ferritin precursor (clone FM2) - maize >gi_22278_emb_CAA43664_ (X61392) ferritin [Zea mays]

Seq. No.	387935
Contig ID	7612_2.R1084
5'-most EST	g2799961
Method	BLASTX
NCBI GI	g2130127
BLAST score	623
E value	8.0e-65
Match length	133
% identity	89
NCBI Description	ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_ (X83076) ferritin [Zea mays]

Seq. No.	387936
Contig ID	7612_3.R1084
5'-most EST	LIB3431-027-P1-K1-B4
Method	BLASTX
NCBI GI	g2130127
BLAST score	447
E value	2.0e-44
Match length	99
% identity	90
NCBI Description	ferritin 1 precursor - maize >gi_1103628_emb_CAA58146_ (X83076) ferritin [Zea mays]

Seq. No.	387937
Contig ID	7628_1.R1084
5'-most EST	LIB3431-047-P1-K1-H10

Seq. No.	387938
Contig ID	7629_1.R1084
5'-most EST	LIB3434-027-P1-K1-C7
Method	BLASTX
NCBI GI	g2130105
BLAST score	273
E value	5.0e-30
Match length	95
% identity	80
NCBI Description	histone H2A type 2 (clone wcH2A-4) - wheat >gi_536892_dbj_BAA07278_ (D38089) protein H2A [Triticum aestivum] >gi_536896_dbj_BAA07280_ (D38091) protein H2A [Triticum aestivum]

Seq. No.	387939
Contig ID	7629_3.R1084
5'-most EST	g287245
Method	BLASTX
NCBI GI	g1154954
BLAST score	308
E value	5.0e-28
Match length	90
% identity	72
NCBI Description	(X94693) histone H2A [Triticum aestivum]

Seq. No.	387940
Contig ID	7632_1.R1084
5'-most EST	g2801155
Method	BLASTX
NCBI GI	g4929757
BLAST score	153
E value	1.0e-09
Match length	132
% identity	32
NCBI Description	(AF151902) CGI-144 protein [Homo sapiens]

Seq. No.	387941
Contig ID	7636_1.R1084
5'-most EST	g2312479
Method	BLASTX
NCBI GI	g3953471
BLAST score	795
E value	7.0e-85
Match length	230
% identity	67
NCBI Description	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq. No.	387942
Contig ID	7641_1.R1084
5'-most EST	LIB3432-036-P2-K1-A5
Method	BLASTX
NCBI GI	g6014652
BLAST score	159
E value	2.0e-10
Match length	172
% identity	31
NCBI Description	(AF187961) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]

Seq. No.	387943
Contig ID	7655_1.R1084
5'-most EST	LIB3431-048-P1-K1-C2
Method	BLASTX
NCBI GI	g2583133
BLAST score	254
E value	1.0e-21
Match length	131
% identity	40
NCBI Description	(AC002387) unknown protein [Arabidopsis thaliana]

Seq. No.	387944

Contig ID	7664_1.R1084
5'-most EST	LIB3431-048-P1-K1-D2
Method	BLASTX
NCBI GI	g6014904
BLAST score	180
E value	5.0e-13
Match length	62
% identity	56
NCBI Description	DAG PROTEIN, CHLOROPLAST PRECURSOR >gi_1200205_emb_CAA65064_ (X95753) DAG [Antirrhinum majus]

Seq. No.	387945
Contig ID	7668_1.R1084
5'-most EST	LIB3431-048-P1-K1-D6
Method	BLASTX
NCBI GI	g5734713
BLAST score	477
E value	9.0e-48
Match length	155
% identity	41
NCBI Description	(AC008075) Is a member of PF_01169 Uncharacterized (transmembrane domain) protein family. [Arabidopsis thaliana]

Seq. No.	387946
Contig ID	7691_1.R1084
5'-most EST	uC-osflcyp169g05b1
Method	BLASTX
NCBI GI	g4938503
BLAST score	222
E value	8.0e-27
Match length	91
% identity	39
NCBI Description	(AL078465) hnRNP-like protein [Arabidopsis thaliana]

Seq. No.	387947
Contig ID	7695_1.R1084
5'-most EST	uC-osflcyp037e09b1
Method	BLASTX
NCBI GI	g2827709
BLAST score	615
E value	1.0e-63
Match length	348
% identity	41
NCBI Description	(AL021684) predicted protein [Arabidopsis thaliana]

Seq. No.	387948
Contig ID	7709_1.R1084
5'-most EST	g701407

Seq. No.	387949
Contig ID	7710_1.R1084
5'-most EST	uC-osroM202024b07b1
Method	BLASTX
NCBI GI	g231587
BLAST score	2418
E value	0.0e+00

Match length	539
% identity	90
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_283001_pir__S25304 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - rice >gi_218147_dbj_BAA01372_ (D10491) mitochondrial F1-ATPase [Oryza sativa]

Seq. No.	387950
Contig ID	7710_2.R1084
5'-most EST	LIB3477-005-P1-K1-D11
Method	BLASTX
NCBI GI	g114420
BLAST score	462
E value	6.0e-46
Match length	109
% identity	86
NCBI Description	ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR >gi_100882_pir__S11491 H+-transporting ATP synthase (EC 3.6.1.34) beta chain, mitochondrial - maize >gi_22173_emb_CAA38140_ (X54233) ATPase F1 subunit protein [Zea mays] >gi_897618 (M36087) F-1-ATPase subunit 2 [Zea mays]

Seq. No.	387951
Contig ID	7713_1.R1084
5'-most EST	uC-osflm202107e11b1

Seq. No.	387952
Contig ID	7727_1.R1084
5'-most EST	LIB3474-002-P1-K1-G8

Seq. No.	387953
Contig ID	7734_1.R1084
5'-most EST	LIB3432-019-P1-K1-B12

Seq. No.	387954
Contig ID	7737_1.R1084
5'-most EST	uC-osf1cyp052h10b1
Method	BLASTX
NCBI GI	g4589965
BLAST score	529
E value	5.0e-54
Match length	137
% identity	72
NCBI Description	(AC007169) putative glyoxalase II [Arabidopsis thaliana]

Seq. No.	387955
Contig ID	7738_1.R1084
5'-most EST	LIB3431-049-P1-K1-H9
Method	BLASTX
NCBI GI	g6093671
BLAST score	388
E value	2.0e-37
Match length	122
% identity	61
NCBI Description	CATIONIC PEROXIDASE 1 PRECURSOR >gi_1491776 (M37636)

cationic peroxidase [Arachis hypogaea]

Seq. No.	387956
Contig ID	7739_1.R1084
5'-most EST	uC-osflcyp009a05b1

Seq. No.	387957
Contig ID	7739_2.R1084
5'-most EST	g2798346

Seq. No.	387958
Contig ID	7741_1.R1084
5'-most EST	LIB3431-042-P1-K1-E10
Method	BLASTX
NCBI GI	g4886280
BLAST score	237
E value	1.0e-19
Match length	115
% identity	44
NCBI Description	(AL050300) putative protein [Arabidopsis thaliana]

Seq. No.	387959
Contig ID	7743_1.R1084
5'-most EST	LIB3431-050-P1-K1-A3

Seq. No.	387960
Contig ID	7747_1.R1084
5'-most EST	uC-osflcyp112e06b1
Method	BLASTX
NCBI GI	g1170507
BLAST score	847
E value	6.0e-91
Match length	171
% identity	94
NCBI Description	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) >gi_100276_pir__S22579 translation initiation factor eIF-4A - curled-leaved tobacco >gi_19699_emb_CAA43514_ (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]

Seq. No.	387961
Contig ID	7748_1.R1084
5'-most EST	LIB3431-050-P1-K1-A8
Method	BLASTX
NCBI GI	g3080391
BLAST score	526
E value	2.0e-53
Match length	125
% identity	76
NCBI Description	(AL022603) putative protein [Arabidopsis thaliana]

Seq. No.	387962
Contig ID	7751_1.R1084
5'-most EST	uC-osflcyp032a12b1
Method	BLASTX
NCBI GI	g4894628
BLAST score	155

E value	4.0e-10
Match length	103
% identity	30
NCBI Description	(AF124369) NT3 [Nicotiana tabacum]

Seq. No.	387963
Contig ID	7753_1.R1084
5'-most EST	LIB3433-040-P1-K1-B2
Method	BLASTX
NCBI GI	g3367596
BLAST score	374
E value	5.0e-53
Match length	156
% identity	71
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	387964
Contig ID	7753_2.R1084
5'-most EST	LIB3479-011-Q6-K1-G3
Method	BLASTX
NCBI GI	g3367596
BLAST score	737
E value	3.0e-78
Match length	177
% identity	76
NCBI Description	(AL031135) putative protein [Arabidopsis thaliana]

Seq. No.	387965
Contig ID	7754_1.R1084
5'-most EST	uC-osflcyp174e09b1
Method	BLASTX
NCBI GI	g2826884
BLAST score	175
E value	3.0e-12
Match length	147
% identity	39
NCBI Description	(AJ223635) transcription factor IIA large subunit [Arabidopsis thaliana]

Seq. No.	387966
Contig ID	7758_1.R1084
5'-most EST	uC-osflcyp162f04b1

Seq. No.	387967
Contig ID	7764_1.R1084
5'-most EST	LIB3431-050-P1-K1-C3

Seq. No.	387968
Contig ID	7786_1.R1084
5'-most EST	LIB3434-004-P1-K1-G5
Method	BLASTX
NCBI GI	g3915186
BLAST score	252
E value	7.0e-27
Match length	147
% identity	45
NCBI Description	UBIQUITIN-CONJUGATING ENZYME E2-21 KD (UBIQUITIN-PROTEIN

	LIGASE) (UBIQUITIN CARRIER PROTEIN) (PEROXIN-4) >gi_3128447 (AF061604) ubiquitin-conjugating enzyme homolog peroxin 4 [Pichia angusta]
Seq. No.	387969
Contig ID	7792_1.R1084
5'-most EST	LIB3431-050-P1-K1-F11
Method	BLASTX
NCBI GI	g4572679
BLAST score	160
E value	2.0e-10
Match length	57
% identity	54
NCBI Description	(AC006954) RSZp22 splicing factor; contains RNA recognition motif [Arabidopsis thaliana]
Seq. No.	387970
Contig ID	7804_1.R1084
5'-most EST	g3769031
Seq. No.	387971
Contig ID	7810_1.R1084
5'-most EST	uC-osrocyp027h04b1
Method	BLASTX
NCBI GI	g1944407
BLAST score	479
E value	1.0e-47
Match length	169
% identity	57
NCBI Description	(D86988) KIAA0221 [Homo sapiens]
Seq. No.	387972
Contig ID	7812_1.R1084
5'-most EST	LIB3431-050-P1-K1-H10
Seq. No.	387973
Contig ID	7818_1.R1084
5'-most EST	LIB3433-036-P1-K1-D6
Method	BLASTX
NCBI GI	g3123264
BLAST score	573
E value	7.0e-59
Match length	136
% identity	82
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279.1_ (Z97337) ribosomal protein [Arabidopsis thaliana]
Seq. No.	387974
Contig ID	7818_2.R1084
5'-most EST	LIB3431-051-P1-K1-A10
Method	BLASTX
NCBI GI	g3123264
BLAST score	441
E value	2.0e-43
Match length	131
% identity	69
NCBI Description	60S RIBOSOMAL PROTEIN L27 >gi_2244857_emb_CAB10279.1_

(Z97337) ribosomal protein [Arabidopsis thaliana]

Seq. No.	387975
Contig ID	7823_1.R1084
5'-most EST	uC-osf1M202089f02b1
Method	BLASTX
NCBI GI	g5103807
BLAST score	584
E value	2.0e-60
Match length	157
% identity	67
NCBI Description	(AC007591) Contains similarity to gb_AF014403 type-2 phosphatidic acid phosphatase alpha-2 (PAP2_a2) from Homo sapiens. ESTs gb_T88254 and gb_AA394650 come from this gene. [Arabidopsis thaliana]

Seq. No.	387976
Contig ID	7825_1.R1084
5'-most EST	LIB3431-058-P1-K1-F5

Seq. No.	387977
Contig ID	7844_1.R1084
5'-most EST	LIB3431-051-P1-K1-C6
Method	BLASTX
NCBI GI	g3881873
BLAST score	452
E value	1.0e-44
Match length	218
% identity	45
NCBI Description	(Z83246) predicted using Genefinder; cDNA EST EMBL:M79771 comes from this gene [Caenorhabditis elegans]

Seq. No.	387978
Contig ID	7847_1.R1084
5'-most EST	g3760854

Seq. No.	387979
Contig ID	7847_2.R1084
5'-most EST	LIB3431-051-P1-K1-D1

Seq. No.	387980
Contig ID	7866_1.R1084
5'-most EST	LIB3432-005-P1-K1-B6

Seq. No.	387981
Contig ID	7887_1.R1084
5'-most EST	LIB3431-052-P1-K1-E12

Seq. No.	387982
Contig ID	7895_1.R1084
5'-most EST	LIB3431-051-P1-K1-H8
Method	BLASTX
NCBI GI	g730241
BLAST score	460
E value	9.0e-57
Match length	273
% identity	45

NCBI Description	DOLICHYL-DIPHOSPHOOLIGOSACCHARIDE--PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) >gi_473947_dbj_BAA06126_ (D29643) similar to Canis oligosaccharyltransferase 48 kDa subunit (M98392). [Homo sapiens]
Seq. No.	387983
Contig ID	7900_1.R1084
5'-most EST	LIB3431-052-P1-K1-A3
Method	BLASTX
NCBI GI	g4757718
BLAST score	276
E value	4.0e-24
Match length	162
% identity	37
NCBI Description	actin-like 6 >gi_4001803 (AF041474) BAF53a [Homo sapiens] >gi_4218064_dbj_BAA74577_ (AB015907) actin-related protein [Homo sapiens]
Seq. No.	387984
Contig ID	7903_1.R1084
5'-most EST	uC-osflcyp154a11b1
Method	BLASTX
NCBI GI	g2911362
BLAST score	622
E value	2.0e-77
Match length	306
% identity	54
NCBI Description	(AF041045) NADPH HC toxin reductase [Zea mays]
Seq. No.	387985
Contig ID	7905_1.R1084
5'-most EST	LIB3432-005-P1-K1-F11
Seq. No.	387986
Contig ID	7916_1.R1084
5'-most EST	uC-osflcyp052f03b1
Method	BLASTX
NCBI GI	g6041792
BLAST score	898
E value	6.0e-97
Match length	257
% identity	67
NCBI Description	(AC009755) unknown protein [Arabidopsis thaliana]
Seq. No.	387987
Contig ID	7928_1.R1084
5'-most EST	LIB3434-065-P1-K1-D2
Method	BLASTX
NCBI GI	g2947060
BLAST score	945
E value	1.0e-102
Match length	272
% identity	66
NCBI Description	(AC002521) putative membrane protein [Arabidopsis thaliana]

Seq. No.	387988
Contig ID	7946_1.R1084
5'-most EST	LIB3431-052-P1-K1-G12

Seq. No.	387989
Contig ID	7965_1.R1084
5'-most EST	g702121
Method	BLASTX
NCBI GI	g6006848
BLAST score	1212
E value	1.0e-133
Match length	281
% identity	81
NCBI Description	(AC009540) unknown protein, 5' partial [Arabidopsis thaliana]

Seq. No.	387990
Contig ID	7975_1.R1084
5'-most EST	LIB3432-047-P2-K11-D8
Method	BLASTX
NCBI GI	g6093977
BLAST score	114
E value	4.0e-14
Match length	61
% identity	76
NCBI Description	CHLOROPLAST 50S RIBOSOMAL PROTEIN L11 >gi_3602936_gb_AAC35597_ (AF041468) ribosomal protein L11 [Guillardia theta]

Seq. No.	387991
Contig ID	7986_1.R1084
5'-most EST	LIB3431-053-P1-K1-C7

Seq. No.	387992
Contig ID	7995_1.R1084
5'-most EST	uC-osf1cyp033b12b1
Method	BLASTX
NCBI GI	g5042413
BLAST score	436
E value	8.0e-43
Match length	201
% identity	44
NCBI Description	(AC006193) Hypothetical Protein [Arabidopsis thaliana]

Seq. No.	387993
Contig ID	8008_1.R1084
5'-most EST	LIB3431-053-P1-K1-F4

Seq. No.	387994
Contig ID	8013_1.R1084
5'-most EST	LIB3432-035-P2-K1-A4
Method	BLASTX
NCBI GI	g3047064
BLAST score	406
E value	3.0e-39
Match length	143
% identity	57

NCBI Description	(AF058825) contains similarity to peptidyl-prolyl cis-trans isomerase (Pfam: pro_isomerase.hmm, score: 23.86 and 28.41 [Arabidopsis thaliana]

Seq. No.	387995
Contig ID	8019_1.R1084
5'-most EST	LIB3431-053-P1-K1-G7
Method	BLASTX
NCBI GI	g3021270
BLAST score	750
E value	8.0e-84
Match length	247
% identity	62
NCBI Description	(AL022347) serine/threonine kinase-like protein [Arabidopsis thaliana]

Seq. No.	387996
Contig ID	8022_1.R1084
5'-most EST	g4714659
Method	BLASTN
NCBI GI	g5091496
BLAST score	81
E value	3.0e-37
Match length	169
% identity	48
NCBI Description	Oryza sativa genomic DNA, chromosome 6, clone P0680A03, complete sequence

Seq. No.	387997
Contig ID	8025_1.R1084
5'-most EST	LIB3431-053-P1-K1-H3
Method	BLASTX
NCBI GI	g4582459
BLAST score	384
E value	8.0e-37
Match length	152
% identity	54
NCBI Description	(AC007071) putative RanBP7/importin protein [Arabidopsis thaliana]

Seq. No.	387998
Contig ID	8038_1.R1084
5'-most EST	g3761223

Seq. No.	387999
Contig ID	8043_1.R1084
5'-most EST	g2310879
Method	BLASTX
NCBI GI	g461812
BLAST score	901
E value	4.0e-97
Match length	337
% identity	51
NCBI Description	CYTOCHROME P450 72A1 (CYPLXXII) (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) >gi_167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] >gi_445604_prf__1909351A cytochrome P450 [Catharanthus

roseus]

Seq. No.	388000
Contig ID	8050_1.R1084
5'-most EST	LIB3431-054-P1-K1-C10
Method	BLASTX
NCBI GI	g1653935
BLAST score	182
E value	4.0e-13
Match length	64
% identity	56
NCBI Description	(D90917) hypothetical protein [Synechocystis sp.]

Seq. No.	388001
Contig ID	8062_1.R1084
5'-most EST	LIB3431-054-P1-K1-D10
Method	BLASTX
NCBI GI	g4678208
BLAST score	474
E value	1.0e-47
Match length	132
% identity	70
NCBI Description	(AC007134) putative sugar transporter [Arabidopsis thaliana]

Seq. No.	388002
Contig ID	8063_1.R1084
5'-most EST	LIB3431-054-P1-K1-D11

Seq. No.	388003
Contig ID	8072_1.R1084
5'-most EST	g428787
Method	BLASTX
NCBI GI	g3776005
BLAST score	1487
E value	1.0e-166
Match length	316
% identity	91
NCBI Description	(AJ010466) RNA helicase [Arabidopsis thaliana]

Seq. No.	388004
Contig ID	8073_1.R1084
5'-most EST	g5667493

Seq. No.	388005
Contig ID	8094_1.R1084
5'-most EST	LIB3432-011-P1-K1-C5
Method	BLASTX
NCBI GI	g3420054
BLAST score	151
E value	2.0e-09
Match length	134
% identity	31
NCBI Description	(AC004680) unknown protein [Arabidopsis thaliana]

Seq. No.	388006
Contig ID	8115_1.R1084

09604465 - 100400

5'-most EST	uC-osf1M202043a11b1
Method	BLASTX
NCBI GI	g2827536
BLAST score	176
E value	2.0e-12
Match length	79
% identity	39
NCBI Description	(AL021633) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388007
Contig ID	8117_1.R1084
5'-most EST	LIB3432-008-P1-K1-H1
Method	BLASTX
NCBI GI	g5734634
BLAST score	365
E value	2.0e-34
Match length	134
% identity	51
NCBI Description	(AP000391) Similar to putative lipase (AC006232) [Oryza sativa]

Seq. No.	388008
Contig ID	8119_1.R1084
5'-most EST	g2427718
Method	BLASTX
NCBI GI	g6041819
BLAST score	313
E value	3.0e-28
Match length	186
% identity	39
NCBI Description	(AC009918) unknown protein [Arabidopsis thaliana]

Seq. No.	388009
Contig ID	8132_1.R1084
5'-most EST	LIB3431-056-P1-K1-B9
Method	BLASTX
NCBI GI	g2264373
BLAST score	357
E value	5.0e-34
Match length	103
% identity	63
NCBI Description	(AC002354) putative NAM/no apical meristem protein [Arabidopsis thaliana]

Seq. No.	388010
Contig ID	8144_2.R1084
5'-most EST	LIB3432-032-P2-K1-E1
Method	BLASTX
NCBI GI	g2688828
BLAST score	352
E value	4.0e-33
Match length	144
% identity	47
NCBI Description	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]

Seq. No.	388011

Contig ID	8157_1.R1084
5'-most EST	LIB3434-017-P1-K1-F4
Method	BLASTX
NCBI GI	g1458245
BLAST score	402
E value	9.0e-39
Match length	253
% identity	39
NCBI Description	(U64834) coded for by C. elegans cDNA cm17a1; coded for by C. elegans cDNA cm7g1; coded for by C. elegans cDNA CEMSE26F; similar to methyltransferases [Caenorhabditis elegans]

Seq. No.	388012
Contig ID	8163_1.R1084
5'-most EST	g2311667
Method	BLASTX
NCBI GI	g5733872
BLAST score	299
E value	8.0e-27
Match length	119
% identity	59
NCBI Description	(AC007932) Similar to gi_4982048 ribosomal protein L18 from Thermotoga maritima genome gb_AE001798. ESTs gb_Z35613, gb_T75951, gb_T22182, gb_T45962, gb_H76281 and gb_AI100025 come from this gene. [Arabidopsis thaliana]

Seq. No.	388013
Contig ID	8172_1.R1084
5'-most EST	g2311115
Method	BLASTX
NCBI GI	g5689238
BLAST score	441
E value	8.0e-53
Match length	126
% identity	85
NCBI Description	(AB024292) histidine-containing phosphotransfer protein [Zea mays]

Seq. No.	388014
Contig ID	8182_1.R1084
5'-most EST	g4714950
Method	BLASTN
NCBI GI	g1261857
BLAST score	54
E value	3.0e-21
Match length	54
% identity	100
NCBI Description	Rice CatA gene for catalase, complete cds

Seq. No.	388015
Contig ID	8184_1.R1084
5'-most EST	LIB3431-022-P1-K1-G12
Method	BLASTN
NCBI GI	g2062705
BLAST score	35
E value	5.0e-10

Match length	36
% identity	38
NCBI Description	Human butyrophilin (BTF5) mRNA, complete cds

Seq. No.	388016
Contig ID	8199_1.R1084
5'-most EST	LIB3431-058-P1-K1-A2
Method	BLASTX
NCBI GI	g1514643
BLAST score	346
E value	2.0e-58
Match length	201
% identity	62
NCBI Description	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]

Seq. No.	388017
Contig ID	8209_1.R1084
5'-most EST	uC-osflcyp028b09b1
Method	BLASTX
NCBI GI	g2582381
BLAST score	1318
E value	1.0e-146
Match length	289
% identity	84
NCBI Description	(AF021220) cation-chloride co-transporter [Nicotiana tabacum]

Seq. No.	388018
Contig ID	8228_1.R1084
5'-most EST	LIB3475-010-P1-K1-G1
Method	BLASTX
NCBI GI	g1421730
BLAST score	956
E value	0.0e+00
Match length	452
% identity	90
NCBI Description	(U43082) RF2 [Zea mays]

Seq. No.	388019
Contig ID	8231_1.R1084
5'-most EST	g3763505
Method	BLASTX
NCBI GI	g4587563
BLAST score	271
E value	1.0e-23
Match length	136
% identity	47
NCBI Description	(AC006550) Similar to gb_U51990 pre-mRNA-splicing factor hPrp18 from Homo sapiens. ESTs gb_T46391 and gb_AA721815 come from this gene. [Arabidopsis thaliana]

Seq. No.	388020
Contig ID	8269_1.R1084
5'-most EST	uC-osflcyp121c05b1
Method	BLASTX
NCBI GI	g3135263
BLAST score	527

E value	2.0e-53
Match length	153
% identity	21
NCBI Description	(AC003058) hypothetical protein [Arabidopsis thaliana]

Seq. No.	388021
Contig ID	8275_1.R1084
5'-most EST	uC-osflcyp075a09b1
Method	BLASTX
NCBI GI	g3004565
BLAST score	300
E value	2.0e-36
Match length	181
% identity	49
NCBI Description	(AC003673) putative protein kinase [Arabidopsis thaliana]

Seq. No.	388022
Contig ID	8289_1.R1084
5'-most EST	LIB3431-059-P1-K1-A2
Method	BLASTX
NCBI GI	g1001355
BLAST score	174
E value	2.0e-12
Match length	87
% identity	41
NCBI Description	(D64006) auxin-induced protein [Synechocystis sp.]

Seq. No.	388023
Contig ID	8296_1.R1084
5'-most EST	LIB3431-059-P1-K1-B10
Method	BLASTX
NCBI GI	g2736155
BLAST score	476
E value	1.0e-47
Match length	122
% identity	75
NCBI Description	(AF022082) sulfolipid biosynthesis protein [Arabidopsis thaliana] >gi_3688184_emb_CAA21212_ (AL031804) sulfolipid biosynthesis protein SQD1 [Arabidopsis thaliana]

Seq. No.	388024
Contig ID	8299_1.R1084
5'-most EST	LIB3432-015-P1-K1-H12
Method	BLASTX
NCBI GI	g6041833
BLAST score	219
E value	2.0e-17
Match length	189
% identity	32
NCBI Description	(AC009853) unknown protein [Arabidopsis thaliana]

Seq. No.	388025
Contig ID	8302_1.R1084
5'-most EST	LIB3432-046-P1-K1-D3
Method	BLASTX
NCBI GI	g1881585
BLAST score	203

E value	7.0e-20
Match length	106
% identity	57
NCBI Description	(U72489) remorin [Solanum tuberosum]

Seq. No.	388026
Contig ID	8308_1.R1084
5'-most EST	LIB3474-011-P1-K1-E9
Method	BLASTX
NCBI GI	g2459430
BLAST score	168
E value	1.0e-11
Match length	69
% identity	51
NCBI Description	(AC002332) putative CUC2 protein [Arabidopsis thaliana]

Seq. No.	388027
Contig ID	8312_1.R1084
5'-most EST	LIB3431-059-P1-K1-C5
Method	BLASTX
NCBI GI	g1848214
BLAST score	197
E value	6.0e-15
Match length	49
% identity	73
NCBI Description	(Y11210) uracil phosphoribosyltransferase [Nicotiana tabacum]

Seq. No.	388028
Contig ID	8323_1.R1084
5'-most EST	LIB3433-026-P1-K1-A4

Seq. No.	388029
Contig ID	8324_1.R1084
5'-most EST	LIB3431-059-P1-K1-D7
Method	BLASTX
NCBI GI	g3894170
BLAST score	171
E value	7.0e-12
Match length	41
% identity	78
NCBI Description	(AC005312) putative glutathione s-transferase [Arabidopsis thaliana]

Seq. No.	388030
Contig ID	8327_2.R1084
5'-most EST	LIB3431-063-P1-K1-E11
Method	BLASTX
NCBI GI	g3738329
BLAST score	257
E value	4.0e-22
Match length	65
% identity	75
NCBI Description	(AC005170) unknown protein [Arabidopsis thaliana]

Seq. No.	388031
Contig ID	8340_1.R1084